AIMST UNIVERSITY

In Commemoration of 20 Years of Academic and Research Excellence of AIMST University, The Faculty of Applied Sciences is proudly organizing

IECBBB-2020

INTERNATIONAL E-CONFERENCE ON BIOTECHNOLOGY, BIOINFORMATICS & BIOMEDICINE

Theme: Challenges and opportunities in Biotechnology Bioinformatics and Biomedicine in the Post-COVID Era

ABSTRACT BOOK

Organized by

Faculty of Applied Sciences, AIMST University, Kedah, Malaysia

Date: 24 – 26 AUGUST 2020

Time: 10:00 – 18:00 MYT (GMT+8)

Co-organizers

UNIVERSITI SAINS MALAYSI

MABIC MALAYSIAN BIOTECHNOLOGY INFORMATION CENTRE

FACULTY OF ENVIRONMENTAL MANAGEMENT PRINCE OF SONGKLA UNIVERSITY

MYBIOSA

INTERNATIONAL E-CONFERENCE ON BIOTECHNOLOGY, BIOINFORMATICS & BIOMEDICINE

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AIMST UNIVERSITY

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FORWARD MESSAGE

Hon. Asst. Commissioner (CD) Prof. Dr. Mohd Baidi Bin Bahari
B.Pharm (USM), Pharm. D. (Uni. of Minnesota)
Acting Vice-Chancellor,
AIMST University

Biotechnology and Bioinformatics is truly a multifaceted field that encompasses Medical, Agricultural, and Pharmaceutical Biotechnology. Biotechnology is one of the fast-growing emerging technologies that can sustain humans with three F‟s: Food, Fuel, and Fibers. In addition to sustaining the human population, with genomics research, it also has the key to the blueprint of human life such as stem cell, regenerative medicine, and personalized medicine. I am happy to remark that the Faculty of Applied Sciences, a research-intensive faculty at AIMST University, has been at the forefront of Biotechnology and Bioinformatics. Active academic and research collaboration with international universities such as Leicester University (UK), Deakin University (Australia), University of Copenhagen (Denmark), and Technical University of Denmark (Denmark) is the hallmark of the faculty. I am proud to mention that the Centre of Excellence in Omics-driven Computational Biodiscovery (COMBio) is one of the key initiatives taken by the faculty to further enhance research and development in bioinformatics. At this juncture, I would like to extend my warm welcome to all the participants of the virtual “International E-Conference on Biotechnology, Bioinformatics & Biomedicine 2020 (IECBBB-2020)”. My heartfelt thanks to all the keynote and plenary speakers for joining this conference. I wish you all the very best for the successful research knowledge sharing and deliberations among the participants of (IECBBB-2020)”.

Hon. Asst. Commissioner (CD) Prof. Dr. Mohd Baidi Bin Bahari
B.Pharm (USM), Pharm. D. (Uni. of Minnesota)
Acting Vice-Chancellor,
AIMST University, Kedah Darul Aman, Malaysia

WELCOME MESSAGE

Senior Professor Dr. Manickam Ravichandran
Dean Faculty of Applied Sciences
AIMST University

I would like to welcome all the eminent keynote and plenary speakers, participants from different parts of the world and staff of AIMST University who are participating in the virtual "International E-Conference on Biotechnology, Bioinformatics & Biomedicine 2020 (IECBBB-2020)". The conference is jointly organized by the Faculty of Applied Sciences, AIMST University, Malaysia with Universiti Sains Malaysia (Malaysia), Madurai Kamaraj University (India), Dayananda Sagar University (India), Prince of Songkla University (Thailand), University of Medical Technology, Yangon, (Myanmar), Yogi Vemana University, (India), Malaysian Biotechnology Information Centre (Malaysia), Ahmednagar College (India), Modern College of Arts, Science and Commerce (India) and Malaysia Biotechnology Students' Association (MYBIOSA). I thank all the co-organizers for their support and contribution and welcome all of you for joining this conference. I want to thank the AIMST University management for plenteous support. Most importantly, my heartfelt thanks go to the organizing committee of IECBBB-2020 for putting together the program very well and organizing the virtual conference during this COVID 19 era. I hope that this conference will provide a good platform for all the researchers to share the research experiences and novel research findings, discuss the challenges encountered and solutions adopted, and have opportunities to establish productive new academic and research collaborations from different parts of the globe. I wish all the participants to have a productive conference and discussion. Good Luck.

Thank you

Best Regards

Senior Professor Dr. Manickam Ravichandran
Dean Faculty of Applied Sciences
AIMST University

PREFACE

Dr. Suresh V. Chinni
Organizing Chairman
International E-Conference on Biotechnology,
Bioinformatics & Biomedicine 2020 (IECBBB-2020)

It gives me immense pleasure to welcome you all to this virtual "International E-Conference on Biotechnology, Bioinformatics & Biomedicine 2020 (IECBBB-2020)". The growth of the biotechnology and bioinformatics industries in recent years is unparalleled and coupled with advancements in molecular modeling, disease characterization, pharmaceutical discovery, clinical healthcare, forensics, and agriculture fundamentally impact economic and social issues worldwide.

The conference is organized by the Faculty of Applied Sciences, AIMST University, Malaysia in collaboration with Universiti Sains Malaysia (Malaysia), Madurai Kamaraj University (India), Dayananda Sagar University (India), Prince of Songkla University (Thailand), University of Medical Technology, Yangon, (Myanmar), Yogi Vemana University, (India), Malaysian Biotechnology Information Centre (Malaysia), Ahmednagar College (India), Modern College of Arts, Science and Commerce (India) and Malaysia Biotechnology Students' Association (MYBIOSA). The conference would be held online (Zoom) from 24th- 26th August 2020. IECBBB-2020 intends to provide a platform for scientists, researchers, and students to exchange knowledge, challenges, recent advances, and future perspectives in the multidisciplinary areas of Biotechnology, Bioinformatics, and Biomedicine.

The COVID-19 pandemic has dramatically affected the health, economy, and social mobility of people in countries around the world. Biotechnology, Bioinformatics and Biomedicine research is an essential activity to advance the development of key interventions to fight off this pandemic, including vaccine development and drug discovery in most of the academic research groups around the world.

The scientific programme of the conference is rich and wide-ranging with 9 keynote talks, 10 invited plenary talks, 42 oral presentations, about 27 E-poster presentations and around 1300+ registered participants from (33 different countries) all over the world.

The hallmarks of this year IECBBB 2020 includes keynote addresses by the eminent speakers namely Dr. Harcharan Singh, Senior Vice President, Technology Solutions, Bioeconomy Corporation, Malaysia will be delivering his talk on "The Malaysian Biotechnology Landscape and Opportunities", Dr. Gowrisankar Rajam, Associate Principle Scientist at MERCK, USA will be delivering his talk on "Novel Vaccine Approaches to Address Unique

Challenges", Dr. Ch'ng Ewe Seng, Advanced Medical and Dental Institute USM, Malaysia is delivering on the "Challenges in Laboratory diagnosis of COVID-19", Senior Prof Dr. Ravichandran, Dean, Faculty of Applied Sciences, AIMST University, Malaysia, will be delivering his talk on "Cold chain free Cholera vaccine (VCUSM14P): A potential live oral bacterial vectored vaccine platform for emerging diseases", Prof. Christopher M. AUSTIN, Deakin University, Australia is delivering his talk on "Metagenomics for Environmental Sciences". Dr. S. Sridhar, Senior Principal Scientist, CSIR IGIB, New Delhi, India, will be delivering his talk on "Personal Genomes to Precision Medicine- Implications for Rare Genetic Diseases". Dr. Mahaletchumy Arujanan, Executive Director, MABIC, Malaysia will be delivering her talk on "Science Communication for Post-Truth Era" Dr. G. Kumaresan Head, Department of Genetics, Madurai Kamaraj University, Tamilnadu, India, will be delivering his talk on "Understanding the Genome Biology and New Therapeutic Strategies for Cancers with Genomic Methods" and Assoc. Prof. Dr. Larry Croft, Deakin University, Australia will be delivering his talk on "How will biotechnology change our future".

All 10 plenary talks are comprehensive and highlight the latest trends & challenges in various fields of biotechnology, bioinformatics, and biomedicine. This book contains abstracts of all invited keynote and plenary speakers, as well as the abstracts of all oral and poster sessions. I wish to thank and acknowledge the support of all co-organizers, patrons, and AIMST University. Nevertheless, the successful organization of this conference is because of the untiring efforts of dedicated and committed members of the organizing team as well as student volunteers who deserve due appreciation and mention.

Dr. Suresh V. Chinni
Organizing Chairman
International E-Conference on Biotechnology, Bioinformatics & Biomedicine 2020 (IECBBB-2020)

AIMST UNIVERSITY

IECBBB-2020

INTERNATIONAL E-CONFERENCE ON BIOTECHNOLOGY, BIOINFORMATICS & BIOMEDICINE

Theme: Challenges and opportunities in Biotechnology, Bioinformatics and Biomedicine in the Post-COVID Era
Date: 24 – 26 August 2020

PROGRAMME

DAY 1: 24 AUGUST 2020 (MONDAY) **SESSION 1**	
OPENING CEREMONY	
9:30 – 9:35 am	Welcome Address by **Assoc. Prof. Dr.Venkata Suresh Chinni**, Conference Chairman
9:35 – 9:45 am	Opening Remarks by **Prof. Dr. Mohd Baidi Bin Bahari,** Acting Vice-Chancellor, AIMST University • **Launching of IECBBB 2020 Abstract book**
CONFERENCE TECHNICAL SESSION	
Chairperson: Senior Prof Dr. M. Ravichandran **Co-chairperson:** Senior Assoc. Prof. Dr. Gokul Shankar	
9:45 – 10:30 am	**KEYNOTE SPEECH - 1** **Dr. Harcharan Singh**, Senior Vice President, Bioeconomy Corporation, Malaysia **Title:** The Malaysian Biotechnology Landscape & Opportunities
10:30 – 10:45 am	Coffee break: Technical talk
10:45 – 11:30 am	**KEYNOTE SPEECH - 2** **Dr. Gowrisankar Rajam,** Assoc. Principal Scientist, Merck, USA, Ex Lab Lead at CDC, USA **Title:** Novel Vaccine Approaches to Address Unique Challenges
11:30 – 12:00 pm	**PLENARY SPEECH 1** **Dr. Alexander Ludwig** School of Biol. Sciences, Nanyang Technological University, Singapore **Title:** Dissecting the epithelial polarity network using proximity proteomics and electron microscopy imaging

ORAL PRESENTATION **SESSION A** **Panel of Evaluators** **Chair Person:** Senior Prof Dr. M. Ravichandran **Co-chairperson:** Senior Assoc. Prof. Dr. Gokul Shankar	
12:00 – 12:10 pm	*Oral Presentation 1* O-1: Ms. Sumalatha Rani Talapati Title: Binding kinetics and crystallographic studies on the interaction of cyclin dependent kinase 2 with a selective and potent inhibitor NU6140
12:10 – 12:20 pm	*Oral Presentation 2* O-2: Mr. Muhammad Sulaiman Rahama Title: Therapeutic Potentials Of *Mangifera indica* Extracts
12:20 – 12:30 pm	*Oral Presentation 3* O-3: Ms. Norhidayah Rosman Title: Limit of detection of a prototype PCR based detection kit for Familial hypercholesterolaemia variants in Malaysia
12:30 – 12:40 pm	*Oral Presentation 4* O-4: Ms. Ng Yee Ling Title: Genetic diversity *Plasmodium knowlesi* apical membrane antigen-1 (PkAMA-1) and *Plasmodium knowlesi* thrombospondin-related apical merozoite protein (PkTRAMP)
12:40 – 12:50 pm	*Oral Presentation 5* O-5: Mr. Tan Hong Jie Title: Effect of Maternal Epigallocatechin Gallate on Blood Pressure and Pregnancy Outcomes in Spontaneously Hypertensive Rats
12:50 – 1:00 pm	*Oral Presentation 6* O-6: Ms. Anna Andrew Title: Expression of Chikungunya virus E2 protein for the development of a rapid diagnostic test
01:00 – 1.20 pm	Q&A Session
Lunch Break	
SESSION 2	
Chair Person: Prof Tang Thean Hock **Co-chairperson:** Assoc. Prof. Dr.Venkata Suresh Chinni	
2:00 - 2:45 pm	**KEYNOTE SPEECH - 3** **Dr.** **Ch'ng Ewe Seng,** Advanced Medical and Dental Institute USM, Malaysia **Title:** Challenges in Laboratory diagnosis of COVID-19
3:00 - 3:30 pm	**PLENARY SPEECH - 2** **Dr. Tan Ju Lin,** NGS, Scientist, GeneSEQ Sdn Bhd, Malaysia **Title:** "Storytelling in Science - Does it matter?"

3:30 - 4:00 pm	**PLENARY SPEECH - 3** **Dr Mohammad Farris Iman Leong Bin Abdullah,** AMDI, USM, Malaysia **Title:** The mind of our heroes and the COVID-19 pandemic: Does COVID-19 affect the mental health of the healthcare workers at the time when we need them most?
4:00 - 5:00 pm	**E-Poster Session I** **Panel members:** **Chairperson:** Dr. Annie Jayachristy **Co-Chairperson:** Dr. Heera Rajandas
Poster Presentation 1 P-1: Ms. Aqila Akmal binti Mohammad Kamal Title: The Effect of Bisphenol A Exposure Below No-Observed-Adverse-Effect-Level (NOAEL) on Uterus of Adult Female BALB/c	
Poster Presentation 2 P-2: Mr. Rocky Vester anak Richmond Title: Characterisation of Artovastatin Liquid Crystalline Nanoparticle as Drug Delivery Vehicle in HepG2 Cells	
Poster Presentation 3 P-3: Ms. Lalitha Devi A/P Rajasegaran Title: Anticancer Effects of Combined Retinoic Acid and Ginger Extract on HeLa Cervical Cancer Cells	
Poster Presentation 4 P-4: Ms. Ainnie Shaherah Title: Growth Performance of Terung Asam in Different Growing Media	
Poster Presentation 5 P-5: Mr. Cheah Hong Leong Title: Small RNA Profiling in *Mycobacterium tuberculosis*	
Poster Presentation 6 P-6: Ms. Teh Hui Wen Title: SNP analysis of Malaysian multidrug-resistance tuberculosis(MDR-TB)	
Poster Presentation 7 P-7: Dr. Sabitha R Title: Promising Tribal Herbs with Hypoglycemic Properties	
Poster Presentation 8 P-8: Ms. Safaa Mahmoud Naes Title: ENT2 gene expression in the different stages of colorectal cancer	
Poster Presentation 9 P-9: Mr. Shifath Bin Syed Title: Antibiograms of Multidrug-resistant *Acinetobacter baumannii* Isolated from Specimens at Kushtia Medical College Hospital	
Poster Presentation 10 P-10: Ms. Raja Nur Firzanah Syaza Binti Raja Sharin Title: Antiproliferative Effect of Lapatinib, An ErbB1/ErbB2 Tyrosine Kinase Inhibitor, on Caco-2 Human Colorectal Cancer Cell Line	
Poster Presentation 11 P-11: Ms. Lim Joejia Title: Process Validation of Cholera Vaccine Formulation	

Poster Presentation 12 P-12: Ms. Kishonthani Krusnamurty Title: Identification and Characterization of Novel non-protein coding RNAs (npcRNAs) associated with Global Transcriptional Regulator, Hfq in Pathogenic Bacteria *Salmonella typhi*	
Poster Presentation 13 P-13: Ms. Richa Prakash Title: Resistome of clinical *Klebsiella pneumoniae* isolates shows the predominance of Ctxm, Oxa, Shv gene variants encoding beta-lactamase & aac(6')-lb encoding bifunctional	
Poster Presentation 14 P-14: Mr. Kartik M Title: Dissecting Complete Genome of *Klebsiella pneumoniae* uncovers the abundant repertoire of antibiotic resistance genes – a GLOBAL snapshot	
ORAL PRESENTATION **SESSION B** **Panel of Evaluators** **Chair Person:** Snr. Assoc. Prof. Dr. Neeraj Kumar Fuloria **Co-chairperson:** Prof. Dr. K. Marimuthu	
5:00 – 5:10 pm	*Oral presentation 7* O-7: Ms. Chidhambara Priya Dharshini K Title: Agricultural Biotechnology
5:10 – 5:20 pm	*Oral presentation 8* O-8: Dr. Senthilkumar Rajagopal Title: GPCR signalling in Inflamation
5:20 – 5:30 pm	*Oral presentation 9* O-9: Dr Prasanna Srinivas R Title: Study of endophytic fungi and their metabolites from the medicinal plant *Withania somnifera*
5:30 – 5:40 pm	*Oral Presentation 10* O-10: Dr. G V Swarnalatha Title: Microalgal Biofuel Production
5:40 – 5:50 pm	*Oral Presentation 11* O-11: Mr Darpan Raghav Title: Curcumin Inhibits the Centrosome Separation in Mammalian Cancer Cells by Perturbing the Functions of Mitotic Kinesin Eg5
5:50 – 6:00 pm	*Oral Presentation 12* O-12: Ms.Nurul Arneida Husin Title: Transcriptome Analysis of Young, Mature and Ripening Stages of Local Durian D24 (*Durio Zibethinus* Murr.) Fruit Pulp Tissues
6:00 – 6:10 pm	*Oral presentation 13* O-13: Dr. Venmathi Maran Balu Alagar Title: Antiparasitic Potential of Medicinal Plant against Zeylanicobdella arugamensis (Hirudinea) and its Chemical Profiling
6:10 – 6:20 pm	*Oral Presentation 14* O-14: Ms. S. Abirami Title: A Molecular Study Delineating the Role of Atorvastatin on Breast Cancer Bone Metastasis Targeting Osteoclastogenic Factors
6:20 – 6:30 pm	*Oral Presentation 15* O-15: Dr. Purabi mazumdar Title: LED Farming of Pennywort : To Keep the Food Supply Chain Thriving during the Covid-19 Pandemic

6:30 – 6:40 pm	*Oral Presentation 16* O-16: Ms. Vinishaa A/P S. Ragu Title: Development of Species-Specific Multiplex PCR to Detect Possible Adulterant DNA in Raw Food Samples
6:40 - 6.50 pm	*Oral Presentation 42* O-42: Mr. Sattam Obeidat Title: O42 Systematic Identification and Characterization of Ae. aegypti Long Non--Coding RNAs
6:50 - 7.00 pm	Q&A Session
End of Day I	

DAY 2: 25 AUGUST 2020 (TUESDAY) **SESSION 3**	
Chair Person: Snr. Assoc. Prof. Dr. Neeraj Kumar Fuloria **Co-chairperson:** Dr. Annie Jayachristy	
9:30 - 10:15 am	**KEYNOTE SPEECH - 4** **Senior Prof Dr. Ravichandran,** Dean, Faculty of Applied Sciences, AIMST University, Malaysia **Title:** Cold chain free Cholera vaccine (VCUSM14P): A potential live oral bacterial vectored vaccine platform for emerging diseases
10:15 – 10:30 am	**Coffee break**
10:30 - 11:15 am	**KEYNOTE SPEECH - 5** **Prof. Christopher M. AUSTIN,** Deakin University, Victoria, Australia. **Title:** Metagenomics for Environmental Sciences
11:15 - 11:45 am	**PLENARY SPEECH - 4** **Dr. Fong Cheng Pan,** Weill Cornell Medicine, New York, USA **Title:** Human embryonic stem cell-derived colon organoids as a platform to model colorectal cancer and COVID-19
11:45 - 12:15 am	**PLENARY SPEECH - 5** **Dr. J. Rajendhran,** Madurai Kamaraj University, Tamilnadu, India **Title:** Prospects and Applications of Metagenomics

ORAL PRESENTATION **SESSION C** **Panel of Evaluators** Chairperson: Dr. Annie Jayachristy Co-chairperson: Snr. Assoc. Prof. Dr. Neeraj Kumar Fuloria	
12:15 - 12:25 pm	*Oral presentation 17* O-17: Mr. Aisamuddin Ardi Zainal Abidin Title: Stability of transgene in *Nannochloropsis sp*.: Potential vaccine delivery system to fish against vibriosis disease
12:25 - 12:35 pm	*Oral presentation 18* O-18: Ms. Bharatee Pandurang Chaudhari Title: A Validated UPLC Method for Simultaneous Estimation of Diacerein and Aceclofenac in Bulk and Pharmaceutical Formulation
12:35 - 12:45 pm	*Oral presentation 19* O-19: Ms. Fatma Diyana Bt Mohd Bukhari Title: Binding Activity of *Plasmodium knowlesi* Duffy Binding Protein Alpha Region II Corresponding to High and Low Parasitaemia Isolates
12:45 - 12:55 pm	*Oral presentation 20* O-20: Mr. Lee Phone Youth @ Zen Lee Title: Development of Point-of-Care Loop mediated isothermal amplification lateral flow (LAMP-LF) assay for detection of *Plasmodium species*
12:55 - 1:05 pm	*Oral presentation 21* O-21: Ms. Maheswari A Title: Anti-Diabetic Effects and Antioxidant Potentials of Green Marine Seaweeds, Collected From Gulf of Mannar
01:05 – 01.15 pm	*Oral presentation 22* O-22: Mr. Navien A/L Tholasi Nadhan Title: *In silico* Selection Of RNA Aptamer Against Progesterone Receptor Using Computational Docking Employing Progesterone Response Elements-Derived RNA
01:15 – 01.30 pm	Q&A Session
Lunch	
SESSION 4	
Chair Person: Assoc. Prof. Dr. Lee Su Yin **Co-chairperson:** Dr. Sivachandran	
2:00 - 2:45 pm	**KEYNOTE SPEECH - 6** **Dr. S. Sridhar** Senior Principal Scientist, CSIR IGIB, New Delhi, **India** **Title:** Personal Genomes to Precision Medicine- Implications for Rare Genetic Diseases
2:45 - 3:15 pm	**PLENARY SPEECH -6** **Prof. K Balakrishnan.** Madurai Kamaraj University, Tamilnadu, India **Title:** "HLA: Molecular Medicine Perspectives".

3:15 - 3:45 pm	**PLENARY SPEECH - 7** **Dr. Susweta Das,** School of Basic and Applied Sciences, Dayananda Sagar University, Bangalore, India **Title:** Epigenetic Modulators – key players in host pathogen cross talk in bacterial infections
3:45 - 4:45 pm	**E-Poster Session II** Panel members: Chairperson: Mr. S. Kurunathan Co-Chairperson: Mr. Jeevandran Sundarasekar
Poster Presentation 15 P-15: Ms. Pershia Title: Evaluation of *in vitro* Antioxidant and Anti -Advanced Glycation End Products Formation (Ages) Effect of Barley, (Hordeum Vulgare) Extract	
Poster Presentation 16 P-16: Ms. Reshma R Title: Extraction of Eco-Friendly Natural Dyes From Indian Almond Leaves Of *Terminalia Catappa* L. And Evaluation of its Anti-Oxidant Properties	
Poster Presentation 17 P-17: Mr. M. Rajesh Kannan Title: ITS based Genus (Clade) level identification of Scleractinian coral endosymbionts in the Palk Bay, southeast coast of India	
Poster Presentation 18 P-18: Mr. Md. Moinuddin Sheam Title: Myco-remediation of Reactive Red Dye by Highly Potential Fungal Strain Isolated from Textile Effluents	
Poster Presentation 19 P-19: Mr. Awosolu Oluwaseun Bunmi Title: Unending transmission of malaria parasite in peri urban community of Ipinsa southwestern Nigeria: Prevalence and risk factors enhancing transmission	
Poster Presentation 20 P-20: Ms. Adina Frank Title: Computational Analysis and Annotation of *Elaeis oleifera* Naringenin-Chalcone Synthase and Palmitoyl Protein Thioesterase	
Poster Presentation 21 P-21: Ms. Avina Frank Title: *In silico* Analysis and Annotation of *Elaeis oleifera* NOI and Metallothionein-like Proteins	
Poster Presentation 22 P-22: Ms. Meroshine Nageswara Rao Title: Styr143 npcRNA gene knockout in *S. typhi* which unregulated completely in biofilm forming pathway.	
Poster Presentation 23 P-23: Ms. Laavanya Rajendhiran Title: Over-expression and purification of *Acinetobacter baumannii* Hfq protein in BL21	
Poster Presentation 24 P-24: Ms. Ang Xin Yee Title: Evaluation of Cold Chain Free Live Attenuated Oral Cholera Vaccine against Enterotoxigenic *Escherichia coli*, as a Dual-Use Vaccine	

Poster Presentation 25 P-25: Ms. Uma Mageswary Mageswaran Title: Preclinical evaluation of prototype cold chain free live attenuated oral cholera vaccine against Enterotoxigenic *Escherichia coli*, as a dual-use vaccine for the diarrhea disease	
Poster Presentation 26 P-26: Dr. Abinaya Subramanian Title: Ficus religiosa in Mitigating Hyperandrogenism in PCOS induced rats: A Phytotherapeutic Approach	
Poster Presentation 27 P-27: Dr. Dasofunjo K Title: Comparative studies on maternal and prenatal exposure to *Piliostigma thonningii* extract on serum lipid profile following acetaminophen induced toxicity on female Wistar rats	
ORAL PRESENTATION **SESSION D** **Panel of Evaluators** Chair Person: Snr. Assoc. Prof. Dr. Subhash J Bhore Co-chairperson: Assoc. Prof. Dr. Sivakumar Pendyala	
5:00 – 5:10 pm	*Oral presentation 23* O-23: Ms. Ravichandran Swetha Title: Screening and identification of cellulose-degrading bacteria from termites: Towards developing a termite and cellulose-based sustainable nutritious solution in resource-limited settings
5:10 – 5:20 pm	*Oral presentation 24* O-24: Ms. Saptadipa Paul Title: Health risk assessment of Macro, Trace-elements and heavy metal in various Indian Antidiabetic Polyherbal formulations
5:20 – 5:30 pm	*Oral presentation 25* O-25: Dr. Selvaraj Mohana Roopan Title: Biosynthesis of copper oxide nanoparticles and its utility in organic synthesis
5:30 – 5:40 pm	*Oral Presentation 26* O-26: Ms. Shoba G Title: Molecular Interaction analysis of Lanosterol derivatives from Laetiporus versisporus as potential inhibitor of BCL-2
5:40 – 5:50 pm	*Oral Presentation 27* O-27: Ms. Tage Yama Title: Isolation and Characterization of Biosurfactant Producing Bacteria from Hot Spring Zone of West Kameng District, Arunachal Pradesh, India.
5:50 – 6:00 pm	*Oral Presentation 28* O-28: Ms. Kirthani Anamalay Title: Evaluation of *in vitro* Antioxidant and Antidiabetic Effect of Water Extract From Oil Palm Fibre
6:00 – 6:10 pm	*Oral presentation 29* O-29: Mr. Mugilan Govindaraju Title: Conversion of Bakery Waste Materials into Compost and Evaluation of Its Physico-Chemical Properties and Phytotoxicity

6:10 – 6:20 pm	*Oral Presentation 30* O-30: Dr. G. Madhumitha Title: Bioactive compound loaded nanoemulsion from edible fruit against insects
6:20 – 6:30 pm	*Oral Presentation 31* O-31: Mr. Irshad P Title: Co-occurrence of mutations in Quinolone Resistance Determining Region (QRDR) observed in global *Escherichia coli* genomes --- alarm for Fluroquinolone therapy in Urinary
6:30 – 6:40 pm	*Oral Presentation 32* O-32: Mr Subham Ghosh Title: Design, Molecular Docking and Drug-likeness Studies of Trioxane Derivatives as Novel Antimalarial Agents
6:40 – 6:50 pm	*Oral Presentation 33* O-33: Mr. Abdulrahman Maina Zubairu Title: Distribution of Available Phosphorus in a Sandy Loam Soil of Nigerian Sudan Savannah
6:50 – 7:00 pm	*Oral Presentation 34* O-34: Ms. Ayesha Siddiqui Title: Phytosynthesis of Silver Nanoparticles Using Plant Extracts of Medicinal Importance
7:00 – 7:10 pm	Q&A Session
End of Day II	

DAY 3: 26 AUGUST 2020 (WEDNESDAY) **SESSION 5**	
Chair Person: Snr. Assoc. Prof. Dr. Subhash J Bhore **Co-chairperson:** Assoc. Prof. Dr. Sivakumar Pendyala	
9:30 – 10:15 am	**KEYNOTE SPEECH – 7** **Dr Mahaletchumy Arujanan** Executive Director, MABIC, Malaysia **Title:** Science Communication for Post-Truth Era
10:15 – 10:30 am	Coffee Break: Technical talk
10:30 – 11:15 am	**KEYNOTE SPEECH – 8** **Dr. G. Kumaresan** Head, Department of Genetics, Madurai Kamaraj University, Tamilnadu, India **Title:** Understanding the Genome Biology and New Therapeutic Strategies for Cancers with Genomic Methods

11:15 – 11:45 am	**PLENARY SPEECH – 8** **Dr Sarah Amirah** (University of Manchester, UK) Title: An Overview of Biotechnological Research & Postgraduate Study in the UK
ORAL PRESENTATION **Panel of Evaluators** Chairperson: Dr. Annie Jayachristy Co-chairperson: Dr. Heera Rajandas	**SESSION E**
12:00 – 12:10 pm	*Oral Presentation 35* O-35: Ms. Dharshini J Title: *In silico* Protein Structure Analysis and Metabolic Pathway Study on Genes Associated with Acute Myeloid Leukemia (AML)
12:10 – 12:20 pm	*Oral Presentation 36* O-36: Dr. Geeta Selvarajah Title: Two Successes out of Three: DNA Barcode Identification of Malaysia Ferns
12:20 – 12:30 pm	*Oral Presentation 37* O-37: Ms. Abirami Sanniraj Title: Knocking-out of potential virulence associated non-protein coding RNA gene (PmiR-137) in *Proteus mirabilis* to understand its role in pathogenesis
12:30 – 12:40 pm	*Oral Presentation 38* O-38: Dr. Adaobi Ekwempu Title: Laboratory Tests ; Clinical Indications during lockdown period
12:40 – 12:50 pm	*Oral Presentation 39* O-39: Ms. Ayisha Aman Title: Bioconversion of agroindustrial waste in to industrially important haloalkaliphilic protease by marine *Bacillus species* under solid state fermentation and formulation of biodetergent
12:50 – 1:00 pm	*Oral Presentation 40* O-40: Ms. Sanyogita Verma Title: Morphological Changes in Planktons, as an Indicators of Seasonal Variations
1:00 – 1:10 pm	*Oral Presentation 41* O-41: Dr. Mowaffaq Adam Ahmed Adam Title: The effect of Aflatoxin B1 and Ochratoxin A on tumor retated genes in MCF7 and MCF10A after the knocdown of cMyc and p53 using siRNA
1:20 – 1.30 pm	Q&A Session
1:30 – 2.00 pm	***LUNCH BREAK***

SESSION 6	
Chair Person: Assoc. Prof. Dr. Gurusamy Prabhakaran **Co-chairperson:** Dr. J. Madhanagopal	
2:00- 2:45 pm	**KEYNOTE SPEECH – 9** **Assoc. Prof. Dr. Larry Croft** Deakin University, Australia **Title:** "How will biotechnology change our future"
3:00- 3:30 pm	**PLENARY SPEECH – 9** **Dr. Enrico Magosso** Universiti Kuala Lumpur, Malaysia **Title:** COVID-19 and Opportunities for Pharmaceutics Researchers
3:30 -4:00 pm	**PLENARY SPEECH – 10** **Dr. Citartan Marimuthu** AMDI, USM, Malaysia **Title:** Whatever you can do, I can do as well: Aptamers as the promising surrogates of antibodies
4:00 -5:00 pm	**Closing Ceremony:** **Announcement of "BEST ORAL & POSTER PRESENTATION AWARD" by : Senior Prof. Dr. M. Ravichandran, Dean, Faculty of Applied Sciences, AIMST University** **Vote of Thanks: Prof. K. Marimuthu**

KEYNOTE SPEAKERS ABSTRACTS

Keynote Talk: 1
The Malaysian Biotechnology Landscape, Opportunities, and Challenges

Dr. Harcharan Singh

Senior Vice President, Bioeconomy Corporation, Malaysia

Abstract: The National Biotechnology Policy (NBP) was launched in 2005 which spells out a comprehensive roadmap for the growth of the Malaysian biotechnology industry focusing on the three core biotechnology sectors (i.e. agricultural, healthcare, and industrial). In addition, to also support key thrust areas critical for the development of bio business such as R&D and technology acquisition; human capital development; financial infrastructure development; legislative and regulatory framework development; strategic positioning; and government commitments. The objective is to create a vibrant biotech ecosystem by attracting local and foreign investment in biotechnology. Biotech companies that establish their manufacturing operations in Malaysia are accorded the BioNexus status which entitles them to targeted facilitation (i.e. introduction to industrial parks, financial institutions, raw material suppliers, university researchers, development programmes, etc.) and application for incentives offered by various government agencies. Over the last 15 years, the Malaysian biotech sector has steadily grown with the approval of over 260 BioNexus status companies throughout the country. The COVID-19 pandemic has dramatically affected the health, economy, and social mobility of people which in turn has affected many businesses. Companies in the biotech sectors have also been impacted by sluggish growth and the need for fresh capital to sustain operations. Countries are now scrambling to develop treatment drugs and a vaccine where various strategies have been deployed. A recent survey conducted on BioNexus companies on how the companies are impacted by COVID-19 indicated there were two key challenges faced. The first challenge is the growing stockpile of end-products that cannot be sold, and the second challenge is the cash flow needed to sustain business operations. These challenges are interrelated, caused by workers unable/scared to travel to work, disruption in the logistics ecosystem, limited raw material supply, and consumers not willing to spend due to the uncertainty created. This presentation will highlight the Malaysian biotech ecosystem, challenges, and opportunities in the biotech industry, and initiatives undertaken to address the COVID-19 pandemic.

Keywords: Agriculture; bioeconomy; biotechnology; health; human capital; technology acquisition

Keynote Talk: 2

Novel Vaccine Approaches to Address Unique Challenges

Dr. Gowrisankar Rajam

Assoc. Principal Scientist, Merck, USA, Ex Lab Lead at CDC, USA

Abstract: Vaccines and vaccination strategies have evolved in tune with the evolution of science and technology. Vaccines can be singled out as the one significant public health achievement responsible for saving millions of lives each year. A chance observation (Jenner) sparked the genesis of these life-saving elixirs. Empowered with the knowledge on both sides of the coin i.e., host and pathogen, these concoctions have metamorphosized into various forms. Adjuvants and delivery mechanisms have expanded the formulation algorithms providing more options to maximize their safety and efficacy. From a simple preparation of live attenuated pathogens or toxins, the field of vaccinology has undergone a series of lateral and vertical changes. Field of tissue culture-infused fresh breath into the area of vaccinology, enabling the generation of a wide range of viral vaccines. Vaccines are probably one of the most critical biological products that reminded the intertwining nature of otherwise siloed fields of science i.e., physical science, chemical science, to name a few. Understanding the chemistry of immunogen, the capsular polysaccharide in Pneumococcus made us realize the limitations of its use as a vaccine in children and led to the development of conjugate vaccines. Nanoparticles borne out of breakthroughs in physical sciences are poised to revolutionize the vaccine delivery and efficacy. Omics…genomics, metabolomics, etc., have made us realize that the vaccinology need not be confined to infectious diseases but can be tuned to address non-infectious disease conditions, including cancer. Therapeutic vaccines that may sound like an oxymoron are indeed a reality. New diseases, new target populations, new challenges but in the realm of vaccinology, the sky is the limit or maybe not!!!

Keywords: Biotechnology; challenges; pandemic; novel vaccine; viral vaccines

Keynote Talk: 3

Challenges in Laboratory diagnosis of COVID-19

Dr. Ch'ng Ewe Seng

Advanced Medical and Dental Institute USM, Malaysia

Abstract: Since the outbreak of a new disease characterized by severe acute respiratory syndrome in December 2019 in Wuhan, China, a novel coronavirus responsible for this disease has been discovered. This novel virus has been named as severe acute respiratory syndrome coronavirus-2 (SARS-CoV2) and the disease as Coronavirus disease 19 (COVID-19). Laboratory diagnosis of COVID-19 has progressed tremendously since the discovery of SARS-CoV2. Many laboratory methodologies have been established with the majorities based on reverse transcription-polymerase chain reaction (RT-PCR). Serological methods to detect developed antibodies against SARS-CoV2, as well as SARS-CoV2 antigen, are now available. Nonetheless, each methodology has its challenges in aiding the diagnosis of Covid-19 and requires cautious interpretation of the test results. This talk focuses on the difficulties of employing and interpreting these test results.

Keywords: COVID-19; challenges; SARS-CoV2; RT-PCR

Keynote Talk: 4

Cold chain free Cholera Vaccine (VCUSM14P): A Potential Live Oral Bacterial Vectored Vaccine Platform for Emerging Diseases

Tew Hui Xian[1], Guruswamy Prabhakaran[1], Kurunathan Sinniah[1], Krishnamoorthy Venkateskumar[2] Chan Yean Yean[3,] and Manickam Ravichandran[1,*]

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Abstract: Cholera due to *Vibrio cholerae* O1 and O139 strains remains a public health concern in South-East Asian countries. Sanitization and vaccines are important measures to control cholera. Our cholera vaccine development journey started with the development of vaccine candidates against *V. cholerae* O139 (VCUSM2) where the *hem*A gene was mutated by systematic allelic replacement methodology. VCUSM2 has all the virulent genes intact, but it is an aminolevulinic acid (ALA) auxotroph due to mutation in the *hem*A gene. It showed good immunological and colonization properties; however, it had reactogenicity property. To reduce the reactogenicity of VCUSM2, zot, and ace virulent genes were deleted, and the wild type *ctx*A gene, the major virulence factor, present in the VCUSM2 was replaced with mutated *ctx*A gene, and the resultant mutant was named as VCUSM14. By site directed mutagenesis. the codons of arginine and glutamic acid at position 7th and 112th, respectively, in CTA of VCUSM14 were substituted with lysine (R7K) and glutamine (E112Q), respectively. VCUSM14 was not reactogenic, but its colonization efficiency in the infant mouse was compromised. To improve the colonization efficiency, the *hem*A gene was reintroduced into VCUSM14, to create a strain with the ALA prototrophic trait, VCUSM14P. VCUSM14P had excellent colonization, and immunological properties that gave 100% protection to wild type challenged rabbits. Recently we have developed a novel cold chain free vaccine formulation of VCUSM14P which is stable and retains its potency at room temperature (25°C ± 2°C, and 60% ± 5% relative humidity) in an ICH-compliant stability chamber for 140 days. One of the unique features of VCUSM14P is that it has intact CTB, which is a known mucosal adjuvant. As the VCUSM14P is a non-toxigenic strain and has built-in adjuvant (CTB), it can be used as an efficient vaccine delivery platform for emerging diseases such as SARS-CoV2 or any emerging diseases. Strategies of developing such affordable cold chain free vaccines have great potential to reach the global immunization program of bottom billion.

***Keywords*:** *Vibrio cholera*; cholera; O139; vaccine; cold chain-free; live; vectored

Keynote Talk: 5

Mitogenomics for Environmental Sciences

Prof. Christopher M. AUSTIN,

Deakin University, Victoria, Australia

Abstract: Background: The molecular genetics and biotechnology revolution has contributed many different methods for accessing genetic information that impacts many fields as diverse as anthropology, medicine, forensics, taxonomy, evolution and conservation and ecology, and selective breeding and genetic improvement in agriculture. Considering the fields encompassed by environmental science, access to readily available and informative molecular markers has been essential, and one specific kind of molecule dominates, viz, mitochondrial DNA. Today, sequences from this molecular still dominate eukaryotic databases and new laboratory methods, and bioinformatics pipelines make the generation and use of whole mitogenomes sequences increasingly accessible. In this presentation, I consider the history and impacts of mitochondrial genetics and the advantages and disadvantages of using mitochondrial genetic information and the future use of this genetic marker. **Methods:** This is a review article that covers several decades of research focused on mitochondrial genes and mitogenomes. In addition to referencing the broader field of environmental science, examples of milestones and applications of mitochondrial genomics will be drawn from my own experience from more than 30 years of research. **Results:** Firstly, the distinctive features of the mitochondrial genome are described. Next, milestones and methods in mitochondrial genetics are mapped, from the first mitogenome to be sequenced, genotyping using restriction enzymes and related methods, the impact of the PCR revolution, the Barcode of Life and associated initiatives, through to the modern-day, which includes the impact of next-generation sequencing and tailored bioinformatics pipelines. Lastly, the value and limitations of using mitochondrial genes and whole mitogenome sequences for environmental research are discussed. **Conclusions:** While the continued evolution of NGS technologies will give ever-greater access to nuclear genomes, mitochondrial genetics will continue to make essential contributions to a diversity of fields within the environmental sciences, especially those requiring species identification from environmental samples.

Keywords: Mitochondria; mitogenomes; molecular markers; Next Generation Sequencing; bioinformatics; genomics

Keynote Talk: 6

Personal Genomes to Precision Medicine- Implications for Rare Genetic Diseases

Dr. S. Sridhar

Senior Principal Scientist, CSIR IGIB, New Delhi, India CSIR Institute of Genomics and Integrative Biology, Delhi, India. Email: sridhar@igib.in

Abstract: Home to a culturally heterogeneous population, India is also a melting pot of genetic diversity. The population architecture characterized by multiple endogamous groups with specific marriage patterns, including the widely prevalent practise of consanguinity provides a niche to understand genetic diseases. Centuries of genetic isolation of population groups have amplified the founder effects, contributing to the high prevalence of recessive alleles, which translates into genetic diseases, including rare genetic diseases in India. Rare genetic diseases are becoming a public health concern in India because a large population size of close to a billion people would essentially translate to a huge disease burden for even the rarest of the rare diseases. Genomics-based approaches have been demonstrated to accelerate the diagnosis of rare genetic diseases. It is also anticipated that genomics-guided decisions would find its place in optimizing therapeutic interventions and minimizing adverse events. The last decade has been transformative in the adoption and implementation of genomics in India. From the first personal genome in 2009, human genomics in India has progressed at a modest but steady pace. Collaborative research initiatives such as the Genomics for Understanding Rare Diseases: India Alliance Network (GUaRDIAN) have attempted to provide genomic solutions for rare diseases in India. The consortium aims to establish a unique collaborative framework in health care planning, implementation, and delivery in the specific area of rare genetic diseases. It is a nation-wide collaborative research initiative catering to rare diseases across multiple cohorts, with over 280 clinician/scientist collaborators across 70 major medical/research centers. Within the GUaRDIAN framework, clinicians refer to rare disease patients, generate whole genome or exome datasets followed by computational analysis of the data and disease modeling for identifying the causal pathogenic variations. The outcomes of GUaRDIAN are being translated as community services through a suitable platform providing low-cost diagnostic assays in India. We discuss how a public-funded collaborative research initiative such as the GUaRDIAN can provide a nation-wide framework for accelerating the diagnosis and management of rare genetic diseases.

Keywords: GUaRDIAN; precision medicine; population; rare genetic diseases

Keynote Talk: 7

Science Communication for Post-Truth Era

Dr. Mahaletchumy Arujanan

Executive Director, MABIC, Malaysia

Abstract: Despite technological advancements, we still live in an era where emotions and personal beliefs become more influential in shaping public opinion compared to science and facts. In this age, we still have anti-vaxxers, flat earthers, and climate change deniers. It is naïve for scientists to think that scientific research and journal papers are enough to garner public acceptance, investments for R&D, and political will. All these are key aspects of the commercialization of research. One blessing from Covid-19 pandemic is enhanced interest among the public on science, and the trust in science among policymakers as a tool to solve global challenges. How do we sustain this? This presentation will first explore why communicating science and engaging the audience outside the scientific fraternity is vital for both development of science and also the personal development of the scientists. The impact of fake news and pseudoscience will also be discussed in the era of post-truth. Some strategies and recommendations will be presented.

Keywords: Biotechnology; Covid-19; communication; research, development

Keynote Talk: 8

Understanding the Genome Biology and New Therapeutic Strategies for Cancers with Genomic Methods

Prof. Dr. Kumaresan

Head, Department of Genetics, Madurai Kamaraj University, Tamilnadu, India

Abstract: Genomic methods are employed in understanding the complexities and functionalities of the genome, and involve analyzing the complete genome or the whole set of genes or factors. This gives an unbiased view and solution to the problem, and hence genomics studies are also known as genome-wide and unbiased approaches and extensively used in various fields of biological and biomedical sciences. Genomic methods involve the investigation of one or more of the genomic components such as mRNAs, miRNAs, lncRNAs, proteome, metabolome, epigenome, etc. For instance, the occurrence of about 14 million polymorphic regions, 20000 genes, few thousands of small RNAs, other non-coding RNAs, and genome-wide epigenetic codes in human genome makes it feasible to understand the genome biology of humans as well as in identifying the biomarkers for various diseases, clinical conditions, and drug responsiveness, upon integration. The whole RNA sequencing and functional genomic interaction studies have made different outlooks to the molecular regulations in the genome and cellular functionalities. Compared to the conventional genomics, the genomic methods offer greater advantages in understanding the complexity of biological conditions as well as in deciphering new therapeutic possibilities. I will describe the power and usefulness of selected genomic methods and data from our recent work having the potential to transform the modalities of disease diagnosis and therapeutics.

Keywords: Genome biology; mRNAs; miRNAs; lncRNAs; non-coding RNAs

Keynote Talk: 9

How will biotechnology change our future?

Dr. Larry Croft

Deakin University, Australia

Abstract: Human technological skill has increased exponentially over the last 100,000 years, linearly with population size. With the recent reverse engineering of the non-human technology which underlies living systems (cellular biology and genes), human abilities are set to expand further. In this talk, I will outline some of the effects this newly acquired technology will have on us in the next few years for ill and for better.

Keywords: Biotechnology; cell biology; genes; technology; population

PLENARY SPEAKERS ABSTRACTS

Plenary Talk: 1

Dissecting the Epithelial Polarity Network Using Proximity Proteomics and Electron Microscopy Imaging

Dr. Alexander Ludwig

School of Biol. Sciences, Nanyang Technological University, Singapore

Abstract: Cell polarity is a fundamental feature of most cell types. It is essential for animal development, tissue morphogenesis and homeostasis, and when compromised leads to severe human disorders and diseases, including cancer. In epithelial cells, apico-basal polarity is established and maintained through the asymmetric cortical distribution of the Par, Crumbs, and Scribble polarity complexes. Apical (Par and Crumbs) and basolateral (Scribble) polarity complexes overlap at the apical-lateral border, which, in mammals, is defined by the apical junctional complex (AJC). The AJC is composed of tight junctions (TJ) and adherens junctions (AJ) and plays a fundamental role in epithelial morphogenesis and plasticity. However, the molecular composition and precise sub-junctional organization of the AJC and its associated polarity regulators are not well defined. In addition, we lack fundamental knowledge about the molecular players that orchestrate polarity signaling downstream of the polarity proteins.

In this talk, I will present recent data showing that proximity proteomics and electron microscopy imaging with the peroxidase APEX2 resolves the organization of the Par and Crumbs complexes in fully polarized mammalian epithelial cells. Our proteomics analyses produced a high-confidence proteome of the apical-lateral border in which TJ and AJ components and apical and lateral compartment markers are spatially resolved. Besides, and intriguingly, while the Par complex is associated with TJ, the Crumbs complex defines a hitherto unidentified polarity domain apical of TJ, which we term the vertebrate marginal zone (VMZ). We further demonstrate that the Crumbs complex recruits to the VMZ proteins implicated in HIPPO growth control signaling and the regulation of the cortical actin cytoskeleton. Taken together, our work defines the spatial and molecular organization of the apical-lateral border in mammalian epithelial cells, reveals an intriguing molecular and spatial conservation of invertebrate and vertebrate cell polarity protein domains, and sheds new light on the molecular mechanisms that govern epithelial polarity signaling. The implications of our findings for epithelial biology and disease, as well as future directions, will be discussed.

Related publication:

Tan, B, Yatim, SMJM, Peng, S, Gunaratne, J, Hunziker, W, and Ludwig, A. The mammalian Crumbs complex defines a distinct polarity domain apical of epithelial tight junctions. Current Biology. Published online June 11 2020. doi: https://doi.org/10.1016/j.cub.2020.05.032

Keywords: APEX2; electron microscopy; epithelial polarity network; proteomics; VMZ

Plenary Talk: 2

NGS in the Food Industry: Authentication, Compliance, and Safety

Dr Ju Lin Tan

NGS, Scientist, GeneSEQ Sdn Bhd, Malaysia

Abstract: While Next-Generation Sequencing (NGS) has seen widespread adoption in academia and the health industry, application in the food industry is limited. GENESEQ Sdn Bhd is a pioneer in this field, and we harness the power of NGS to assess food safety issues and to ensure compliance with domestic, international, and religious standards. Food fraud is an issue in the food industry, especially when this problem can cost the global food industry $30 to $40 billion per year. Other than financial impact, food fraud can also pose health risks, and damage a company's reputation. The global supply chains have been disrupted by COVID-19, and this issue is likely to diminish the level of surveillance, resulting in a rise of food fraud. In order to prevent such issues from exacerbating, we use NGS to help food operators to better manage their food safety system within the complex supply chain. Using targeted amplicon sequencing, identification of all the animal and plant species and bacterial populations within a processed food sample is now a reality. Furthermore, NGS facilitates the identification of bacterial populations in a food facility, and this application fits well into the Environmental Monitoring Program. With this information at hand, food operators will have the ability to be preventive rather than reactive in their food safety programs. This talk describes the use of targeted amplicon sequencing of the mt16S DNA for animal identification, ITS2 DNA for plant identification, and the 16S rRNA region for identification of bacterial populations, and highlight some interesting findings using this method.

Keywords: Compliance; DNA; food industry; NGS; safety

Plenary Talk: 3

The Mind of Our Heroes and the COVID-19 Pandemic: Does COVID-19 Affect the Mental Health of the Healthcare Workers at the Time When We Need Them Most?

Mohammad Farris

AMDI, USM, Malaysia

Abstract: The severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) virus is a highly infectious and contagious virus belongs to the coronavirus family has caused a major health hazard globally. Human as a social being needs to engage in various daily routines and social activities in order to safeguard their mental well-being. As a result of quarantine or lockdown for a prolonged period and due to the pandemic itself, the affected people are very likely to develop a wide range of symptoms of psychological stress and disorder, including low mood, insomnia, stress, anxiety, anger, irritability, emotional exhaustion, depression, and post-traumatic stress symptoms. Low mood and irritability specifically stand out as being very common. A comprehensive review of recently published literature on the psychological impact of COVID-19 pointed out that common psychological complications reported in healthcare workers during the COVID-19 outbreak were depression, anxiety, posttraumatic stress disorder, stress, and sleep disturbance. The specific predisposing and protective factors reported among healthcare workers were work-related while attempted and completed suicide related to COVID-19 among healthcare workers were also reported in case series and case reports. The findings of this comprehensive review outlined a worrying trend of psychological complications in healthcare workers due to COVID-19. However, insufficient understanding of its predisposing and protective factors warrants a more robust future studies design (e.g. longitudinal, case-control). Establishing these factors is crucial to prompt a concerted effort to ameliorate psychological complications of the outbreak through treatment and prevention plan. In this talk, I will focus on: (1) the psychological sequelae of COVID-19 among healthcare workers, (2) the associated predisposing and protective factors of these psychological complications, and (3) what are the learning points which the government or health authorities should focus on to safeguard the mental health of healthcare workers at the time of a global pandemic?

Keywords: Anger; anxiety; COVID-19 pandemic; disorder; insomnia; stress

Plenary Talk: 4

Human Embryonic Stem Cell-Derived Colon Organoids as a Platform to Model Colorectal Cancer and COVID-19

Dr. Fong Cheng Pan

Weill Cornell Medicine, New York, USA

Abstract: Recent advances combining human embryonic stem cell (hESC) gene-editing technology, cell-type-specific differentiation protocols, and organoid culturing techniques offers an unlimited source of cell type-specific isogenic organoids that can be used to model disease biology, facilitate drug discovery, and provide key insights for developing personalized therapies. Through modulation of signaling pathways that are known to regulate embryonic colon development, we have established hESC differentiation protocol for the progressive generation of definitive endoderm, hindgut endoderm, and subsequently enrichment of colon organoids. These hESC-derived colon organoids expressed pan-intestinal marker CDX2 and colon-specific marker SATB2, indicating that they are *bona fide* colon organoids. Besides, single-cell RNA sequencing results showed that the wild-type COs contained all major colonic cell types, including enterocytes, goblet cells, neuroendocrine/enteroendocrine cells, transit-amplifying, and stem cell populations. In this talk, I will focus on using this hESC-derived colon organoid platform to (1) model colorectal cancer, (2) study tropisms of SARS-CoV-2, and (3) identify drug targets for COVID-19.

1. Yang L, Yuling Han Y, Nilsson Payant BE, Gupta V, Wang P, Duan X, Tang X, Zhu J, Zhao Z, Jaffré F, Zhang T, Kim TW, Harschnitz O, Redmond D, Liu L, Naji A, Ciceri G, Guttikonda S, Bram Y, Chandar V, Nguyen D, Hoagland D, Huang Y, Xiang J, Wang H, Chen HJ; Studer L, **Pan FC***, Ho DD, tenOever BR, Evans T, Schwartz RE, Chen S, Cioffi M, Houghton S, Lyden D, Borczuk A. (2020). A human pluripotent stem cell-based platform to study SARS-CoV-2 tropism and model virus infection in human cells and organoids. (***Cell Stem Cell, in press*****) (*co-corresponding author).**

2. Duan X, Han Y, Yang L, Nilsson-Payant BE, Wang P, Zhang T, Xiang J, Xu D, Uhl S, Huang Y, Chen HJ, Wang H, tenOever B, Schwartz RE, Ho DD, Evans T, **Pan FC***, Chen S. Identification of drugs blocking SARS-CoV-2 infection using human pluripotent stem cell-derived colonic organoids. (Under review in *Nature*) (*co-coresponding author)

Keywords: Biotechnology; COVID-19; health; human embryonic stem cell; SARS-CoV-2

Plenary Talk: 5

Prospects and Applications of Metagenomics

Dr. J. Rajendhran

Department of Genetics, School of Biological Sciences, Madurai Kamaraj University, Madurai – 625 021; Email: jrajendhran@gmail.com

Abstract: The biosphere is dominated by microorganisms, yet most microbes in nature have not been studied. However, the majority of these microbes have never been cultured, and their enormous genetic richness has remained untapped. Recent microbial surveys based ribosomal RNA genes suggest that about 90 to 99% of the existing microorganisms in any environment are uncultivable. Alternatively, the genomes of microorganisms are now accessible without culturing through metagenomic approaches. The genomes of the total microbiota found in nature, which is termed as the metagenome, contain vastly more genetic information than is contained in the culturable subset. Cloning of fragments of DNA isolated directly from the natural environments provides a method to access genetic information of all microorganisms. The metagenomic approach allows the analysis of genetic material derived from total microbiota of the associated environment, and hence, the metagenome searches result in the identification of novel genes and biodegradation pathways. The metagenomic library can be screened for suitable enzymes using appropriate functional or sequence-based approaches. The genomes of the human microbiota, collectively defined as the "human microbiome", provide traits that humans did not evolve on their own. The influence of gut microbiome in obesity has been demonstrated. Research on gene expression in the microbial community is expanding, and the recent developments in the area of metagenomics and the Human Microbiomics are expected to yield novel biomolecules and therapeutic agents.

Keywords: Applications; DNA; metagenome; microbiome; microbiota

Plenary Talk: 6

HLA based Diagnostics and Therapeutics

Dr. Balakrishnan

Madurai Kamaraj University, Tamilnadu, India

Abstract: The genetic loci involved in the rejection of foreign organs/tissues are known as the Major Histocompatibility Complex (MHC) and are highly polymorphic cell surface molecules encoded by the MHC. The primary biological role of HLA molecules is in the regulation of immune response. In the clinical setting, the use of Human Leukocyte Antigen (HLA) testing is to match organ and tissue transplant recipients with compatible donors. The leukocyte-agglutinating antibodies (leukoagglutinins) were observed in sera from multiparous women and previously transfused patients. The human MHC maps to the short arm of chromosome 6 (6p.21.3) and spans approximately 3,600 kilobases of DNA. The class-I region of MHC complex contains the classical HLA-A, HLA-B, and HLA-C genes and the class II region contains HLA-DR,-DQ, and DP genes. MHC class I and class II alleles and linked genetic factors have been shown to contribute considerably to individual differences in susceptibility to several pathogens including viruses. HLA-class I and class II alleles are shown to be associated with several diseases such as tuberculosis, leprosy, diabetes, cervical cancer, and a host of other diseases. Further, the HLA genes/ molecules are exploited as drug targets in treatment options for lymphomas. Shared epitopes of HLA molecules are well illustrated as diagnostic markers in autoimmune diseases and cancers. It is possible to predict vaccine candidates based on MHC-HLA-Peptide binding prediction analysis. For example, HLA-A2 is a predominant class I allele among all ethnic groups. HLA alleles, haplotype, and extended haplotypes are important molecular targets for studies on population genetics, susceptibility studies donor screening in transplant programmes, therapeutics development, and vaccine designing. The paper presents the applications of HLA genes as a diagnostic marker and as a molecular target in developing therapeutics.

Keywords: Cervical cancer; Diagnostics; diabetes; leprosy; therapeutics; tuberculosis

Plenary Talk: 7

Epigenetic Modulators – Key Players in Host-Pathogen Cross Talk In Bacterial Infections

Dr. Suswetha

School of Basic and Applied Sciences, Dayananda Sagar University, Bangalore, India

Bacteria have evolved to be more powerful than we humans could ever anticipate. The current era is witnessing emerging superbugs along with a rapid rise in multidrug resistance menace making therapeutic regimes challenging for bacterial infections. We know infectious diseases are the outcome of molecular cross-talk between host and the pathogen that can tilt the balance either in favour of the pathogens spread or clearance. In this cross-talk, pathogenic bacteria can affect the chromatin structure and transcriptional program of host cells by influencing diverse epigenetic factors and take control of the hosts' immune system. In this line, my talk will discuss our findings in Mastitis - a fatal mammary gland infection caused majorly by bacterial pathogens. I will share how two closely related strains of Staphylococcus aureus induced alteration of epigenetic modulators (histone acetylation and microRNA expression) influencing the differential expression of pro and anti-inflammatory genes in the host. The molecular cross-talk of two strains of S. aureus with the host showed how the host transcriptional program could be exploited and modified, leading some strains towards possible rapid clearance, whereas others persist inside the host. Elucidating bacterial infectious disease in connection with the epigenome can offer new avenues for therapeutic interventions.

Keywords: Bacteria; epigenetic; host; Pathogen; *Staphylococcus*

Plenary Talk: 8

An Overview of Biotechnological Research & Postgraduate Study in the UK

Dr. Sarah Amirah

University of Manchester, UK

Abstract: Biotechnology is an evolving research field that covers a broad range of themes and signifies a new biological approach to a wide range of industries. Biotechnology is known to be divided into four different sectors, namely white (industrial), red (pharmaceutical/medical), green (food and agriculture), and blue (environment/marine). Here, we will cover some of the current and prominent research themes in each sector. Metabolic engineering is one of the most dominant research areas in biotechnology currently, and *Saccharomyces cerevisiae* is known as an established biotechnological workhorse for the production of various compounds including food products, biopharmaceuticals and biofuels. Previously, the Ashe lab has shown that the biofuel n-butanol can be produced by expressing a Clostridial butanol synthesis pathway in yeast. However, the titre of n-butanol produced is below what would be viewed as industrially significant. Interestingly, in some of these butanol production strains, there is a prominent level of 2,3-butanediol (2,3-BD). 2,3-BD represents an important high-value chemical with numerous industrial applications ranging from synthetic perfumes, plasticisers, food and pharmaceuticals. In this talk, we will discuss several metabolic engineering strategies that have been applied to improve bio alcohols production in yeast.

Keywords: Agriculture; biopharmaceuticals; biotechnology; n-butanol; *Saccharomyces cerevisiae*

Plenary Talk: 9

COVID-19 and Opportunities for Pharmaceutics Researchers

Dr. Enrico Magosso

Universiti Kuala Lumpur, Malaysia

Abstract: The ongoing pandemic caused by the SARS-CoV-2 has brought numerous challenges in most, if not all, aspects of human life. Since COVID-19 was declared a pandemic by the WHO, health-related scientific fields have received widespread attention in the public eye. The focus of the scientific community has become an all-out search for any possible treatment or adjuvant in the treatment of SARS-CoV-2. As for August 2020, according to the WHO database, amongst vaccines, 29 candidates are undergoing clinical trials, with six candidates reaching phase-3 clinical trials. Furthermore, there are 138 vaccine candidates in various stages of pre-clinical phase investigations. Intuitively, besides the search for a novel vaccine, many other pharmacological approaches of established agents are under investigation. Such well-known drugs that are already on the market, from various antiviral drugs, to antimalarial drugs chloroquine and hydroxychloroquine, from anti-heartburn famotidine to antidepressant fluvoxamine to corticosteroids, offer the opportunity of investigating novel delivery systems. Therefore, from a strict pharmaceutical technology point of view, repurposing old or established drugs, may represent an arguably faster approach to find, if not a cure, at least ad adjuvant candidate against COVID-19. While the issue of repurposing known drugs represents a challenge, it also opens opportunities for the pharmaceutical scientists involved in delivery systems.

Keywords: COVID-19; chloroquine; opportunities; pharmaceutics; SARS-CoV-2

Plenary Talk: 10

Whatever You Can Do, I Can Do As Well: Aptamers as the Promising Surrogates of Antibodies

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Abstract: Since its discovery in 1990 by a process known as Systematic Evolutions of Ligands by Exponential Enrichment (SELEX), aptamers have been used in a spectrum of applications, on par with the protein-based antibodies. Compared to antibodies, aptamers are much cheaper, with no batch-to-batch variations, more feasible for functional group conjugation, and generally exhibit target-induced conformational change for a much more pronounced signal transduction. The much sought-after aptamer-based application is in the diagnostics, whereby aptamers act as the target-binding modules and the event of aptamer-target recognition is made manifest in terms of signal changes. In our laboratory settings, we have isolated aptamers against multiple targets from cancer biomarker to the microbial biomarkers. We have demonstrated the application of aptamers in several aptanostics (aptamer-based diagnostics) assay such as apta-Western blot, apta-dot blot, aptamer-linked immunosorbent assay (ALISA) and aptahistostaining, in much the same way as antibodies. It is time to conclude that whatever you can do, I can do as well!

Keywords: Aptamers; ALISA; biotechnology; ligands; SELEX

ORAL PRESENTATION ABSTRACTS

O1

Binding Kinetics and Crystallographic Studies on the Interaction of Cyclin-Dependent Kinase 2 with a Selective and Potent Inhibitor NU6140

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Abstract: Background: Cyclin-dependent kinase 2 (CDK2) is the important cell cycle protein target for therapeutic intervention in various proliferative diseases, including cancer. Numerous CDK2 inhibitors have been discovered and their crystal structures with CDK2 or CDK2/Cyclin A complex have been published. NU6140 is a potent and selective ATP-competitive inhibitor of CDK2. This study aims to understand the binding kinetics of CDK2 with NU6140 and elucidate the structural features of their complex. We have investigated the binding kinetics of NU6140 with CDK2 using Surface Plasmon Resonance (SPR) technology. NU6140 displayed dose-dependent binding to CDK2 and exhibited typical kinetic behavior with an equilibrium dissociation constant, Kd of around 800 nM. In thermal stabilization studies, NU6140 increased the melting temperature of CDK2 by 4.8 ℃. X-ray crystal structure of CDK2 with NU6140 elucidated to understand the various interactions that stabilize the complex demonstrated that NU6140 binds in the ATP binding pocket, interacting with Leu 83 and Glu 81 directly. The binding was further stabilized by water mediated interaction with Asp 145. Based on the SPR binding kinetics and crystal structure, further modifications on NU6140 are proposed, which may significantly increase the antitumor activity. **Methods:** Thermal shift assay was performed using the ABI Prism 7500 instrument (Applied Biosystems, USA) using SYPRO Orange dye as an indicator. Surface plasmon resonance (SPR) spectroscopy experiments were performed using Biacore T200 (GE Healthcare Biosciences (India). X-ray data were collected at the MX2 beamline at Australian Synchrotron (AS) and the crystal structure was determined using BlueIce, XDS, CCP4 package suite version 7.1. software. **Results:** The results illustrate the binding kinetics and various interactions involved in the CDK2 - NU6140 complex formation and provide information for the proposal of additional interactions with CDK2 which can further stabilize the complex.

Keywords: CDK2, NU6140, SPR, Crystal structure

O2

Therapeutic Potentials of *Mangifera indica* Extracts

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Abstract: The aim of this study is to ascertain the therapeutic potentials of *Mangifera Indica* bark. The fresh bark of *Mangifera indica* was collected, air dried and ground to powder, the crude extract was prepared using chloroform, ethanol and distilled water, the dried sample of 50g each of the *Mangifera indica* bark yielded 9.11g, 5.4g and 1.8g for chloroform, ethanol and distilled water as solvents respectively, the antimicrobial screening analysis revealed that the crude extracts inhibited the growth of *Staphylococcus aureus* at virtually all the concentrations but had no effect on the tested fungi. Furthermore, the crude extracts were also subjected to phytochemical screening in which alkaloids, flavonoids, and steroids were found to be present and terpenoids were absent in all the three crude extracts. It could be concluded that the crude extracts of the *Mangifera indica* have an antibacterial effect as a result of tested phytoconstituents.

Keywords: Therapeutic, Crude Extract, Phytoconstituent, *Mangifera indica*,

O3
Limit of detection of a prototype PCR based detection kit for Familial Hypercholesterolaemia Variants in Malaysia

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Abstract: Background: Early detection of familial hypercholesterolaemia (FH) pathogenic variants among patients as the inherited disease is vital to prevent the risk of cardiovascular disease at an early age. Current criteria for diagnosing FH rely on NGS sequencing of patients' DNA, which is expensive and time-consuming. Thus, a novel PCR-based FH screening kit was developed for the detection of pathogenic variants unique to the Malaysian population targeting low-density lipoprotein receptor *(LDLR)* and apolipoprotein B *(APOB)* genes of FH. **Methods**: A PCR-based prototype was developed that targeted 11 *LDLR* and *APOB* genes variants of FH. Preliminary evaluation of the prototype performance was performed, as well as the determination of the Limit of Detection (LoD). This study included 22 specific primer sets as well as the synthetic targets DNA that targeted wild-type (WT) and pathogenic-type (MUT) variants of LDLR, and APOB genes of FH were designed. LoD of the kit was determined using synthetic target DNA in a serial dilution from 1ng up to 10^{-10}ng. **Results:** The preliminary sensitivity and specificity of six positive and negative clinical samples, as well as 22 positive and negative control DNA, was 100%. Single band with correct product size was detected on most of the FH variants of the *LDLR* and *APOB* genes even on the lowest dilution factors (10^{-10}) as the outcome for LoD. Thus, the optimal detection of all these positive controls towards the primers was determined to be 1ng/µl with the optimized conventional PCR protocol. **Conclusions:** The development of a novel prototype that showed 100% sensitivity and specificity in preliminary testing with the lowest detection limit of 10^{-10}ng. The PCR detection kit will prove useful as a cheap and fast alternative for FH pathogenic variants detection.

Keywords: Familial hypercholesterolaemia, *LDLR*, *APOB*, Malaysia, limit of detection, polymerase chain reaction

O4

Genetic diversity *Plasmodium knowlesi* apical membrane antigen-1 (PkAMA-1) and *Plasmodium knowlesi* thrombospondin-related apical merozoite protein (PkTRAMP)

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Background: The simian malaria parasite and also the fifth human malaria parasite, *Plasmodium knowlesi* is prevalent in Southeast Asia especially Malaysia. *Plasmodium knowlesi* apical membrane antigen-1 (PkAMA-1) and *Plasmodium knowlesi* thrombospondin-related apical merozoite protein (PkTRAMP) are potential to be the considerations in malaria vaccine development as they play crucial roles in the invasion of the parasite into the host's erythrocyte. Genetic diversity is a common consideration among the approaches for vaccine development of malaria. The number of reported *P. knowlesi* cases were higher in Malaysian Borneo compared to Peninsular Malaysia. This study investigates the genetic diversity of PkAMA-1 and PkTRAMP in *P. knowlesi* clinical samples from Malaysian Borneo and Peninsular Malaysia. **Methods:** Blood samples (n=40) were collected from *P. knowlesi* malaria patients from Malaysian Borneo and Peninsular Malaysia. The PkAMA-1 and PkTRAMP genes were amplified from DNA samples using PCR, and subsequently cloned into *Escherichia coli* and sequenced. Software MEGA7 and DnaSP version 5.10.00 programmes were used to analyze the genetic diversity and natural selection of both PkAMA-1 and PkTRAMP. **Results:** PkAMA-1 and PkTRAMP sequences were obtained. The analysis showed that PkAMA-1 and PkTRAMP were under purifying selection. Phylogenetic analysis showed the sub-group formation for Peninsular Malaysia and Malaysian Borneo. **Conclusions:** This study is the first to compare the genetic diversity and natural selection of PkAMA-1 and PkTRAMP from Malaysian Borneo and Peninsular Malaysia. PkAMA-1 and PkTRAMP were under purifying selection.

Keywords: *Plasmodium knowlesi*, apical membrane antigen-1, thrombospondin-related apical merozoite protein, genetic diversity

O5

Effect of Maternal Epigallocatechin Gallate on Blood Pressure and Pregnancy Outcomes in Spontaneously Hypertensive Rats

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Abstract. Background: Chronic hypertension during pregnancy is associated with maternal-fetal morbidity and mortality. Epigallocatechin gallate (EGCG) has been recommended as a blood pressure lowering agent due to its potent antioxidant, anti-inflammatory properties, as well as its direct vasodilatation effect. This study proposes that EGCG might be useful in treating chronic hypertension during pregnancy. This study aims to (i) determine effect of oral EGCG on blood pressure and pregnancy outcome (gestation period, birth weight, and little size) of SHR dams, and (ii) determine the effect of perinatal EGCG on blood pressure of SHR offspring. **Method**: SHR dams were given oral EGCG (30 mg/kg *b.w.*) from day-1 of pregnancy until day-21 postpartum. Pregnancy outcome (gestation period, litter size and birth weight) were recorded. Systolic blood pressure of the SHR dams was recorded up to day-21 postpartum, while SBP of the SHR offspring was recorded up to 13 weeks of age. **Result**: EGCG treated SHR dams has lower SBP compared to the untreated groups at day-7, 14 and 21 of pregnancy, as well as day-14 and 21 postpartum ($p<0.001$). Gestation period, little size and birth weight of the EGCG treated group was comparable to the untreated group. SBP of the SHR offspring that received maternal EGCG was comparable to their age-matched controls up to 13 weeks of age. No sign of toxicity or mis-behavior were observed in both SHR dams and offspring throughout the experimental period. **Conclusion**: EGCG reduced maternal blood pressure with no side effects on the pregnancy outcome. The findings of this study further suggest that EGCG could be an antihypertensive agent that safe to be consumed during pregnancy.

***Keywords*:** EGCG, SHR, pregnancy outcome, blood pressure

O6

Expression of Chikungunya virus E2 protein for the development of a rapid diagnostic test

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Abstract. Mosquito-borne diseases are a major public health concern. Similar to the dengue virus, Chikungunya virus (CHIKV) causes febrile illnesses and human transmission is mainly by *Aedes* mosquitoes. Co-circulation of these two viruses and similarity in clinical symptoms contributes to the challenge of making an accurate diagnosis of the infection. There is a need to develop a rapid, sensitive, and user-friendly diagnostic tool to confirm CHIKV infection for appropriate intervention. Envelope 2 (E2) protein is at the outermost region of the CHIKV and is responsible for attachment during viral infection. Studies have indicated that E2 protein is the major target of neutralizing antibodies and thus serves as a suitable target antigen for the development of a diagnostic test. The present study aimed to isolate, clone, and express the *E2* gene to produce the recombinant CHIKV E2 protein. Total RNA was extracted from CHIKV isolated in the Institute of Health and Community Medicine, UNIMAS, and the *E2* gene was amplified by a reverse transcription-polymerase chain reaction. The amplified *E2* gene was purified and cloned into the pET-14b vector. Positive clones were selected, verified, and subsequently transformed into the *E.coli* BL21 (DE3) pLysS strain. Expression of recombinant CHIKV E2 protein in *E.coli* was induced with 0.5 mM isopropyl-beta-thiogalactosidase for 2 hours and yielded an insoluble protein in the form of inclusion bodies. The inclusion bodies were isolated and solubilized in 6M urea before purification through column chromatography and subsequent verification by western blot. The 24 kDa recombinant CHIKV E2 protein was successfully expressed and purified with a final product yield of ~200 mg/l. The protein was reactive against anti-CHIKV positive sera and anti-CHIKV polyclonal antibody on a western blot with no cross-reactivity with anti-dengue positive pooled sera. The resulting recombinant CHIKV E2 protein can serve as a potential target for the development of CHIKV rapid diagnostic tests.

Keywords: Chikungunya virus; diagnostic test; envelope 2 protein

O7

Unraveling the Nutritional and Anti-Diabetic Properties of Kattu Yanam- A Traditional Rice Variety of Tamil Nadu

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Abstract: Background: Kattu Yanam, an indigenous rice variety of Tamil Nadu is very well known for its antidiabetic property and low glycemic index. The present study was aimed at revealing the nutritional property of Kattu Yanam rice in comparison with other two rice varieties like White Ponni rice and IR64 along with its antidiabetic efficiency through *in vitro* and *in vivo* studies. **Methods:** The nutritional profiling of the three rice varieties was carried out based on the standard AOAC methods. For revealing the antioxidant properties, DPPH radical scavenging assay was performed. The anti-diabetic properties of the indigenous rice were analyzed *in vitro* through α-amylase and α-glucosidase inhibition assay and *in vivo* through Streptozotocin-induced diabetic animal model studies. **Results:** The nutritional profiling of the Kattu Yanam rice showed that it contained lowered sugar levels and fat content, increased dietary fiber, and protein content and it was also found to produce lower calories of energy when compared with the other two rice varieties. The DPPH radical scavenging assay of the two extracts of Kattu Yanam rice viz., ethanolic, and aqueous extracts exhibited good antioxidant properties. The GC-MS analysis of the two extracts of the Kattu Yanam rice exposed that it contains a good number of phytocompounds in it. The *in vitro* α- Amylase and α- Glucosidase inhibition showed the minimum inhibitory concentration (IC50) of 42.575 ± 4.516 mg/ml and 16.686 ± 2.013 mg/ml respectively. The *in vivo* studies results showed that the ethanolic extract of Kattu Yanam rice significantly ($p<0.05$) reduced blood glucose levels. Furthermore, histological studies revealed the ability of the extracts in maintaining the normal liver cell architecture thus featuring its safety. **Conclusion:** Based on the results present study establishes the nutritional property of Kattu Yanam rice Kattu Yanam the indigenous rice variety of Tamil Nadu that can be employed in the management of Diabetes Mellitus.

Keywords: Kattu Yanam rice; diabetes; antioxidant property; phytocompounds.

O8

GPCR Signaling In Inflammation

Anti-Inflammatory Effect Of Non-Essential Amino Acid - Glycine

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Abstract: Background: Glycine is the most important and simple, non-essential amino acid in humans, animals, and many mammals. There are overwhelming reports supporting the role of dietary supplementation of glycine are effectual in treating metabolic disorders in patients with cardiovascular diseases, several inflammatory diseases, obesity, cancers, and diabetes. Glycine blocks the increases in intracellular calcium ions in specific cells caused by many structurally different stimuli like alcohol, endotoxin, peptidoglycan, polysaccharide, bile acids, peroxisome proliferators, etc. Aim: a) The aim of the present study was to investigate the anti-inflammatory effect of glycine, a non-essential amino acid in an in vitro model and the PKC isozymes responsible for the action of alcohol were investigated using translocation as a measure of activation. b) To identify the alcohol-induced G protein-coupled receptor expression in HUVEC. Methods: Human Umbilical Vein Endothelial cells damage was induced by ethanol (5%), and glycine was subsequently administered at a dose of 300 µM for 24 hrs. Translocation of PKC isozymes to the membrane studied by western blot. Conventional PCR was performed. Results: Administration of alcohol significantly elevated the inflammatory cytokines Tumor necrosis factor-α (TNF-α) and Interleukin 6 (IL-6), the activity of myeloperoxidase and depleted reduced glutathione (GSH) concentration compared with the control group. Subsequently, glycine supplementation to alcohol induction significantly lowered the TNF-α and IL-6, reduced the activity of myeloperoxidase and normalized the glutathione concentration compared with untreated alcohol induction groups. Exposure of the cells to ethanol (5%) led to the translocation of PKC α and ε. Toll-like receptor 2 [TLR-2] was detected by RT-PCR. Conclusion: Thus, the present study demonstrates that the inhibitory effect of glycine by virtue of its ability to optimize the activity of myeloperoxidase, normalize the concentrations of inflammatory cytokines and reduced glutathione. To understand the physiological significance of PKC α and ε translocation to the membrane by alcohol, further studies are warranted to elucidate the mechanisms involved in the activation of GPCR.

Keywords: Antiperoxidative Activity; GPCR; Inflammation; Protein kinase C; Toll-like receptor; Translocation

O9

Study of Endophytic Fungi and Their Metabolites from the Medicinal Plant *Withania Somnifera*

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Abstract. Background: Soil is a medium with macro and micronutrients helping in the growth of micro-organisms, which is supported by the root exudates of plants. It is a complex set of interactions influenced by humification and cycling of elements. The study of endophytes in the rhizosphere and rhizoplane of plant roots play an important role in understanding the symbiotic associations. The endophytic fungi can influence the plant at different stages of growth and production of metabolites. A study of endophytes in medicinal plants has played an important role in exploring the metabolites produced by the endophytes. **Methods**: The plant root bits were processed in 5% sodium hypochlorite and 70% alcohol and the endophytic fungi were isolated on PDA media. The screened fungal isolates were cultured in broth to study for secondary metabolites. The broth was purified and studied for antibacterial properties and screened for the antibacterial compounds. **Results**: The fungal endophytes isolated from *Withania somnifera* reported dominant fungal species *Gliocladium deliquescens, Mycelia sterilia, Phoma glomerata, Phoma humicola,* and *Fusarium xylarioides.* The fungi *Fusarium xylarioides* and *Phoma humicola* were reported to inhibit both Gram-positive and Gram-negative bacteria. These fungal isolates were found to produce metabolites rich in aldehydes, esters, and ketones. They showed the efficacy of antibacterial property on *Escherichia coli* and *Staphylococcus aureus.* **Conclusions**: The plant *W. somnifera* has antimicrobial activity and the endophytic fungal isolates of the plant also showed antibacterial activity, specifically the *Fusarium xylarioides* and *Phoma humicola* producing aldehydes, esters, and ketones.

Keywords*:* Endophytic fungi; *Fusarium xylarioides*; *Phoma humicola;* Antibacterial activity.

O10

Microalgal Biofuel Production

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Abstract. Objectives: The flue gases emitted by thermal power plants, oil refineries, and other industries containing about 15% CO2 are the major contributors to global warming. Microalgae could be an efficient system for bio-mitigation of CO2 due to their faster growth rate, ability to fix CO2 from the atmosphere, flue gases, and chemically fixed soluble carbonates and conversion to biomass containing value-added products. Therefore, it is necessary to evaluate and select efficient microalgal isolates for bio-mitigation of CO2 and production of biofuel. **Methodology:** Microalgal isolates from natural habitats were supplemented with 5, 10, 20, and 30% CO2 in LDPE based photobioreactors for 16 days (16:8 light: dark cycle; 25±1 oC). The biomass was harvested and freeze-dried at the end of the incubation period. The microalgae were evaluated for the ability to tolerate and sequester CO2 in terms of specific growth rate, productivity, carbon content, CO2 fixation rate, and biomass yield. The obtained biomass was analyzed for lipid contents and fatty acid profiles. **Results and conclusion:** Indigenous microalgal isolate was able to sustain and grow under elevated levels of CO2 with enhancements in biomass yield, productivity, specific growth rate, CO2 fixation rate, chlorophyll, carotenoid, and lipid content. Results suggest that the indigenous microalgal isolates have the potential for CO2 sequestration with their biomass as a source of value-added products like lipid which can be used as biofuel.

Keywords: Microalgal, photobioreactors, Biofuel Production

O11

Curcumin Inhibits the Centrosome Separation in Mammalian Cancer Cells by Perturbing the Functions of Mitotic Kinesin Eg5.

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Abstract: Background: Curcumin is a well studied polyphenol which has shown tremendous anti-cancer potential against different cancer types. Curcumin is known to induce cell cycle arrest at G2/M phase in various cell lines with defects in mitosis like inhibition of centrosome separation followed by impaired chromosomal segregation; however, the underlying molecular phenomenon remains elusive. Hence, we decided to investigate the anti-mitotic mechanism of curcumin in detail. **Methods:** The HeLa cells were treated with different concentrations of curcumin for 24 h and the centrosomes and microtubules were visualized by immunostaining the γ-tubulin and α-tubulin respectively. For a detailed *in-vitro* investigation, the recombinant human mitotic kinesin Eg5 (Eg5-437H) was over-expressed in *E. Coli* BL21 cells and was subsequently purified to homogeneity. Tubulin was purified by two cycles of temperature-dependent polymerization and depolymerization. The interaction of curcumin with recombinant Eg5 was studied extensively by performing fluorescence spectroscopy, computational docking, FRET, and circular dichroism. The effect of curcumin on the ATPase activity of Eg5 was studied by performing a standard malachite green ATPase assay. The impact of curcumin on the interactions between Eg5 with microtubules was studied by performing a co-sedimentation assay. **Results:** Curcumin blocked the HeLa cells at mitosis, inhibited the centrosome separation, and induced monopolar spindles in a concentration-dependent fashion. Curcumin bound to the purified Eg5-437H with a strong affinity and perturbed its secondary structure. Evidence from competition experiments, FRET, and computational docking indicated that curcumin bound to Eg5 at a novel druggable site which is 33 Å away from TRP127. Further, curcumin inhibited the ATPase activity of Eg5 motor and perturbed the dynamic interactions between Eg5 and microtubules. **Conclusions:** The data suggest that the application of curcumin in combination with a potent Eg5 inhibitor such as ispinesib might provide a therapeutic advantage for the treatment of cancer.

Keywords: Curcumin; Eg5; FRET; mitosis; monopolar; tubulin

O12

Transcriptome Analysis of Young, Mature and Ripening Stages of Local Durian D24 (*Durio Zibethinus* Murr) Fruit Pulp Tissues

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Abstract: Background: Durian (*Durio zibethinus* Murr.) is an economically significant fruit and known for its unique aroma. A variety of physiological and biochemical changes take place during the fruit ripening process, and thousands of genes play essential roles in various metabolic pathways to make an edible durian fruit. This study analysed the Durian fruit transcriptome to discover patterns of gene expression and understand their regulation. **Methods:** The Illumina Hi Seq platform was used for sequencing. Principal component analysis of the transcriptome separates the fruit samples into three groups corresponding with stages of fruit growth of early (90 days post anthesis), mature (120 days post anthesis) and ripening (127 days post anthesis). The data were analysed using three different combinations of mapping aligners and statistical methods, namely HISAT2+DESeq2, Tophat+Cufflinks, and HISAT2+edgeR. **Results:** Analysis showed that over 110,351,584 clean reads were mapped to the Durian genome, yielding 11,394; 17,833 and 24,351 of differential expressed genes in both up and down-regulated categories using CuffDiff, DESEq2, and edgeR. In all tested cases, edgeR called more genes as differentially expressed. A large number of the identified differentially expressed genes were linked to the ripening processes. These include genes in functional categories such as general transporter, plant hormone signalling, ethylene signalling, cell wall degradation, volatile aromatic compounds production, receptor and protein kinase response, and stress response. The members of the gene families of nine xyloglucan transglycosylase/hydrolase (XTH), five cellulose, four polygalaturonase, and four U-box domains were highly up-regulated during ripening, indicating their involvement in fruit softening. In addition, several genes involved in the synthesis of aromatic volatiles and transcription factor families were identified. Analysis of the novel transcript led to the identification of new 280 unknown transcripts, presumably involved in various biological functions. GO classification of the differentially expressed genes among different growth stages revealed that most of the expressed genes were enriched for metabolic process, cellular process, and response to a stimulus. The results showed that the majority of genes with an increased expression upon transition from the mature to the ripening stage were mainly involved in the metabolism of cofactors and vitamins, nucleotide metabolism and carbohydrate metabolism. The significant genes from the young to the mature stage were associated primarily to the carbohydrate metabolism, metabolism of cofactors and vitamins, and amino acid metabolism. **Conclusion:** As a whole, transcriptomics-based gene expression analysis output provided insights into the dynamic developmental changes in Durian fruit pulp tissue. The research findings provide a foundation for understanding Durian fruit development-specific genes and understanding biological processes. The research findings of the project will be discussed during the conference.

Keywords*:* DEGs; fruit ripening; RNA Seq; transcriptome

O13

Antiparasitic Potential of Medicinal Plant against Zeylanicobdella arugamensis (Hirudinea) and its Chemical Profiling

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Abstract. Global aquaculture has been increasing rapidly and due to the intensification of fish hatcheries, farms faced several fish health issues that caused the economic loss. Among these, the leech *Zeylanicobdella arugamensis* (Hirudinea: Piscicolidae) has been reported to impact hybrid groupers and other hosts. The objective of this study was to test the antiparasitic potential of the various chromatographic fractions of crude methanol extracts of a tropical shrub *Dillenia suffruticosa* and determined the phytochemical composition using high-resolution LCMS QTOF to identify and narrow down the various metabolites responsible for antiparasitic properties. Seven fractions of the methanol extract of *D. suffruticosa* were obtained through flush column chromatography techniques. Various concentrations of the fractions were prepared and tested against the parasitic leech. Bioassay conducted with fresh leeches exhibited significant mortality induced by several fractions. Chemical profiling with LC–QTOF-MS showed the presence of secondary metabolites representing triterpenoid, sterol, flavone, glycoside, phenolic, pyrrolizine, fatty acid, and fatty amide functional groups. Thus, our study indicated that *D. suffruticosa* fractions contained potent bioactive compounds with antiparasitic potential.

Keywords: Aquaculture, Antiparasitic activity, Hybrid groupers, *Zeylanicobdella arugamensis, Dillenia suffruticosa,* LCQTOFMS analysis, Secondary metabolites

O14

A Molecular Study Delineating the Role of Atorvastatin on Breast Cancer Bone Metastasis Targeting Osteoclastogenic Factors

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Abstract. Almost 80% of breast cancer patients with advanced malignancy show bone metastases since bone provide fertile soil to the metastasized cancer cells. Bone metastases of breast cancer are mostly associated with osteolytic lesions where abrupt osteoclast activity plays an important role in increasing bone resorption. In healthy conditions, bone is built by the action of bone residential osteoblasts (bone forming cells) and osteoclasts (bone resorbing cells), when bone resorption is balanced by bone formation. In bone metastasis, breast cancer cells that have already reached bone microenvironment secrete growth factors and cytokines, which either directly or indirectly enhance osteoclast activity, responsible for perturbing bone homeostasis. The excess osteoclast activity not only resorbs bone but also releases some growth factors embedded within the bone. These released factors, in the bone microenvironment, further effectuate the activity of breast cancer cells. Thus, targeting this vicious cycle could be an important therapeutic strategy in treating bone metastasis of breast cancer. Cholesterol-lowering Atorvastatin limits osteolytic metastasis of breast cancer. Thus, Atorvastatin treatment might prevent inhibition of osteoclast activity within metastatic bone cells. This study reports how Atorvastatin arrested the breast cancer-induced TRAP and MMP activity, and expressions of osteoclastogenic genes (TRAP, Cathepsin K, and NFATc1) in pre-osteoclast RAW264.7 cells.

Keywords: Breast cancer; metastasis; Osteoclast; Atorvastatin.

O15

LED Farming of Pennywort: To Keep the Food Supply Chain Thriving during the Covid-19 Pandemic

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Abstract: Background: The agriculture sector especially smallholder farmers in Malaysia has been adversely affected by reduced agricultural labour and disruption in demand and supply chain as a result of COVID-19 pandemic. Indoor farming using light-emitting diodes (LED) is offer advantages to reduce labour dependency, maximize production, and promote sustainable farming. To compare the efficiency of LED light on indoor farming, a largeleaf pennywort *spp; Hydrocotyl bonariensis* growth was tested under natural light and different spectral compositions of LED lights. **Methods:** Productivity and nutritional quality of *H. bonariensis* assayed for plants grown under natural light and four different spectral compositions of LED lighting: 1) Red and blue (R:B = 83:35) 2) Red and blue with a higher blue irradiance (R:B = 83:65) 3) Red, blue and green (R:B:G = 83:35:12), and 4) Red, blue and ultraviolet A (R:B:U = 83:35:10). **Results:** The ratio of red to blue light has a substantial influence on plant growth and leaf biomass in *H. bonariensis*: Plants grown under the system with a higher level of blue irradiance showed the highest leaf number, total leaf area, leaf biomass, plant height, total antioxidant content, total phenol, and total flavonoid content compared to plants are grown under natural light in a greenhouse or the other LED conditions. The addition of green LED had a neutral effect on plant growth and total antioxidant, phenol and flavonoid content while the addition of ultraviolet A LED had a negative effect on plant growth and total antioxidant and phenol content. **Conclusion:** These findings provide fundamental information for the design of light sources, which will be useful for sustainable indoor farming of *H. bonariensis* and other pennywort species.

***Keywords*:** Antioxidant; LED; nutraceuticals; pennywort; total phenol; total flavonoid

O16

Development of Species-Specific Multiplex PCR to Detect Possible Adulterant DNA in Raw Food Samples

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Abstract: Background: Food adulteration has become a growing concern nowadays which calls for more stringent monitoring. Various DNA-based methods are being used in authenticating meat sources but most are not specific in detecting types of adulterant or only specific to a few of them. Thus, this study was conducted to develop and optimize a species-specific multiplex PCR assay targeting the porcine specific repetitive region of LINE-1 (L1) retrotransposons and several mitochondrial regions of poultry and other meat species for the identification of multiple species in raw food samples. **Methods:** Four primers were combined in a multiplex PCR assay and it was validated for specificity. Genomic DNA was extracted from 12 different meat samples. Multiplex PCR was optimized using gradient PCR and tested with all 12 genomic DNA samples. **Results:** The optimization of this multiplex PCR assay was for all four primer pairs (IC, *SUS*, POU, and OM II) in a single reaction. All primer pairs bind to respective templates and showed specific bands. **Conclusion:** This species-specific multiplex PCR has the advantage of detecting various possible adulterant meat in raw food samples. It can be an alternative assay in detecting common meat species from raw meat as it is convenient, effective, and cost-efficient.

Keywords: *Porcine DNA; Species-specific; Multiplex PCR; Food authentication; Halal food industry*

O17

Stability of Transgene in *Nannochloropsis* sp.: Potential Vaccine Delivery System to Fish Against Vibriosis Disease

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Abstract: Background: Aquaculture is one of the most important sectors in agriculture but the occurrence of diseases causes a significant loss. In the aquaculture industry, vibriosis is one of the highly virulent diseases caused by gram-negative bacteria from the genus *Vibrio*. Vaccination has been proven to be effective in treating the disease but has been proven to be laborious. This study focused on the use of transgenic microalgae, *Nannochloropsis* sp. as a vaccine carrier. High stability of transgene expression is essential for functional genomics studies using transformation approaches and for the application of genetic engineering. **Methods:** Transgenic *Nannochloropsis* sp. harbouring an outer membrane protein kinase (*OmpK*) gene fragment of the *Vibrio* species namely V1, V2, CV1, CV2, CPV1, and CPV2 were utilized in this study. The stability of *OmpK* gene in transgenic *Nannochloropsis* sp. over several generations was evaluated. DNA and RNA from the *Nannochloropsis* sp. transgenic lines were extracted and subjected to PCR amplification of *OmpK* gene fragment. **Results:** The *OmpK* gene fragment was successfully amplified and expressed up to the fifth generation (F5). For V1, V2, CV1, and CV2 the gene was presented and expressed in F4 and F5; but for CPV1 and CPV2 the *OmpK* genes were presented upto F4. **Conclusions:** Based on the results obtained present study concludes that *Nannochloropsis* sp. is suitable as vaccine carriers and recommends *Nannochloropsis* sp. utility to ameliorate vibriosis as a vaccine carrier.

Keywords: Microalgae, *Nannochloropsis* sp., transgenic, vaccine, vibriosis

O18

A Validated UPLC Method for Simultaneous Estimation of Diacerein and Aceclofenac in Bulk and Pharmaceutical Formulation

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Abstract: Background: Present study was intended to develop and validate a simple, exceptionally cost-effective, accurate, quite precise, and highly reproducible analytical method for simultaneous estimation of Diacerein and Aceclofenac in bulk and Pharmaceutical formulation. The new Ultra Performance Liquid Chromatography technique was developed. **Methods:** The separation has been done on column ACQUITY UPLC BEH Shield C18 (50 x 2.1 mm), 1.7µm (40°C temperature). The mobile phase contains acetonitrile and water (ACN: WATER) (60:40), pH 4.5 with orthophosphoric acid (OPA). The flow rate was set at 0.4 ml /min and detected at 268 nm with a PDA detector. The mobile phase was sonicated for 15 min. before use. 5µl of samples of standard stock solution and Tablet solution were injected. Different trials were performed to separate diacerein and aceclofenac. The total run time of the detection was 4 min. The developed method was validated against different validation parameters. **Results:** The retention times were obtained at 1.762 min. and 2.891 min. for Diacerein and Aceclofenac respectively. With an accuracy of less than 2% RSD, LOQ for Diacerein and Aceclofenac was found as 2.98µg/ml and 5.9041µg/ml respectively similarly LOD was 0.9841 µg/ml and 1.9467 µg/ml. Precision %RSD for intraday and interday was found as 0.19 and 0.18 for Diacerein , 0.44, and 0.16 for Aceclofenac. Linearity was found in the range of 2.5-17.5 µg/ml and 5-35 µg/ml for Diacerein and Aceclofenac respectively. The method was found robust for changes in the flow rate, the ratio of the mobile phase, and detection wavelength. **Conclusions:** Based on the results present study concludes that the developed method was found to be satisfactory and can be used successfully for the determination of Diacerein and Aceclofenac simultaneously in the bulk and pharmaceutical dosage form.

Keywords: **U**PLC; Diacerein; Aceclofenac; accuracy; estimation

O19

Binding Activity of *Plasmodium knowlesi* Duffy Binding Protein Alpha Region II (*PkDBPαII*) Corresponding to High and Low Parasitaemia Isolates

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Abstract: **Background:** Invasion of *Plasmodium knowlesi* merozoite into human erythrocytes involves molecular interaction between the parasite's Duffy binding protein (*PkDBPαII*) and the Duffy antigen receptor for chemokines (DARC) on the erythrocytes. This study investigates the binding activity of human erythrocyte with *PkDBPαII* of *P. knowlesi* isolates from high and low parasitaemic patients in an erythrocyte binding assay. **Method:** The *PkDBPαII* gene of *P. knowlesi* from high and low parasitemia clinical cases were transfected into COS-7 mammalian cells and allowed to interact with erythrocytes at 1% hematocrit. The number and size of rosettes formed following transfection were determined in order to evaluate the binding activity. The size of rosettes was measured using Imaging Software NIS-Element Basic Research Version 3.07. **Result:** The PkDBPαII of *P. knowlesi* isolated from low parasitaemia cases produced a significantly higher number of rosettes with human erythrocytes compared to high parasitaemia case isolates (65.50 ± 12.85 and 17.17 ± 5.50, respectively). Interestingly, PkDBPαII of isolates from high parasitaemia cases formed significantly larger rosettes with human erythrocytes compared to rosettes formed by PkDBPαII of isolates from low parasitaemia cases (18,019.67 ± 12,991.67 μm^2 and 1,315.44 ± 622.98 μm^2, respectively). **Conclusion:** Association between rosetting and parasitemia levels remains to be clarified. Future studies need to be conducted to elucidate the role of PkDBPαII in erythrocytes invasion and its possible association with the parasitemia level.

Keywords: Duffy Binding Protein; malaria; *Plasmodium* spp.

O20

Development of Point-of-Care Loop mediated isothermal amplification-Lateral flow (LAMP-LF) assay for detection of *Plasmodium* species

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Abstract. Point of care (POC) diagnosis is a medical diagnostics test done at the time and place of patient care. Loop mediated Isothermal Amplification (LAMP) is potentially an ideal alternative molecular diagnosis method due to the fact that it is highly specific, efficient and does not require expensive equipment (Notomi, 2000). Whereas, Lateral flow assays (LFA) is a paper-based platform for the detection of analytes in complex mixtures. Coupling the methods together (LAMP-LFA), encompasses all the benefits of specificity, sensitivity and efficiency in a 'simple to read test strip' suited for point of care diagnosis. This research tackles the coupling of molecular diagnostics in a time efficient manner, from the process of DNA extraction to the endpoint interpretation in less than 2 hours.

Keywords: *Plasmodium*, Lateral flow assays, specificity, sensitivity

O21

Anti-Diabetic Effects and Antioxidant Potentials of Green Marine Seaweeds, Collected From Gulf of Mannar

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Abstract: Background: Marine seaweeds are known to exhibit potential biological activity, where phenolic compounds possess a variety of biological functions. The important pharmacological aspect of using marine polyphenols as a strong natural antioxidant and it has been suggested to play a vital role in the alleviation of diabetes mellitus. **Method:** The present study aims to investigate the antioxidant potential of four green marine seaweeds namely *Chaetomorpha crassa*, *Caulerpa racemosa*, *Caulerpa verticillata*, and *Caulerpa scalpelliformis* in the management of Type 2 diabetes mellitus. *In vitro* evaluation of the antioxidant activity was assessed by employing ABTS, Phosphomolybdenum assay and Metal chelation activity methods. **Results:** The results showed that among four marine seaweeds, the ethanolic extracts of *Caulerpa verticillata* has recorded the highest total flavonoid content (66.19±0.002mg QE/g) and antioxidant activity in ABTS (96.95±0.411 %), Phosphomolybdenum assay (323.28±0.006µM) and Metal chelation activity (71.92±0.48%). The IC50values of *C verticillata* was found to be 0.42mg/ml for ABTS and 0.78mg/ml for Metal chelation activity respectively. In addition, ethanolic extracts of *C verticillata* showed a highly significant inhibition of α-amylase (70.64±0.39% with IC50 of 0.420mg/ml) and α-Glucosidase (64.07±0.33% with IC50 of 0.068mg/ml) in a dose-dependent manner. **Conclusion:** From the results, it is understood that that *C. verticillata* could be a good choice to reduce the hyperglycemic condition by inhibiting the carbohydrate hydrolyzing enzymes and maintain the tolerable oxidative stress.

Keywords: Green marine seaweeds, Antioxidants, ABTS, Phosphomolybdenum, Metal chelation, α-amylase, α-Glucosidase.

O22

In Silico Selection of RNA Aptamer against Progesterone Receptor Using Computational Docking Employing Progesterone Response Elements-Derived RNA

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Abstract: Background: Aptamers are single-stranded DNA or RNA oligonucleotides generated by SELEX that exhibit high binding affinity and specificity against a wide variety of target molecules based on their unique tertiary structural conformation. The tediousness and rigor associated with certain steps of the conventional SELEX intensify the efforts to adopt in silico approaches in developing RNA aptamers. That said, we report an in silico selection of RNA aptamer to the progesterone receptor (PR) using RNA sequences derived from human progesterone response elements (PREs). PRE has a natural affinity against the progesterone receptor and therefore the derived RNA sequences can serve as a potent pool of molecules for the in silico selection of RNA aptamers. Methods: Sixty-four different RNA analogs of the corresponding PRE sequences were subjected to secondary and tertiary structure determination and their likelihood to emerge as PR aptamer was examined using PatchDock. The sequence with the highest score was selected as the candidate for binding validation. These in silico predictions need further confirmation by a method such as gel shift assay. Results: In its entirety, we selected a candidate RNA (PRapt31; 5′-AGAACACCUUGUUCU -3′), which showed the highest docking scores of 10806. Conclusion: In conclusion, PRapt-31 is identified as the potential aptamer using the in silico-based aptamer selection. The selected aptamer will be validated by in vitro binding assay.

Keywords: in silico; RNA aptamer; progesterone receptor; docking

O23

Screening and identification of cellulose-degrading bacteria from termites: Towards developing a termite and cellulose-based sustainable nutritious solution in resource-limited settings

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Abstract. Background: Cellulose ($C_6H_{10}O_5$) is an organic compound consisting of a linear chain of several hundred to thousands of β (beta) linked D-glucose units found in a plant cell's walls. Humans are incapable of digesting cellulose, due to the lack of cellulolytic enzymes. On the other hand, other organisms (mostly animals) such as herbivores such as cows, koalas, horses and termites, all digest cellulose. Termites are among the most successful groups of insects on earth, colonizing most landmasses and have the ability to digest cellulose using enzyme mostly from symbiotic cellulolytic microorganisms present in their gut and within themselves. Cellulose is one of the most abundant materials on Earth and is one of the unused materials by humans as we are incapable of digesting it. Hence the overall aim of this project is towards developing a termite based or enzyme cocktail based method to produce a nutritious solution that can be used as food in resource-limited settings. **Method:** As the preliminary work in this study, we have collected three species of termites from AIMST University, Kedah, Malaysia. CTec2 (Novozymes), cellulase mix that can degrade cellulose to fermentable sugars was used as a control cellulase enzyme. The activity of cellulase was measured by DNS (3,5-dinitrosalicylic acid) method through the concentration of reducing sugars liberated using this method. One per cent solution of carboxymethylcellulose (CMC) was used as a substrate. Carboxymethylcellulose agar (CMCA) was used to qualitatively detect the cellulose digesting capability of the termite homogenate. Using 16S rRNA PCR, DNA sequencing and BLAST analysis, the bacteria isolated from the termites were identified and their cellulose digesting properties were analyzed. **Results:** In this study, we have optimized the cellulase assay and demonstrated cellulase activity from the termite lysate. This finding was further substantiated by CMCA method in which all the termite homogenates showed zones of cellulase activity. The organisms isolated from four of the termite samples were successfully identified as *Kosakonia oryzendophytica* (1A), *Bacillus paranthracis* (1B), *Bacillus megaterium* (3D1) and *Bacillus pumilus* (5D1). The partial 16S rRNA gene sequence of the isolate *K. oryzendophytica* (1A) was submitted to Genbank with accession number MN991174. **Conclusion:** In this study, we have demonstrated that the termite homogenate had cellulolytic activity. Furthermore, 4 strains of bacteria having cellulase activity was identified. The outcome of this study will form a base for research and developing a termite and cellulose-based sustainable nutritious solution in a resource-limited setting.

Keywords: Termite, cellulase, cellulose, bacteria

O24

Health risk assessment of Macro, Trace-elements and heavy metal in various Indian Antidiabetic Polyherbal formulations

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Abstract. Background: Diabetes mellitus, a global pandemic, can be holistically managed with the use of Polyherbal formulations which is an accessible form of treatment in developing countries due to fewer side effects, economical and easily available. Commercial polyherbal formulation lacks systemic based scientific study, thus it is suspected to be associated with several contaminations and related toxicities, one of which is considered to be elemental health hazards. Therefore, the present study is designed to assess six selected Antidiabetic Polyherbal formulations from the Indian market for their element contents, quality, and health risk assessment. **Methods:** Concentrations of 35 essential and non-essential trace-elements were quantified by Handheld X-ray spectrophotometer and health risk assessment was calculated by estimated daily intake (EDI) and Total hazard quotient (THQ). **Results:** Elements were found to be in a vast range of concentration in the tested APH. Among the 35 elements analyzed, Ca (23100±0.033ppm) and K (14800±0.021 ppm) in "MH" and Zn (15600±0.025 ppm) in "DB" were found to be the highest. Lowest concentrations of Rb and Nb (3±2 ppm) were observed in the formulation "MH" and "SN" respectively. THQ of all the elements was calculated to be less than unity except for Rb in the formulation "MA". Rb is rarely associated with toxicities as it is rapidly excreted in sweat and urine**.** V, Co, Ni, Cu, As, Se, Y, Ag, Sn, Sb, Ba, W, and Hg were absent in all the APH. **Conclusion:** Results of the present study indicated the presence of essential elements some of which are important for the management of diabetes and hence can be considered as safe for use.

Keywords: Antidiabetic Polyherbal formulation, Heavy metals, Trace elements, Marco elements, Health risk assessment, Handheld X-ray spectrophotometer.

O25

Biosynthesis of Copper Oxide Nanoparticles and Its Utility in Organic Synthesis

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Abstract: Background: In recent, Biosynthesis has been considered as one of the eco-friendly approaches to prepare various nanomaterials. Also, while preparing such nanomaterials it's not much toxic or non-toxic when compared to their bulk materials due to the support of biomolecules. **Methods:** Exclusively in the current paper, we have scrutinized the biosynthesis of copper oxide nanoparticles by utilizing plant extract. We procured the leaf powder from the commercial Ayurveda shop in Vellore District. The plant extract has been acted as reducing, capping, and stabilizing agents. **Results:** This process has been carried out at 60 ^{o}C for the duration of 3 h. The calcination process has been further continued for 3 h at 300 ^{o}C. The isolated CuO NPs has been confirmed with the support of UV–Vis absorption spectroscopy, Scanning Electron Microscopy (SEM), Transmission Electron Microscopy (TEM), and Energy Dispersive X-Ray Analysis (EDAX) analysis. The synthesized CuO is a spherical size with a range of up to 30 nm. Further, the synthesized nanoparticles have been utilized in organic synthesis. **Conclusions:** We have successively synthesized CuO NPs via bio-approach and successfully utilized in organic synthesis.

Keywords: Biosynthesis; CuO; nanomaterials; Organic Synthesis.

O26

Molecular Interaction analysis of Lanosterol derivatives from *Laetiporus versisporus* as potential inhibitor of BCL-2

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Abstract. Background Edible mushrooms are rich in bioactive compounds which have various medicinal values such as anti cancer activity, anti-diabetic activity and immunogenic activity. In this study, lanosterol derivatives from *Laetiporus versisporus* namely laetiposide B, laetiposide E, laetiposide F, laetiposide G, eburicoic acid, trametenolic acid and sulfurenic acid were taken for docking analysis against Bcl-2 to predict inhibitory mechanism. **Materials And Methods:** The bioactive compounds from of *Laetiporus versisporus*, were docked with the BCL2 protein that was dysregulated by the downstream consequence of perturbed signaling cascades and not by mutations in HCC. Structures of bioactive compounds were prepared using Chemsketch, optimised and converted into its 3D PDB structure. The target protein, BCL-2 was retrieved from RCSB PDB. The protein and ligands were docked using Autodock 4.2 software and interaction visualized using Biovia Discovery studio. **Results:** Among the seven lanosterol derivatives, the Trametenolic acid revealed promising inhibitory potential against BCL-2 with binding energy of –9.38 kcal/mol and forms three hydrogen bond interactions as compared to its known standard cyclophosphamide having binding energy of –6.68 kcal/mol and three hydrogen bond interactions. **Conclusion:** From the molecular interaction studies, lanosterol derivatives from *Laetiporus versisporus* shows that these compounds may act as hepatocellular carcinoma and has to be taken up for experimental work against hepatocellular carcinoma.

Key Words: *Laetiporus versisporus, Lanosterol,* hepatocellular carcinoma, BCL-2, Molecular docking

O27

Isolation and Characterization of Biosurfactant Producing Bacteria from Hot Spring Zone of West Kameng District, Arunachal Pradesh, India

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Abstract: Background: Biosurfactants are surface-active compounds synthesized by microbes like bacteria, fungi, and yeast. These molecules increase the biodegradation of insoluble pollutants. In this study biosurfactants were produced and characterized for the first time using bacteria isolated from the Dirang hot spring area of West Kameng District, Arunachal Pradesh. **Methods:** The Streak plate method was used for bacterial isolation. Screening and the kinetic study was performed by using the technique of emulsification assay. Characterization of isolated bacteria was done by performing Gram staining and biochemical tests. Optimization of different carbon sources for biosurfactant production was done by using three different oils i.e., Crude oil, coconut oil, and kerosene oil. **Results:** 22 bacterial isolates were isolated from the collected samples.12 biosurfactant producing bacteria were selected from these isolates, out of which 3 most efficient isolates were identified as *Pseudomonas* sp., *Micrococcus* sp., and *Stenotrophomonas* sp. Kinetic study showed the maximum biosurfactant production by *Pseudomonas* sp. (59.50%) on the 6th day of incubation followed by *Stenotrophomonas* sp. (59.09%) and *Micrococcus* sp. (52.94%) on the 8th day of incubation. Optimization of different carbon sources showed that the best carbon source for *Pseudomonas* sp. and *Stenotrophomonas* sp. was kerosene with 52.94% and 40.08% of production respectively. *Micrococcus* sp. showed the maximum production of 41.17 % with crude oil. The results of this study confirmed that there is a high diversity of biosurfactant producing bacteria in the ecosystem of Dirang Hot spring and by application of these bacteria in environmental problems can be assisted. **Conclusions:** The present study highlights and discusses the bisurfactant producing bacteria that are present in these hot springs which produced a significant biosurfactant that can reduce the stress of that area by reducing the surface tension between the molecules.

Keywords: Biosurfactant producing bacteria; Biosurfactant; Hot Spring; West Kameng District.

O28

Evaluation Of *In Vitro* Antioxidant and Antidiabetic Effect Of Water Extract From Oil Palm Fibre

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Abstract. Background: Malaysia is one of the leading agricultural countries in the world with exports, including palm oil. Many bioactive compounds have been reported extracted from Palm oil but not much on oil palm fibre. However, there are a few reports on the biological activities of Pyroligneous acid and Lignin extracted from oil palm fibre. **Aim**: The current research focused on the evaluation of in vitro antioxidant and antidiabetic effect of water extract from oil palm fibre **Method:** In vitro evaluation of free radical scavenging ability of water crude extract of the Oil palm fibre (OPF) was done on free radical generated by DPPH, nitric oxide, hydrogen peroxide, lipid peroxidation, FRAP and metal ion chelating. The in vitro antidiabetic study was done by evaluating the inhibitory effect of OPF on the activities of alpha-amylase, and alpha-glucosidase and acarbose were used as a standard drug. The oil palm fibre extract concentration ranged from 10µg/ml to 100µg/ml. **Result:** The results showed OPF inhibited the free radicals generated by DPPH, Nitric oxide, hydrogen peroxide, Lipid peroxidation, FRAP and metal ion chelating and inhibited the activities of alpha-amylase, and alpha-glucosidase compared to standard drug acarbose. **Discussion and conclusion:** OPF possess a powerful free radical scavenging property and antidiabetic properties through the inhibition of alpha-amylase, and alpha-glucosidase activities. OPF possess *in vitro* antioxidant and antidiabetic property.

Keywords: Oil palm fibre; antidiabetic; antioxidant; alpha-amylase; alpha-glucosidase

O29

Conversion of Bakery Waste Materials into Compost and Evaluation of Its Physico-Chemical Properties and Phytotoxicity

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Abstract: Background: Compost is considered a soil-amending product that can be used for soil improvement and to increase the productivity of organic vegetable crops. Composting can be an alternative solution for solid waste management. **Methods:** In this research, various bakery wastes and a bulking agent such as cow dung were used to produce compost. The bin composting method was applied in this research. Commercial Effective Microorganism was used to study its effectiveness in composting bakery waste compared to the common way of composting. Six compost trials were designed by using different ratios of feedstocks such as creamy and non-creamy bakery waste, paper boxes, eggshells, cow dung, dry leaves, and Effective Microorganism (EM). For the assessment of the maturity, stability, and quality of the compost, various physical and chemical parameters were monitored routinely such as temperature, pH, electrical conductivity (EC), moisture content, color, appearance, odor, water holding capacity (WHC), phytotoxicity and colour intensity of water extract, total organic carbon (TOC), total nitrogen (N), phosphorus (P), potassium (K) and C/N ratio. **Results:** All the 6 compost trials had reached the 4 important phases of temperature which are mesophilic, thermophilic phase, second mesophilic phase (cooling phase), and maturation phase. The pH, EC, N, P, K of every compost trials comply with standard compost requirements. Phytotoxicity study proved that all the compost trials were phytotoxic-free when tested with *Phaseolus vulgaris (Green Bean*). The water holding capacity of all the 6 trails ranges from 2.18 to 4.30 g water/g dry material. Compost trials C1, C2, C5, and C6 achieved C/N ratio ranged from 10.84 to 12.95 which is considered within the satisfactory limit. **Conclusion:** The results showed that bakery waste can be turned into compost and the quality of the compost without the addition of effective microorganisms and eggshells is better.

Keywords: Bakery waste, composting, food waste, effective microorganism, physicochemical analysis

O30

Bioactive compound loaded nanoemulsion from edible fruit against insects

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Abstract: Background: Nanoscience is the study of structure and materials within nanometers that is used to increase the bioavailability of herbal drugs. **Methods:** The aim of this work is to presents the Nano formulation for increasing the aqueous solubility. The nanoemulsion of bioactive compound from *C. edulis* was formulated using surfactants as an emulsifier. The *C. edulis* extract mediated synthesis of nanoparticles were prepared by standard protocol and this nanoparticles used to load the bioactive compound from *C. edulis*. Initially, nanoparticles were well dispersed in emulsifier and further loaded with bioactive compound. **Results:** The Prepared formulations were characterized by UV-Vis spectrophotometry, FT-IT, SEM, Zeta potential and nanoparticle analyzer. The formulated was assessed by using three different agriculture insects. The particles were having spherical shape and the insecticidal activity was showed significant results. **Conclusions:** These synthesized formulates were found to be more effective against tested insects.

Keywords: *C. edulis*; nanoformulation; nanoparticles; insecticidal activity.

O31

Co-occurrence of mutations in Quinolone Resistance Determining Region (QRDR) observed in global *Escherichia coli* genomes - alarm for Fluroquinolone therapy in Urinary Tract Infection

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Abstract. Background: Fluoroquinolones (FQ) have been the most preferred treatment for Urinary Tract Infection (UTI) caused by *Escherichia coli*. Unfortunately, the rapid rise in resistance mechanisms has complicated the treatment regimes. One of the most prominent mechanisms has been spontaneous mutations in Quinolone Resistance Determining Region (QRDR) of *gyr* A, *par* C and *par* E. The present study aimed to capture these mutations in QRDR region by dissecting the available whole genome sequences of *Escherichia coli* strains from Urinary Tract Infection patients originating from different parts of the world (Australia, Brazil, Colombia, Canada, China, Hongkong, Mexico, Saudi Arabia, Sweden, Slovakia, South Korea, Taiwan, UK, USA). **Methods:** Exhaustive screening of available genome data in NCBI revealed a total of 1074 complete genome (PacBio). The study retrieved the complete genome background information (n=1074) and segregated the cluster belonging to *E. coli* from UTI (n=30) for the year (2016-2019). The genomes were annotated and analyzed for detection of quinolone resistance genes, explicit mutations in QRDR, phylogenetic analyses (Multi Locus Sequence Typing-MLST) by using bioinformatics pipeline. **Results**: *E. coli* strains (n=7/30) showed the presence of quinolone resistance genes (*qep*A1, *oqx*A, and *oqx*B) in the plasmids. Further, we observed point mutations viz., S83L, and D87 N in *gyr*A (n=14); S80I and E84V in par C (n=10) and I529L in *par*E (n=9) as the predominant mutations across the strains (n=18). Importantly, the study found co-occurrence of S83L, D87N (*gyr*A) + S80I, E84V (*par*C) + I529L (*par*E) as the predominant combination of mutation pattern in UTI - *E. coli* strains (n=9). MLST revealed these strains belonged predominantly to the global clonal strain ST131. **Conclusion**: The UTI- *E. coli* genome showed co-existence of a common pattern of mutations in *gyr*A coding for DNA gyrase and *par*C and *par*E coding for topoisomerase IV as the predominant mode across the global isolates.

Keywords: Urinary Tract Infection, *E. coli*, QRDR, Mutations, Whole Genome

O32

Design, Molecular Docking and Drug-likeness Studies of Trioxane Derivatives as Novel Antimalarial Agents

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Abstract: ***Background:*** Malaria remains one of the most devastating infectious diseases affecting millions of people every year across the globe. *Plasmodium falciparum*, the deadliest malaria parasite, is responsible for most of the mortality associated with malaria infections. Artemisinin-based Combination Therapies (ACTs) are currently the frontline treatments against *P. falciparum* malaria. Because of the widespread emergence of drug-resistant strains of *P. falciparum*, the clinical utility of existing drug therapies including ACTs in the treatment of malaria has been increasingly limited. It has become a serious health concern which, therefore, necessities to develop novel drug molecules and/or alternative therapies to combat, particularly resistant *P. falciparum* malaria. The objective of the study was to develop 1,2,4-trioxane derivatives as novel antimalarial agents that would be effective against resistant *P. falciparum*. ***Methods*:** In our study, fifteen newer trioxane derivatives were designed by molecular modification of the 1,2,4-trioxane scaffold as possible antimalarial agents. Molecular modeling studies of trioxane derivatives were performed based on the CADD approach using Biovia Discovery Studio (DS) 2018 software. The protein-ligand docking study was carried out against *P. falciparum* falcipain 2 (FP-2) (PDB id: 3BPF) protein using the simulation-based docking protocol LibDock by flexible docking method. The assessment of drug-likeness, ADMET properties, and toxicity was also investigated. ***Results:*** The docking protocol was validated by re-docking procedure which confirmed the accuracy of the docking method with acceptable RMSD of less than 2 Å. Results of the docking study showed that among fifteen compounds three trioxane derivatives were found to possess a promising binding affinity with LibDock scores in the range between 117.16 to 116.90. Drug-likeness, ADMET, and toxicity properties were found to be satisfactory. ***Conclusion*:** Finally, it can be concluded that newly designed 1,2,4-trioxane derivatives can be further studied for *in vitro* and *in vivo* antimalarial activities for their possible development as potent antimalarial agents against resistant *P. falciparum* malaria.

***Keywords*:** 1,2,4-Trioxane; Pharmacophore; *P. falciparum*; Drug resistance; Molecular docking; Antimalarial

O33

Distribution of Available Phosphorus in a Sandy Loam Soil of Nigerian Sudan Savannah

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Abstract. This study was conducted to determine the distribution of available phosphorus in the Sandy Loam of the University of Maiduguri Teaching and Research Farm. Samples were collected based on pedological horizons and analyzed for Physico-chemical properties. The content of soil Phosphorus was found to be low, ranging from 2.80 – 9.10 mg/kg and was irregularly distributed all profiles studied. The soil reaction was slightly acidic to near neutral (6.02 – 6.92). A correlation analysis was run between the available phosphorus and soil pH, OC, CEC, clay content, and Total Nitrogen. A highly significant correlation was found to be between the soil pH and the available P ($r = 0.6284$, $p = 0.05$). Similarly, a significant correlation was observed between available P with O.C, CEC, and clay content. The low available P content of these soils suggested that supplemental P application is necessary for optimum production of field crops

Keywords: **Phosphorus content, Sandy Loam, Sudan Savannah**

O34

Photosynthesis of Silver Nanoparticles Using Plant Extracts of Medicinal Importance

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Abstract: Background: Utilization of nanotechnology with biotechnology is the most promising approach in the past decade. Antimicrobial resistance is increasing day by day due to multiple factors therefore; development of novel drugs is a need of current medical research. **Methods:** This study demonstrates the formation of silver nanoparticles by utilizing various plant extracts of *Sida cordifolia, Withania somifera, Grewia asiatica, Trigonella foenumgracecum, Acorus calamus, Punica granatum, Camellia sinensis, Callicarpa macrophylla, Cinnamomum tamala, Areca catechu, Foeniculum vulgare,* and *Syzygium aromaticum*. This method is rapid, easy, and an evaluation of the chemical and physical methods is an eco-friendly alternative. Antibacterial activity of formed silver nanoparticles was tested against six pathogenic cultures *Enterococcus sp., Klebsiella sp., Proteus sp., Pseudomonas sp., Shigella sp., and Streptococcus sp.* **Results:** Results of the present study demonstrated the formation of silver nanoparticles which showed significant inhibition of the tested pathogenic microorganisms. Thus, this study revealed that the silver nanoparticles synthesized by this green route have an inhibitory effect on the tested pathogenic strains. These plant extracts could be the great potential for the formulation of drugs against various infectious agents. **Conclusions:** This study found that plants can be a better source for the synthesis of SNPs using plant extracts for making nanoparticles that are affordable, quite simply scaled up and environmentally benign. The synthesis of silver nanoparticles by the use of plants is a quite new, fresh, and innovative approach that leads towards a truly green chemistry pathway. This renewable approach has a wide range of advantages such as to scale-up processes, for economical viability in a very safe way.

Keywords: Antimicrobial; Nanoparticles; Pathogens; Photosynthesis

O35

In silico Protein Structure Analysis and Metabolic Pathway Study on Genes Associated with Acute Myeloid Leukemia (AML)

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Abstract. Purpose: Acute myeloid leukemia (AML) is a blood cancer that forms when the blast is formed from bone marrow and the cells are not completely matured. According to the National Organization of Rare Disorder, AML is found to affect 5 in 100,000 people in the United States. Although AML is a rare disease because it affects very few people but the survival rate is very less. AML is caused by a genetic modification which is chromosomal translocations that aim the transcription factors such as members of the core binding factor family. In normal circumstances, these cells must develop into white blood cells and ward off infections. In AML, abnormal white blood cells along with red blood cells and platelets are formed and start to take up the place of normal blood cells. It is found that the mutated gene undergoes transcription and translation processes to produce the mutated protein. There is a list of proteins that are associated with AML formation in humans. **Methods:** In this study, we had listed out the genes which are found to be mutated and associated in AML formation. Five protein sequences were selected and retrieved from UniProt. **Methods:** database. The sequences were then subjected to protein modeling using the Swiss Model database. After running the protein sequence in the Swiss Model, several results were obtained such as the protein model, Ramachandra plot, protein size, and residue numbers. These results are used to analyze the protein structure. A metabolic pathway study for each protein is also done using the KEGG pathway database. This study shows how the protein is associated with different cell activity which could lead to AML **Results:** The result of this study maps out a clear pathway on how the mutated gene causes AML in humans and also a clear picture of their neighboring metabolic pathways which are eventually affected. **Conclusion:** There are many genes associated with the formation of AML in humans and leading them to be also diagnosed with other diseases due to the disruption in the normal metabolic pathways. These results can be used for extensive studies concerning AML in the future and can be a reference for other researchers for targeted gene study.

Keywords: Acute Myeloid Leukemia (AML), UniProt, Swiss Model, KEGG Pathway, metabolic pathway.

O36

Two Successes out of Three: DNA Barcode Identification of Malaysia Ferns

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Abstract: Background: The COVID-19 crisis is a wake-up call to reset our attitude and approach to nature. Identifying and understanding the relationships among the species in our shared space is vital for human flourishing. Morphological identification in plants requires taxonomist, access to type species and taxonomic literature – all not readily available, and impeded by payment barriers. DNA barcoding which compares a DNA sequence with an online database of sequences of all species has democratized species identification. However, the method still needs optimization, and the database lacks samples from all geographical regions. This study aimed to test the feasibility of identifying three Malaysian ferns based on the BLAST and tree topology analysis of non-coding *trnH-psbA*, and *trnL-F* DNA sequences. **Results:** The BLAST analysis of *trnH-psbA* and *trnL-F* loci was consistent in identifying two of the unknown species as *Pteris vittata* and *Pronephrium triphyllum* respectively. While tree topology did not support the identity of *P. triphyllum*, morphology confirmed identifications of both *P. vittata* and *P. triphyllum.* In the third species, the BLAST analysis of the two loci did not provide consistent species assignment but tallied at genus level assignment, that is, it was another species of Pteris. Tree topology based on *trnL-F* suggests it is not *Pteris majestica*, and morphology indicated that the identification using *trnH-psbA* as *Pteris natiensis* is more likely. **Conclusion:** DNA barcoding is unable to confirm the identification of all species, though it narrows down the possible identities for a morphological search. One possible reason why barcoding is not always successful is the incomplete database. We recommend populating the database with sequences of more species, including those from different geographical regions to reflect the intraspecific variation. We also support the usage of more than one locus and data analysis method in DNA barcoding for confidence in the assigned identities.

Keywords: Ferns, species identification, DNA barcoding, trnH-psbA, trnL-F

O37

Knocking-out of potential virulence associated non-protein coding RNA gene (PmiR-137) in *Proteus mirabilis* to understand its role in pathogenesis

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Abstract. Background: *Proteus mirabilis* is a Gram-negative, facultatively anaerobic rod-shaped bacterium, best known for its form of multicellular surface mobility termed swarming. *P. mirabilis* causes symptomatic urinary tract infections (UTI) such as catheter-associated urinary tract infections (CAUTI), urolithiasis, acute pyelonephritis, and wound infections. Our recent study revealed 240 Hfq-associated novel non-protein-coding RNAs (npcRNAs) in *P. mirabilis*. One npcRNA of interest is PmiR-137, which is predicted to regulate the virulence by association with the mRNA of fimbriae and flagella proteins. **Objectives:** To understand the function of PmiR-137 by knocking-out the gene from *p. mirabilis* genome. This is followed by the characterisation of the knock-out strain. **Material and methods**: Plasmid pkD46 was transformed into *P. mirabilis* and screened using an ampicillin marker. **The DNA fragment** with a kanamycin resistance gene, FRT sites, and 100 bps of homologous sequence from the flanking regions of PmiR-137 gene was amplified by PCR and transformed into *P. mirabilis* with pkD46. To detect PmiR-137 mutants, the transformed colonies were selected on kanamycin plate and verified using FRT-specific primers. **Results**: The plasmid with lambda red-recombinase gene, pkD46 was successfully transformed into *P. mirabilis*. The DNA fragment was further transformed into *P. mirabilis* with pKD46. Based on the screening of colonies with several specific primers, the knock-out of PmiR-137 from *P. mirabilis* was successful. Conclusion: We successfully knock-out PmiR-137 from *P. mirabilis*. Further confirmation of this knock-out will be carried by sequencing analysis and the mutant strain will be used to study the functional characterization of PmiR137.

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

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

O38

Review of Clinical Symptoms and Laboratory Tests during COVID-19 Lockdown in Jos, Plateau State, Nigeria

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Abstract. Background: Corona Virus Disease (COVID-19) is a Public Health challenge affecting more than 90% of the world's countries as reported by WHO in 2020. Preventing symptoms for the disease include fever, cough, general body pains, and headache. Laboratory tests result play an important role in evidence-based diagnosis and therapeutic management of patients. Evaluating the pattern of presenting clinical symptoms and laboratory requests by physicians during the COVID-19 lockdown will provide surveillance useful for the implementation of bioinformatics. This study sought to describe the different types of clinical symptoms and laboratory tests common during this period due to the pandemic. **Methods:** A retrospective study was conducted at Kauna Specialist Hospital, Jos, Plateau State, Nigeria from March 2020 to June 2020. The demographic characteristics of the patients were retrieved from the Laboratory Outpatients register. Data generated were analyzed using Excel and presented using frequency distribution, percentages, means, maximum, and minimum. **Results:** A total of five hundred and sixty-eight (568) records were retrieved from the outpatients' book. Out of this, 199(35%) were males while 369(65%) were females. Mean, minimum and maximum ages for the female attendees were 31years, 2years, and 65years respectively while those for the male attendees were 28years, 2years, and 70years respectively. A total of 1,012 laboratory requests were made which comprised Malaria parasite 383(37.8%), Widal test 282(27.9%), Full blood count 234(23.1%), Urine analysis 39(4%). Based on the reported clinical symptoms, the majority of the patients presented with headache, fever and body pains 527(62.5%), chest pain, cough and sore throat 81(9.6%), nausea/vomiting, abdominal pains and watery stool 191(22.7%). **Conclusion:** While this study suggests that symptoms similar to that of COVID-19 were mostly presented, there were however no laboratory tests requested for the screening of this deadly infection, since the majority of the laboratory tests were more diagnostic than therapeutic. More work is needed in this environment on the inclusion of bioinformatics in routine Healthcare provision.

Keywords: COVID-19; Laboratory tests; Clinical Symptoms; Bioinformatics

O39

Bioconversion of Agroindustrial Waste into Industrially Important Haloalkaliphilic Protease by Marine *Bacillus* Specie Under Solid State Fermentation and Formulation of Biodetergent

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Abstract: Background: In recent years, agriculture waste quantity has been raised rapidly all over the world. This contributes to environmental pollution. One strategy in industrial biotechnology is to utilize these waste for the production of industrially important enzymes through microbial fermentation. This study aimed to isolate protease producing bacteria from various marine sources. This study also demonstrates the utilization of different agroindustrial substrates for enhanced protease production by isolated bacteria. **Methods:** A total of twenty-two marine isolates were isolated and purified. Based on qualitative gelatin hydrolysis assay strain MV9 showed maximum enzyme index and hence selected for further studies. Phenotypic identification of bacterial culture was done based on Bergey's Manual of Determinative Bacteriology. Qualitative assays were done for the assessment of the influence of salinity and pH on bacterial growth and protease production. Quantitatively, the effect of agroindustrial substrates as a carbon source on the production of protease using solid-state fermentation by MV9 was also analyzed. Two diluents were used to soak agroindustrial residues. **Results:** The isolate MV9 was characterized as *Bacillus* species. This strain grew well for up to 10% NaCl with proteolytic activity, while the isolate was also tolerated alkaline pH with remarkable production of protease. Based on these consequences, the strain is characterized as haloalkaliphilic. The results of solid-state fermentation showed that Diluent # 1 containing rice husk gave maximum units, while the use of wheat husk as substrate boosted protease activity with Diluent # 2. Due to the alkaliphilic nature of protease from MV9, washing assays of protease were also carried out and the outcomes were significant, as crude protease effectively removed blood stains from cotton fabric. **Conclusion:** These outcomes suggest the efficient use of agro-industrial waste as a carbon substrate and potential applications of alkaline protease in the detergent industry.

Keywords: Protease; Haloalkaliphilic; Solid-state fermentation; Biodetergent

O40

Morphological Changes in Planktons, as Indicators of Seasonal Variations

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Abstract: The morphological changes that occur in certain species of invertebrates in accordance with environmental condition are called Cyclomorphosis. The phenomenon has been noted in the dinoflagellates, rotifers, cladocerans, and much strikingly in the copepods. The degree to which the Cyclomorphosis is developed within different populations of the same species is variable. Although the seasonal incidence of the change is determined by environmental factors, there may also be certain other inherited diversity in different species to react to these factors. The seasonal changes of form in certain Rotifers are so striking that the summer and winter forms of the same species would certainly be supposed to represent different species by an observer, unacquainted with the facts. Although there is no significant change in the physiological processes in these planktons but a great change in the morphology as well as existence of polymorphism is observed, rather to some extent it is true that the cyclomorphic changes do have some adaptive significance too. It involves the alternation of different morphological units in a species in accordance with the climatic as well as environmental changes. The total body size may increase, decrease, or remain the same throughout the cycle, depending on the species. The change that occurs in the shape of Lorica, size, and number of outer ornamentation like spines and the shape of mastax in accordance with body shape is remarkable. The polymorphic forms and the morphological changes in accordance with the environment in the case of some of the zooplankton and Phytoplankton is discussed.

Keywords*:* Zooplankton, Phytoplankton, Cyclomorphosis, Environmental factors, Seasonal Variations

O41

The effect of Aflatoxin B1 and Ochratoxin A on tumor retated genes in MCF7 and MCF10A after the knockdown of *cMyc* and *p53* using siRNA

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Abstract. Background: Mycotoxin contamination of food commodities caused by fungal strains such as *Aspergillus* and *Penicillium* is common in countries with tropical weather. Mycotoxins have been reported to cause severe food poisoning, liver damage, and carcinogenic to kidney and liver cells. In this study, the effect of Aflatoxin B1 on MCF7 cells with a knocked down *cMyc* and the effect of Ochratoxin A on MCF10A cells with a knocked down *p53* was investigated to determine the level these toxins would affect these cells in the absence of genes function. **Methods:** The first step was the designing of *T7-cMyc* and *T7-p53* primers through E-RNAi design of RNAi construct website. cDNA from MCF7 and MCF10A was used to amplify *p53* and *cMyc* gene along with the T7 promotor using PCR. The final PCR product was used to synthesize siRNA using in vitro transcription and T7-p53, *T7-cMyc* primers. MCF7 and MCF10A were seeded in the density of $0.3x10^5$ in 6 well plates using respected growth media for each cell line and were allowed to reach the confluence of 1.2×10^6. Once cells are confluence, the old media was aspirated, and cells were washed with 1_X PBS buffer two times. siRNA prepared was used to transfect the cells by the means of lipofectamine 2000, and cells were incubated for different time points to determine at which time point the gene knockdown was at maximum. Once the desired time point with the maximum knockdown was identified, fresh media containing (Aflatoxin B1 1.2 µg/ml) for treating MCF7 and (Ochratoxin A 5.7 µg/ml) for MCF10A was added to the cells and cells were incubated for 48 hours at 37° C with 5% CO2. RNA was extracted to conduct gene expression analysis using real-time quantitative polymerase chain reaction (RT qPCR) for the selected oncogenes and tumor-suppressing genes. **Results:** Knocking down *p53* in MCF10A caused *BRAC1*, *BRCA2*, *HER1*, *HER2* and *cMyc* to be upregulated and post treatment, *BRCA2*, *HER1*, *HER2* and *cMyc* were downregulated. Knocking down cMyc in MCF7 upregulated BRCA1, BRCA2, p53, *HER1*, and *HER2* but post treatment, *BRCA1*, *BRCA2*, *p53*, *HER1*, and *HER2* were downregulated. **Conclusion:** The exposure to both toxins post gene knockdown using siRNA caused changes in gene expression of tumor-related genes within MCF7 and MCF10A. This change in gene expression could make cells malignant and increase the risk of breast cancer.

Keywords: Mycotoxins, Aflatoxin B1, Ochratoxin A, MCF7, MCF10A, siRNA, cMyc, p53.

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O42

Systematic Identification and Characterization of *Ae. aegypti* Long Non--Coding RNAs

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Abstract. Dengue is a mosquito-borne viral disease that is caused by dengue virus (DENV). It is flu-like fever, which can develop into severe dengue haemorrhagic fever, causing serious illness and death, in tropical and sub-tropical areas. Dengue is transmitted by mosquitoes of the genus Aedes, and *Ae. aegypti* is the primary vector. Despite many attempts to control the spread of dengue such as by mosquito control, most are not efficient yet. Studying molecular interaction between the mosquito vector and virus will provide insight into molecular mechanisms underlying virus infection. Protein-coding genes have been studied extensively in *Ae. aegypti*, especially in virus host interaction. Whereas, in the last few years, long non-coding RNAs (lncRNAs) have gained the attention of many scientists due to their potential functions in many biological processes, including virus infection. LncRNAs are RNAs that are more than 200 bp in size and do not code for proteins. This research aims to systematically identify and characterize lncRNAs in *Ae. aegypti*. A total of 117 public RNA-sequencing libraries were used as raw inputs in the lncRNA prediction pipeline. In this project, a total of 4,689 novel lncRNAs transcripts were identified in *Ae. aegypti*, of which 2,064 were intergenic, 2076, and 549 were intronic and antisense respectively. Similar to previous studies, it was found that lncRNAs in *Ae. aegypti* share many characteristics with lncRNAs in other species, such as low expression, low GC content, short in length, and low sequence conservation. These newly identified lncRNAs will enrich the annotation of the *Ae aegypti* genome reference. Results from this study will provide a valuable bioinformatics resource for future research in *Ae. aegypti,* especially in the field of non-coding genes.

Keywords: Long non-coding RNA, *Aedes aegypti.*

POSTER PRESENTATION ABSTRACTS

P1

The Effect of Bisphenol A Exposure below No-Observed-Adverse-Effect-Level (NOAEL) on Uterus of Adult Female BALB/c

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Abstract: Background: Endocrine Disrupting Chemical (EDC) has the ability to disrupt the homeostasis of endocrine systems and lead to adverse effects in reproductive tissues. The wide use of Bisphenol A in the manufacture of daily products, from home appliances to food packaging,make it one of the most studied EDC. Exposure of BPA below No-Observed-Effect-Level (NOAEL) is considered safe for human exposure. However, emerging reports regarding the detrimental effects of doses below NOAEL in reproduction have raised concerns. This study aims to observe the effects of BPA exposure below NOAEL on the uterus of sexually mature female BALB/c mice. **Methods:** The mice aged 8 to 12 weeks were randomly allocated into three groups. Group 1 (control) received the vehicle comprising tween 80 + distilled water (1:9 v/v), Groups 2 and 3 received BPA at doses of 1 mg/kg bw/day group and 3 mg/kg bw/day respectively. Treatments were administered via oral gavage for 7 days. The morphology of the uterus was analyzed. **Results:** Bodyweight, as well as relative uteri weight to body weight, were not significantly different between the three groups. Although not significant, a decreasing trend in the height of lumen was observed in Groups 2 and 3 mice, as well as the height of endometrium of Group 2 compared to the Control Group mice. On the other hand, an increment trend was observed in myometrium height of Group 2 and 3 mice, as well as endometrium height of Group 3 compared to Control Group. Because of the trends observed further studies on different doses and different organs are required. **Conclusion:** Based on the results obtained in the present study it can be concluded that Bisphenol A exposure below the No-Observed-Adverse-Effect-Level (NOAEL) has the potential to interrupt normal uterine development.

Keywords: Bisphenol A; uterus; NOAEL; reproduction

P2

Characterization of Atorvastatin Liquid Crystalline Nanoparticle as Drug Delivery Vehicle in HepG2 Cells

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Abstract. Background: Atherosclerosis is the accumulation of plaque on the arterial wall that increases the risk of potentially serious health problems, including stroke, myocardial infarction, and angina. Statin, a cholesterol lowering drug is the most common therapy used but discontinuation of this drug has been reported due to concern towards its toxicity. Treatment via nanoparticle-drug internalization provides a site-specific and possibility to develop a controlled released treatment. **Methodology:** Liquid crystalline nanoparticle (LCN) is prepared from a binary mixture of citrem and soy phosphatidylcholine (SPC) with the weight ratio of 1:1. Resulting materials subsequently exposed to high-energy input (ultrasonification) to synthesis the nanocarrier. The structure and its crystallographic space groups will be determined via Small-angle X-ray scattering (SAXS) and transmission electronic microscopy (TEM) for visualization. Zetasizer will be utilized to detect the particle size, zeta potential, and molecular weight. The further characterization for melting point and surface adsorption is conducted through differential scanning calorimetry (DSC) and Fourier transform infrared spectroscopy (FTIR) were also conducted. The encapsulation efficiency of Artovastatin was conducted prior to in vitro drug loading and release study. The cytotoxicity profile of the system on HepG2 cells will be determined via MTT Assay. **Result:** The formulation was predicted to self-assemble into bicontinuous cubic phase (V2) - cubosome with the topology of either Ia3d, Pn3m, and $Im\bar{3}m$. The atorvastatin is positioned inside the lipid bilayer of the structure. The stiffness and high viscosity of the nanoparticle ensure a slow-release matrix for drugs. **Conclusion:** This study on the physicochemical characteristic and profiling of the nanoparticle provides a better understanding of its potential as a drug nanocarrier for atorvastatin in atherosclerosis treatment.

Keywords: atherosclerosis, statin, nanoparticle, cholesterol, cytotoxicity

P3

Anticancer Effects of Combined Retinoic Acid and Ginger Extract on Hela Cervical Cancer Cells

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Abstract: Cervical cancer is the second most commonly diagnosed cancer in developing countries and the recurrence after primary therapy, mainly due to the existence of survived drug-resistant cancer stem cells (CSCs) within the tumour. This study was aimed at identifying the anticancer effects of Retinoic acid-ginger extract combined therapy on HeLa cells representing an invasive form of aggressive adenocarcinoma of the cervical. The Cell-titre-glo and Caspase 3/7 assay, as well as Isobologram-combination index analysis, were conducted to examine the anticancer effect of Retinoic acid (RA) and ginger extract (GE) on HeLa cells viability, ability to induce apoptosis and the RA-GE drug relationship respectively. The Hela cells were treated with RA (5-50uM), GE (25-200uM) and a combination of RA (5-50uM) + GE at (IC25:55uM and IC50:100uM) respectively.. The combined RA-GE significantly reduced HeLa cell viability compared to the solo drug treatment respectively in a dose-dependent manner by 11.44-68.14% (RA), 20.69-87.63 (GE), 51.21-96.76% (combined RA-IC50ginger extract), respectively. Besides, the IC50 concentration of RA in HeLa cells was successfully reduced from 25.60uM to 6uM when combined with IC50ginger extract. Microscopy images of Solo RA-treated HeLa cells exhibited a more differentiated phenotype up to 25uM while ginger extract-treated HeLa cells appeared apoptotic from 40uM onwards. However, the combined RA-IC50ginger extract treatment induced a significant level of apoptosis in HeLa cells from as low as 6uM RA concentration compared to solo treatment, with RA (IC50:1.04%, negligible), ginger (IC25:1.21%, IC50:1.25%), ginger IC25 and RA IC50 (1.36%) and ginger IC50 with RA 6uM (1.71%). The combined RA-IC50ginger extract also exhibited an apparent synergistic effect (CI: 1.30-0.23) on HeLa cells. In conclusion, these findings altogether suggest that the RA-ginger extract therapeutic strategy may be potent anticancer agents for the targeted therapy of cervical cancer cells and other CSCs-enriched cancers.

Keywords: Ginger extract, Retinoic acid cervical cancer apoptosis cancer stem cells

P4

Growth Performance of Terung Asam in Different Growing Media

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Abstract: Background: Terung asam (*Solanum lasiocarpum*), a popular indigenous fruit vegetable in Sarawak, has become an economically important fruit not only to local people but also to tourists who come to Sarawak. However, one of the challenges in planting this crop is lacking knowledge particularly in finding suitable media for its growth, eventually inhibiting local farmers from successfully growing the crop. Among all media available, a mixture of soil and organic compost is commercially preferred in planting terung asam. **Methods:** This study was conducted to investigate the effects of four media (M1: soil, M2: soil and organic compost, M3: soil and cocopeat and M4: soil, organic compost, and cocopeat) on the germination and growth performance of terung asam seedlings. The experiment was tested in a randomized complete block design (RCBD) with 10 replicates. **Results:** The results showed seeds planted in M4 medium produced the highest germination rate of 96.67% and were significantly different ($p < 0.05$) from those sown in other growth media. However, the performance of the seedlings in terms of height, stem diameter, number, and length of leaves showed a significant increase ($p < 0.05$) in M2 medium while the least increase was recorded in seedlings grown in M1 medium. **Conclusion:** This study has proven that germination and growth performance of terung asam seedlings were greatly affected by growing media and M2 medium is therefore recommended to be used in planting terung asam.

Keywords: Terung asam; growing media; seed germination; plant growth parameters

P5

Small RNA Profiling in Mycobacterium tuberculosis

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Abstract: Background: *Mycobacterium tuberculosis* is highly resistant to an adverse environment. Despite being crucial for the development of new diagnostic markers and therapies, the understanding of the transcriptional frameworks of *M. tuberculosis* remains to be elucidated. Therefore, this study aimed to identify small regulatory RNAs (sRNAs) in *M. tuberculosis* and characterize their regulatory responses to relevant stress conditions. **Methods:** After being exposed to different stress conditions, *M. tuberculosis* was subject to the isolation of total RNA, which served as the starting material for constructing cDNA sequencing libraries. The sequencing data were subjected to bioinformatics analyses to identify transcription start sites (TSSs) and novel sRNAs, as well as to characterize the expression profiles of *M. tuberculosis*. Besides, the differentially expressed genes (DEGs) identified for each stress condition were also subject to gene ontology (GO) term enrichment. **Results:** A total of 8,173 TSSs and 2,082 sRNA candidates were discovered in this study. TSS maps enabled the identification of promoters, 5'-untranslated regions (5'UTRs), and riboswitches, as well as facilitated the genomic localization of sRNA candidates, one of which is transcript antisense to Rv0757 that encodes PhoP, which is a two-component transcriptional regulator that modulates responses to oxidative stress and metal uptake. Besides, the differential expression analysis detected 183, 119, 109, 112, and 140 DEGs under iron, isoniazid, kanamycin, starvation, and surfactant stress conditions, respectively. Enriched GO terms for these DEGs include polyketide synthase complex, phthiocerol biosynthetic process, DIM/DIP cell wall layer assembly, fatty acid biosynthetic process, etc. **Conclusions:** Discovery of abundant sRNA candidates in this study underscored the regulatory complexities of *M. tuberculosis*. However, potential regulatory mechanisms and functions in *M. tuberculosis* still need to be characterized and validated.

Keywords: Small RNA; *M. tuberculosis*; transcriptome; RNA-seq; stress responses

P6

SNP analysis of Malaysian multidrug-resistance tuberculosis (MDR-TB)

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Abstract: Background: Tuberculosis (TB), caused by *Mycobacterium tuberculosis*, is a contagious disease among mankind. TB is an airborne disease that generally affects the lungs. Drug resistance has become a major problem in TB treatment leading to multidrug resistance tuberculosis (MDR-TB) strain. World Health Organization defined MDR-TB is resistant to both isoniazid (INH) and rifampicin (RIF). MDR-TB is a major challenge to public health and national TB control and prevention. The resistance in MDR-TB is mostly conferred by single nucleotide polymorphism (SNP) in genes encoding drug targets or drug-converting enzymes. These polymorphisms give rise to phenotypic diversity, thus causing resistance to antibiotics. The rapid advancement of biocomputational tools and high-throughput next-generation sequencing has aided in the identification of SNP mutations in the bacterial genome. We aim to predict and validate the novel mutations and their functional effects by using biocomputational tools. **Method:** Whole-genome sequencing was carried out on 24 TB clinical strains isolated in Malaysia and their assembled genome sequences were aligned to the reference genome of MTB H37Rv for SNP calling using the alignment program MUMmer. **Results:** We successfully identified 12 novel SNPs in genes associated with drug-resistance including enzymatic activity, biosynthesis of mycolic acid, the polymerases that catalyze the transcription of DNA to RNA, and bifunctional enzyme. **Conclusion:** SNPs identified provide insights into the relationship and correlation between the SNPs and antibiotic resistance. Further verification of these novel SNPs in this project is still ongoing.

Keywords: *Mycobacterium tuberculosis*, single nucleotide polymorphism (SNP), multidrug-resistant

P7

Promising Tribal Herbs with Hypoglycemic Properties

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Abstract: Background: Diabetes is a dreadful disease spread across the world alarmingly. WHO projects that diabetes will be the seventh leading cause of death in 2030. The existing treatment methods for diabetes, including various synthetic agents, do not cure the disease entirely and also imposes multiple side effects. Physicians are in the lookout for alternative treatment methods that are safe, effective, and economical. As per the Siddha system, Tridosham or Vatham, Pitham, and Kapham in a state of equilibrium potentiate well-being of the human body. Herbs like *Wrightia tinctoria, Plumbago zaylanica, Terminalia chebula, Persea macrantha, Phyllanthus emblica, Coscinium fenestratum,* and *Zingiber officinale* are mentioned in ethanomedicinal literature for various therapeutic properties which include hypoglycemic Type 2 Diabetes. In this context, the new oral anti-diabetic drug-Ethanolic extract of PHF present interesting therapeutic properties. **Methods:** Collection of fresh crude drugs were dried under shade. They were ground powders individually and sieved and weighed equal amount of all herbal drugs & transferred herb powder into mud pot. Pot is tightly cover with a cloth and sealed. Sealed pot is buried under the soil and fully covered with sand**.** Allowed it to ferment for 24 hr**.** After fermentation transferred to glass bottle and stored and used for further, extraction and evaluation studies. **Results and Conclusion:** From the results, we concluded that streptozotocin-induced hyperglycemia, polydipsia, and polyphagia. Administration of ethanolic extract of PHF (200 &400mg/kg) to STZ-diabetic rats reduced the blood glucose level near to normal levels and restored the body weight, food and water intake, and oxidative defense after 28 days treatment. Thus the extract possesses an anti-diabetic effect and protective effect of pancreative β cells.

***Keywords*:** Polyherbal formulation, anti-diabetic, Type 2 diabetes, Ethnomedicine.

P8

ENT2 Gene Expression in the Different Stages of Colorectal Cancer

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Abstract. Background: Equilibrative nucleoside transporter 2 (ENT2) is a bidirectional transporter that localizes on the cell membrane. ENT2 mediates the uptake of purine and pyrimidine nucleosides and other nucleobases. Since nucleoside-derived drugs are used in the clinic, especially as an anti-cancer therapy, ENT2 expression may correlate or predict the treatment responses and prognosis of cancer patients. Therefore, the main objective of this study is to determine the ENT2 expression level and roles in supporting the pathogenesis of colorectal cancer. **Methods**: We assessed ENT2 gene expression level in a panel of human colorectal cancer (CRC) cell lines, representing four CRC stages (Duke A, B, C, and D), and normal colon cells using the quantitative real-time polymerase chain reaction (RT-qPCR). Two independent reference genes, GAPDH and HPRT-1, were used for normalization. The human CRC cell lines ENT2 expression fold change relative to normal colon cell line was determined by using the 2-ΔΔCT method. **Results**: We identified that ENT2 expression was significantly higher ($P < 0.05$) in all CRC cell lines as compared to CCD-841CoN normal colon cell line. We found that the ENT2 expression level was 215, 248, 462, and 110 fold higher in Dukes A, B, C, and D stages of CRC, respectively. The ENT2 expression level was the highest in Duke's C stage. Interestingly, the ENT2 expression level was lower in Duke's D stage as compared to the Duke's A stage of the CRC cells. **Conclusion:** Our RT-qPCR data revealed the upregulation of ENT2 gene expression in all CRC stages, however Duke's D (which is considered as metastatic CRC) was the lowest. The change in the expression of ENT2 transporter may play a crucial role in cancer progression and therapeutic mechanisms. Therefore, more investigations are required to evaluate the role of ENT2 in metastatic CRC to improve the therapeutic methods of CRC.

Keywords: ENT2, Colorectal cancer, Chemotherapy, Nucleoside Analogues

P9

Antibiograms of Multidrug-resistant *Acinetobacter baumannii* Isolated from Specimens at Kushtia Medical College Hospital

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Abstract. *Acinetobacter baumannii* is an opportunistic, hospital dwelling pathogen which is responsible for hospital-acquired infections like Ventilator-associated pneumonia (VAP), several respiratory and urinary tract infections, meningitis, wound sepsis and numerous skin/soft tissue infections (SSTIs). The emergence of this notorious bacteria is profoundly observed by recent outbreaks throughout the world. The dominance of this pathogen thrives over the healthcare units, because of its ability to resist every existing first-line antibiotics, reminding the fear of the pre-antibiotic era to the world. This study aimed to isolate and identify A. baumannii from clinical samples and to determine their antimicrobial resistance pattern to commonly prescribed drugs to find out multidrug-resistant *A. baumannii* (MDRAB). Four different samples were collected from Kushtia Medical College Hospital. *A. baumannii* was isolated and identified based on their growth, physiological, and biochemical characteristics. Their antibiograms were studied through the standard disk diffusion method, and antibiotic susceptibility patterns were interpreted. Ceftriaxone, ciprofloxacin, erythromycin, imipenem, and colistin were used to evaluate the sensitivity of the isolates. Out of four specimens, the pathogen was recovered from hospital drain water, hospital dust, and urine sample. Though the isolates showed similar growth and physiological characteristics along with similar biochemical profiles, they differ considerably in their sensitivity against several antibiotics. The least resistance showing antibiotic was colistin (22%) and then imipenem (33%). Aside from isolate DW04, HD19, HD20, HD24, all isolates found multidrug-resistant (resistant to ≥ 3 antibiotics group). The recovery of MDRAB, including imipenem-resistant *A. baumannii* from different clinical specimens, and their antibiotic resistance pattern hint emergence of a formidable pathogen of nosocomial origin. The findings of the study seek up-gradation of current patient maintenance practices in healthcare units of our country to limit the prevalence of antibiotic-resistant *A. baumannii*.

Keywords*: Acinetobacter baumannii*; Antimicrobial Resistance; Multi-Drug Resistant; Nosocomial Infection

P10

Antiproliferative Effect of Lapatinib, an ErbB1/ErbB2 Tyrosine Kinase Inhibitor, on Caco-2 Human Colorectal Cancer Cell Line

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Abstract: Background: Lapatinib is a dual ErbB1 and ErbB2 tyrosine kinase inhibitor. It is effective in ErbB2-positive breast cancer treatment. However, it has been associated with several side effects, particularly diarrhoea. The underlying mechanism of lapatinib-induced diarrhoea remains unclear. This is a preliminary observation on the effect of lapatinib on Caco-2, human colon adenocarcinoma cell line. Caco-2 is selected as it is able to differentiate into enterocytes-like phenotype and able to form high barrier integrity, hence, it is chosen as a model to reflect human normal small intestinal epithelium. **Methods:** Caco-2 cell line was cultured in DMEM F-12 culture medium, which was supplemented with 20% foetal bovine serum (FBS), 1-2% antibiotic and antimycotic and 2 mM L-glutamine in 25 cm^2 flasks in a 37°C incubator with 5% CO_2. The half maximal inhibitory concentration (IC_{50}) of lapatinib on Caco-2 cell was evaluated via MTS assay. Caco-2 was treated with a range of concentrations of lapatinib (0-100 μM) and incubated at four-time points, 24, 48, 72, and 96 hours. An equivalent serial dilution of DMSO was used as a control treatment. The dose-response then was plotted to obtain IC_{50}. **Results:** Lapatinib showed different IC_{50} values at different time-points. No IC_{50} value was observed at 24 hours. Recorded IC_{50} values are 28 ± 12.806 μM, 29 ± 2.513 μM and 14 ± 1.642 μM at 48, 72 and 96 hours, respectively. **Conclusions:** Lapatinib showed on antiproliferative activities on Caco-2 at 48, 72, and 96 hours. Further investigations are currently underway to determine the underlying mechanisms of lapatinib-induced diarrhoea.

Keywords: *Caco-2; Cell viability assay; Cytotoxicity; Lapatinib; Proliferation*

P11

Stability Studies on Cold-Chain Free Oral Cholera Vaccine Formulations at Different Storage Conditions

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Abstracts: Background: Cholera is an acute diarrhoeal disease caused by the *Vibrio cholerae* serogroup O1 or O139. A prototype cold chain free vaccine was developed at AIMST University which eliminates repetitive dosing in contrast to all the existing cold chain dependent WHO/FDA licensed whole-cell killed or live oral cholera vaccines and it is stable at room temperature for 140 days. Thus, this study is focused on the stability of vaccine formulations at different storage conditions. **Methods:** The vaccine formulations were prepared and stored at different storage conditions: 25°C ± 2°C and 60% ± 5% humidity, 30°C ± 2°C and 65% ± 5% humidity and 40°C ± 2°C and 70% ± 5% humidity. The viability, purity, and stability of the vaccine candidate in the formulation during the extended storage period were assessed by Gram staining, selective media, PCR, and Biochemical tests. **Results:** The vaccine formulation F23 had shown very stable viability at 25°C - 30°C with 60% - 65% relative humidity after 220 days of storage with approximately 10^7 CFU/mL recovery number of cells. New liquid vaccine formulations P1 and C1 were developed and showed similar stability to F23 with recovery number of cells approximately 10^7 CFU/mL for 238 days. **Conclusions:** The newly developed liquid live oral vaccine formulation P1 and C1 were performed better due to its free-flowing form and easier to be administered. However, the protective efficacy of these vaccine formulations should be further studies in animal models.

Keywords: Stability, Cold-chain free, Live, Vaccine, *Vibrio cholerae*

P12

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

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Abstract. Most of the cellular pathways involved in bacterial pathophysiology is regulator by non-protein coding RNAs (npcRNAs). In Gram-negative bacteria the binding of Hfq protein to RNA chaperone in npcRNA, facilitates its binding to the targeted mRNAs. Hfq gene is conserved in a wide variety of bacteria and is involved in many cellular functions such as stress adaptation and regulation of gene expression. The main objective of this study is to sequence the transcriptional regulator Hfq bound transcriptome in Salmonella typhi at different growth phases which the bacteria listed in top drug-resistant bacteria that pose the greatest threat to human health released by the World Health Organization in 2017. The second objective is to annotate the sequences for the identification of the novel npcRNAs and the submission of the sequences to the GenBank. Lastly, to confirm the novel npcRNA expression profile during the different growth phases of the S. typhi by Northern blot analysis or reverse transcription PCR. The expression of the npcRNA at the different growth phases might be involved in virulent regulation and pathogenicity of *S. typhi*. Polymerase Chain Reaction uses the amplified the Hfq gene and recombined in pET 28b+ to overexpress Hfq protein. Affinity column will be used to purify bounded RNAs. The RNA will be sequenced using the Illumina genome analyzer sequencing platform. Bioinformatics software will be used to analyze the sequenced data to identify the un-annotated intergenic transcripts and NCBI database BLASTn performs to filter the annotated mRNA and npcRNA genes in other organisms respectively. We believe that the identification and characterization of npcRNAs from S. typhi will fill the gaps in understanding the regulatory pathways of the organism. It will also set a platform for further research in developing new technology for npcRNA based detection method, exploring novel drug targets and development of RNA based vaccines.

Keywords: Non- protein-coding RNAs, Hfq protein, S. typhi, growth phase

P13

Resistome of clinical *Klebsiella pneumoniae* isolates shows the predominance of *Ctxm, Oxa, Shv* gene variants encoding beta-lactamase & *aac(6')-Ib* encoding bifunctional aminoglycoside modifying enzymes

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Abstract. Background*: Klebsiella pneumoniae* is considered an immediate threat across the globe due to the emergence of Multi-Drug Resistance (MDR) associated with hospital-acquired infections and community-acquired infections. It is crucial to investigate the resistance gene pool hidden in these strains to pave the way for novel therapeutic strategies and also guide the appropriate treatment regimen. The present study aimed to characterize the available genome of *Klebsiella* strains originating from burn patient; perirectal; skin swab; wound swab; urine; abdominal drainage fluid; tracheal secretion; nasal swab; anal swab and other random clinical samples from tertiary-care hospitals. **Methods:** A cluster of the available complete genome in the database covering different diseases was selected for investigation of resistome. The available genome of *Klebsiella pneumoniae* (n=20) was downloaded and subjected for a specific bioinformatic pipeline to determine the antibiotic resistance genes (ARGs) in both plasmid and chromosome. Further genome-based Multi Locus Sequence Typing (MLST) was employed to determine the phylogenetic relationship. **Results:** The analyses revealed the presence of multiple ARGs in the range 4-32 ARGs per *Klebsiella pneumoniae* strain attributing to antibiotic resistance towards multiple classes of antibiotics. Beta-lactam (100 %) and aminoglycoside (85%) were found to be the most prevalent across the strains with bla_{CTXM}, bla_{OXA}, bla_{SHV} genes encoding beta-lactamase and aac(6')-Ib gene encoding bifunctional enzymes capable of multiple modifications of aminoglycoside antibiotics as predominant ARGs. This indicates the potential of *K. pneumoniae* infection to outpass the effect of these antibiotics, making them ineffective. MLST analyses identified 12 different Sequence Types viz., ST147 (n=6); ST258 (n=3) and singletons (ST 11, 14, 15, 23, 29, 244, 258, 340, 505 and 3851). **Conclusion**: The co-occurrence of several ARGs is a major challenge in the treatment of hospital-acquired infections. The results suggest the need for rapid molecular assays targeting the major ARGs in the clinics to guide appropriate therapeutic regimne.

Keywords: *Klebsiella pneumoniae*, Resistome, Antibiotic Resistance Genes, MLST , Multidrug-resistance.

P14

Dissecting Complete Genome of *Klebsiella pneumoniae* uncovers the abundant repertoire of antibiotic resistance genes – a GLOBAL snapshot

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Abstract. Background: The rapidly growing repertoire of antibiotic resistance genes (ARG) in ESKAPE pathogens due to continuous horizontal transfer emphasizes that PCR based investigation targeting a handful of antibiotic resistance genes in clinical isolates is insufficient to gain complete insights of their weapons for resistance. Dissecting the resistome at the whole-genome level is the need of the hour. The current study focussed to capture the Whole Genome Sequence (WGS) repertoire of antibiotic resistance genes in clinical *Klebsiella pneumoniae* (KP) strains originating from different parts of the world in the period of 2005 to 2020. **Methods**: The study employed WGS analyses for a cluster of 100 *Klebsiella pneumoniae* complete genome was available in the NCBI database by using a systematic bioinformatics pipeline. The ARG distribution in the contigs of the genome was further analyzed and segregated to determine the location of ARGs in the plasmids and chromosomes. **Results**: Multiple ARGs were detected in the range of 4 - 33 ARGs per KP strain attributing resistance towards multiple antibiotics (Aminoglycoside; Beta lactam; Fosfomycin, Macrolide, Phenicol, Sulphonamide; Quinolone; Trimethoprim). The highest ARG frequency observed was for Quinolone (99), Beta lactam (99), and Aminoglycoside (77). Systematic investigation revealed 72 KP strains harbouring ARGs in the PLASMID ranging from 6 - 30 ARGs per KP strain. The predominant ARGs detected were quinolone resistance determinant *oqx*A and *oqx*B gene (n= 103 & 101); *ctxm-15* & *tem-1b* beta lactamase (n = 43) and *aac (6')-lb* aminoglycoside modifying enzyme (n= 35). **Conclusions:** The WGS analysis revealed the huge armamentarium of resistance power hidden in *Klebsiella pneumonia* plasmids which usually goes undetected in clinics leading to abuse of antibiotics. This observation reemphasizes the need for dedicated research towards formulating conjugation inhibitors as a possible avenue to curtail the dissemination of antibiotic resistance. The study also recommends the value of WGS to unveil the potential of emerging superbugs.

Keywords*: Klebsiella pneumoniae*; Whole Genome Sequence, Antibiotic resistance genes, Plasmids, Global strains

P15

Evaluation of *In-vitro* Antioxidant and Anti -Advanced Glycation End Products Formation (Ages) Effect of Barley, (Hordeum Vulgare) Extract

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Abstract. Background: Barley, (Hordeum vulgare), cereal plant of the grass family Poaceae and its edible grain which is rich in functional ingredients, such as gamma-aminobutyric acid, flavonoids, saponarin, lutonarin, superoxide dismutase, K, Ca, Se, tryptophan, vitamins (A, B1, C, and E), dietary fiber, metallothioneins, and polyphenols. Barley possesses various pharmacological benefits such as antidiabetic effect, enhances immunity, protects the liver, antidepressant effects; improves gastrointestinal function, anti-inflammatory, hypolipidemic, prevents hypoxia, reduces hyperuricemia, cardiovascular diseases and, improves cognition. However, no report on the antioxidant and anti-advanced glycation end products formation effect of Barley. Glycation is a non-enzymatic reaction between a reducing monosaccharide and an amine group in proteins, lipids, or nucleic acids forming an unstable Schiff base, a secondary aldimine. This undergoes further rearrangement to form a stable Amadori product which then leads to the irreversible formation of an advanced glycation product (AGE). Oxidative stress and AGEs in hyperglycemia condition play a vital role in aging, diabetes Mellitus (DM), and cardiovascular complications. **Aim:** Therefore, this experiment aimed to evaluate the antioxidant and anti-advanced glycation end products formation effect of Barley. **Method:** In vitro evaluation of free radical scavenging ability of barley, was done on free radical generated by DPPH, nitric oxide, hydrogen peroxide, lipid peroxidation, FRAP, and metal ion chelating, and reducing power. In-vitro antiglycation activity was done using BSA-MGO, BSA-Glu, and glycated haemoglobin. **Result:** The results showed barley blocked the formation of AGE as shown by the results of BSA-GLU, BSA-MGO, glycated haemoglobin and inhibited the free radicals generated by DPPH, Nitric oxide, hydrogen peroxide, Lipid peroxidation, FRAP and Metal ion chelating. **Discussion and conclusion:** Barley possesses antioxidant and antiglycation properties. The mechanism of action seems to be via the blockage of free radical formation, decreasing reactive carbonyl. Further research is ongoing to evaluate the mechanism of action.

Keywords: barley, anti-advanced glycation, antioxidant, diabetes mellitus, Oxidative stress.

P16

Extraction of Eco-Friendly Natural Dyes from Indian Almond Leaves of Terminalia Catappa L. and Evaluation of Its Antioxidant Properties

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Abstract. The major objective of extracting dyes from sources of the plants is to reduce or prevent environmental pollution. In the recent days, having a global concern over the usage of eco-friendly and biodegradable materials, numerous research work is being considerably undertaken around the world on the application of natural dyes over synthetic dyes in textile industries. The use of natural dyes for textile dyeing has been decreased to a very large extent after the discovery of synthetic dyes. In the present study, we have made an attempt to study the preparation of natural dyes, which is an alternative to the use of synthetic dyes, from the solvent extracts of Indian almond leaves, *Terminalia catappa L*. in four periods such as young green leaf, mature green leaf, orange red leaf and brown leaf. The plant sample containing brown leaves were extracted using three different solvents like ethanol, methanol and double distilled water by heating at 100°C for 30 minutes. Phytochemical tests were performed and it confirmed the presence of metabolites like phenols, tannins etc. The dyes were tested for antibacterial activity using disc diffusion method, which revealed that the ethanolic and distilled water extracts showed remarkable activity against *Pseudomonas aeruginosa* and *Staphylococcus aureus* and antioxidant activity was also carried out using DPPH assay and levels ranging from 0.04-0.59 were recorded. Thus, the work concluded that the pigment extracted from Indian almond leaves can be used as natural dyes and also for healing wounds.

Keywords; natural dyes, Indian almond leaves, DPPH, tannic acid, antimicrobial activity

P17

ITS based Genus (Clade) level identification of Scleractinian coral endosymbionts in the Palk Bay, southeast coast of India

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Abstract. Background: Coral reefs have entered an era of "ecological crisis" as climate change drives fatal reef loss worldwide. Coral growth and bleaching susceptibility are regulated by their endosymbiotic association with dinoflagellate, zooxanthellae in the family Symbiodiniaceae. The phyletic diversity of endosymbionts depends on various environmental conditions including temperature, solar radiation, light, and salinity. As part of the pioneering research on molecular diversity of coral endosymbionts of Palk Bay, India, the present study mainly focuses on the genus (clade) level identification of endosymbionts of Mandapam and Veedhalai regions using ITS marker since it is a potential genetic marker to infer phylogenetic relationship of both infrafamilial as well as infrageneric levels. **Methods:** In this study, a total of ten coral colonies (eight from Mandapam and two from Veedhalai) sampled from Palk Bay at a depth of 2 meters by SCUBA techniques. The fragment was individually subjected to isolation of endosymbiont by the airbrushing method. The genomic DNA of endosymbiont was extracted using the method described by Rowan and Powers (1991) and Chen et al., (2003). Gene-specific ITS primers were used for PCR amplification (Santos *et al*., 2001) and the size of ITS was ~750bp. **Results:** Amplified PCR products were sequenced bidirectionally. Nucleotide sequence analysis shows that the Mandapam coast harboured endosymbionts of the genera *Durusdinium* (Clade 'D') and *Cladocopium* (Clade 'C') while the corals of Veedhalai region detected only the genus *Durusdinium* 'D'. The constructed phylogenetic tree was supported to the known genera *Durusdinium* and *Cladocopium* with Bootstrap values. **Conclusion:** Present study confirms the dominance of thermotolerant endosymbionts (genus *Durusdinium* 'D') in the reef corals of Palk Bay, India. It indicates the coral under thermal stress due to increasing Sea Surface Temperature (SST). The studying genetic diversity of endosymbiont communities is useful to understand the long-term responses of reef corals to global climate change.

Keywords: Corals; Endosymbiont; Palk Bay; ITS Marker; *Durusdinium*; *Cladocopium*

P18

Mycoremediation of Reactive Red Dye by Highly Potential Fungal Strain Isolated from Textile Effluents

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Abstract. Besides the detrimental impacts on the aquatic ecosystem, fabric colorants often have a hazardous effect on human health. These problems are more serious in Bangladesh, one of the largest exporters of apparel. Biodegradation of fabric colorants by microorganisms is a prospective and sustainable approach over the conventional physio-chemical methods and fungi mediated mycoremediation is also a significant decontamination approach of these dyes. This study aimed to isolate potential fungal strains from textile effluent that are capable of degrading reactive red (RR) dye, a widely used dye in local thread dyeing industries. Dye degradation assay was performed in potato dextrose broth supplemented with 50 mg/l RR dye by inoculating different fungal strains. A photo-electric-colourimeter was used to analyze the decolorizing potentiality of fungal strains after aerobic incubation under static conditions. For molecular characterization and identification, the PCR product has been performed for partial sequencing. Primarily, six fungal strains were isolated and one strain (TEF-3) exhibited 97.41% degradation of RR dye at a concentration of 50 mg/l after 96 h of incubation. Thus, this fungus has the prospectiveness to be utilized in the textile wastewater treatment plant.

Keywords*:* Bioremediation; Myco-remediation; Reactive red dye; Textile effluents; Internal transcribed spacer

P19

Unending Transmission of Malaria Parasite in Peri Urban Community of Ipinsa Southwestern Nigeria: Prevalence and Risk Factors Enhancing Transmission

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Abstract: Background: Malaria is a vector borne infectious disease caused by *Plasmodium* spp. it is a major public health problem worldwide, particularly in Africa. This study was conducted to investigate the prevalence and risk factors affecting malaria transmission in the peri urban community of Ipinsa, southwestern Nigeria. **Methods:** Thick and thin smear was prepared and examined under the x100 objective lens of the light microscope to confirm the prevalence of *Plasmodium falciparum* in blood samples. Questionnaires were used to collect information such as sex, age, location, and variables for economic status. Out of 300 subjects who volunteered, 235 (78.3%) were infected with *P. falciparum.* **Results:** The study revealed that females had a lower infection prevalence of 125 (76.7) compared to their male counterparts with 110 (80.3). Age group was related to the malaria infection in this study area. While the highest rate of infection was observed among ≤5, the least was observed among the subjects within the age group 11-15 years ($P<0.05$). Similarly, with parasite density, males had lower parasite density (1806 parasite/µL of blood) compared to females who have a higher parasite density (2068 parasite/µL of blood). In the same vein, those who were more than 21 years had a lower density than those of ≤5 years. The economic variable which is determined by income was significantly related to malaria infection ($P<0.05$). Subjects earning ≤18000 Naira/month had a higher malaria prevalence of 85.2%, while subjects earning ≥31000 Naira/month had lower malaria prevalence (56.9%) and there was a significant difference ($P<0.05$). **Conclusions:** The outcome of this study is proof that malaria is prevalent in the study area and appropriate control intervention should be made available to the populace to ameliorate infection conditions.

Keywords: Transmission; malaria; *P. falciparum*; prevalence; risk factors

P20

Computational Analysis and Annotation of *Elaeis oleifera* Naringenin-Chalcone Synthase and Palmitoyl Protein Thioesterase

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Abstract: Background: American Oil Palm or *Elaeis oleifera* (*Eo*) is a palm that has a low yield of palm oil but has a better oil quality compared to African oil palm (*Elaeis guineensis*). Naringenin-chalcone synthase(CHS) and palmitoyl protein thioesterase (PPTE) are the functional contributors to flavonoids biosynthesis and fatty acid biosynthesis, respectively. The main aim of this project was to annotate *Eo*CHS and *Eo*PPT. **Methods:** The *Eo*CHS and *Eo*PPT cDNA sequences were retrieved from the nucleotide database of NCBI. The *Eo*CHS and *Eo*PPT cDNA(s) and the deduced proteins were annotated by employing various bioinformatics tools to know their attributes. The multiple sequence alignment (MSA) was performed using ClustalX 2.1, and phylogenetic analysis was completed using TreeViewX. Secondary structures and 3-Dimensional (3D) structures were predicted using the Phyre2 server. **Results:** The annotation of cDNA of *Eo*CHS suggests that it contains an open reading frame (ORF) which encodes for a peptide that contains 389 amino acids (aa). The annotation of cDNA of *Eo*PPTE indicated that it includes an ORF which encodes for a peptide that contains 332 aa. The primary analysis of predicted secondary structures showed that the *Eo*CHS contains 15 alpha-helices and 11 beta-strands, whereas the *Eo*PPTE contains 14 alpha-helices and 11 beta-strands. For the 3D structure prediction of *Eo*CHS and *Eo*PPTE, the suitable templates c1cm and d1ei were used respectively based on the coverage score. The phylogenetic analysis showed that the *Eo*CHS and *Eo*PPTE are closely related to their counterparts from *E.guineensis*. **Conclusions:** This study predicted the secondary structures and 3D structure of *Eo*CHS *and Eo*PPT. The predicted 3D structures will serve as a foundation for further studies on both enzymes.

Keywords: 3-D structure; American Oil Palm; Biotechnology; cDNA; naringenin chalcone synthase; palmitoyl protein thioesterase.

P21

In Silico Analysis and Annotation of *Elaeis oleifera* NOI and Metallothionein-like Proteins

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Abstract: Background: The American Oil Palm [*Elaeis oleifera (Eo*)] is an oil-producing plant species grown only within tropical belt. It is known for quality oil used in both food and non-food industries. Nitrate induced like protein (NOI) and Metallothionein like protein (MT) are known to play an essential role in plants defense mechanism and regulation of homeostasis, respectively. Hence, a better understanding of *Eo*NOI and *Eo*MT is necessary. Therefore, this study aimed to annotate *Eo*NOI and *Eo*MT. **Methods:** The *Eo*NOI and *Eo*MT cDNA sequences were retrieved from NCBI. The *Eo*NOI and *Eo*MT cDNA(s) and the deduced proteins were reannotated by using bioinformatics tools to confirm their salient features. Multiple sequence alignment (MSA) was performed before phylogenetic analysis, followed by, prediction of the secondary and tertiary structure of both proteins. **Results:** The annotation of *Eo*NOI and *Eo*MT cDNA sequences suggests that it contains an open reading frame (ORF) which encodes for a peptide that contains 228 amino acids and 62 amino acids, respectively. The primary analysis of predicted secondary structures showed that the *Eo*NOI contains 4 alpha-helices and 1 beta-strands whereas *Eo*MT contains only 4 beta-strands and no alpha-helices. The model prediction of *Eo*NOI was based on the Pseudomonas (AvrB) template _c2nu protein and as for *Eo*MT was based on template _c1qj from Sea urchin. The prediction of the 3D model of *Eo*NOI has >90% confidence level while the prediction of 3D model of *Eo*MT was 74.5% confidence level as the coverage was low (25%). The phylogenetic analysis of both proteins showed its close relation with their counterparts from *E.guineensis*. **Conclusions:** This study predicted the secondary structures and 3D structure of *Eo*NOI and *Eo*MT. The annotation and predicted secondary structures and 3D structures of both proteins will serve as a basis for the further molecular modeling work that needs to be done.

Keywords: American Oil Palm; Biotechnology; cDNA; metallothionein-like protein; nitrate induced-like protein; 3-D structure

P22

StyR-143 non-protein coding RNA gene knock out in *Salmonella* Typhi which upregulated completely in biofilm formation pathway

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Abstract. A total of 97 non-protein coding RNA (ncpRNA) were identified and characterized in *Salmonella enterica* serovar Typhi(*S.* Typhi) which is a human-specific pathogenic bacterium. From the 97 ncpRNAs, 33 were particularly expressed in S.*typhi* which was associated with the pathogenesis of the bacterium. From the 33 npcRNA, the number of npcRNAs was associated with the metabolic pathway of biofilm formation in S.*typhi*. The formation of biofilm in S.*typhi* is associated with one of the important pathogenicity where it allows the bacterial cell to colonize in the liver of the infected individual to achieve successful transmission to other hosts. In this study one of the npcRNA which assists the biofilm formation in the bacterial cell were chosen to perform gene knock out. This npcRNA is known as Stry143 which one of the RNA upregulated completely in the bacterial cell where forming the biofilm in the exponential growth stage. A gene knockout of the StyR-143 was performed using the electroporation method which is one of the efficient methods to perform the transformation in the S.*typhi* compared to the heat shock method. In this gene knockout study pKD46 plasmid which is also known as the recombineering plasmid system which consists of ampicillin resistant cassette as the selective marker and lambda red genes which facilitate the gene knockout of Styr143 in the FTIR region of the bacterial genome. A special kanamycin cassette which about 1.5kbps with the homologous block which specific to the Styr143 of npcRNA in the bacterial genome where design which inserted into the genome at the Styr143 region. **Objectives:** To knock-out the npcRNA of StyR-143 from *S.* Typhi genome. **Material and methods:** Plasmid pkD46 was transformed into P. mirabilis and screened using ampicillin marker. The DNA fragment with kanamycin resistance gene, FRT sites, and 100 bps of homologous sequence from the flanking regions of PmiR-137 gene was amplified by PCR and transformed into P. mirabilis with pkD46. To detect PmiR-137 mutants, the transformed colonies were selected on kanamycin plate and verified using FRT-specific primers. **Conclusion:** The confirmation of the knock out strain will be performed by using FRT primer and by sequencing analysis. After the confirmation of the knock out strain, transcriptome sequencing, physiological and morphological will be carried out.

Keywords: *S.* Typhi; gene knockout; pkD 46; StyR-143; biofilm formation;

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P23

Over-expression and purification of Acinetobacter baumannii Hfq protein in BL21

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Abstract. Background: Acinetobacter baumannii has emerged as an opportunistic bacterial pathogen with the rapid evolution of drug resistance. Due to the increase in A. baumannii infections, there is a high need to find new strategies or new targets for effective treatment of diseases caused by this pathogen. Recently, non-protein coding RNAs emerged as the important mediators of bacterial virulence regulation and performing their function by binding to RNA chaperone Hfq protein, forming ribonucleoprotein complex. In this study, we would like to establish a method to identify novel npcRNAs by sequencing the cDNA library of Hfq protein-bound RNA from A. baumannii. Methods: The Hfq gene from A. baumannii was amplified and cloned into pET-28b+ vector. The ligated mixture was transformed into TOP-10 cells and this transformed bacterial colony was screened by antibacterial (Kanamycin) selection and further confirmed by PCR methods. The recombinant plasmid was transformed into E. coli BL21 and induced the expression with IPTG. The overexpressed Hfq protein was purified using Ni-NTA affinity chromatography. Results: Hfq gene had been successfully amplified, digested with an appropriate restriction enzyme and cloned into pET-28b+ vector. The recombinant plasmid was successfully transformed into TOP10 and BL21. A highly purified Hfq protein was obtained and confirmed by SDS PAGE analysis. Conclusion: We had successfully purified Hfq protein from A. baumannii. The identification and characterization studies will be carried out by RNA binding study for the selection of the npcRNA that binds to the protein.

Keywords: Acinetobacter baumannii; Hfq protein; pET-28b+ vector; npcRNAs;

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P24

Evaluation of Cold Chain Free Live Attenuated Oral Cholera Vaccine against Enterotoxigenic Escherichia coli, as a Dual-Use Vaccine

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Abstracts: Background: Diarrheal disease, the second-leading cause of death among infants and young children worldwide is predominantly caused by two major enteric pathogens Vibrio cholerae and Enterotoxigenic Escherichia coli (ETEC). The pathogenesis of both pathogens is quite similar. The cholera toxin (CT) produced by *V. cholerae* O1 and the heat-labile enterotoxin (LT) of ETEC is structurally, functionally, immunologically identical. There is no vaccine exclusively licensed for ETEC. However, the existing cholera vaccine Dukoral, with its rCTB component affords short-term cross-protection against ETEC infection. In this direction, the present study is focused to evaluate the prototype cholera vaccine developed at AIMST University for its cross protectivity against ETEC strains. **Methods:** In this study, the purity of the ETEC strains was assessed by Gram staining, selective media, PCR, and Biochemical tests. The LPS isolation kit (Biovision) was used to isolate the LPS of ETEC 2947 and H10407 strain. The cross-protectivity of the vaccine against ETEC strains was evaluated by performing ELISA to determine the anti-LTB and anti-LPS ETEC antibodies in vaccinated rabbit serum samples. The ELISA methods were standardized. **Results:** The purity of ETEC strains has been proven and the LPS of ETEC strains were successfully isolated and used for ELISA purposes. There were significant 30 fold increase of Anti-LTB IgG antibodies and a 2-8 fold increase of Anti-LTB IgA were found in all the vaccinated rabbit serum samples. However, no antibodies against LPS of ETEC 2947 and H10407 strains were evaluated in all the vaccinated rabbit serum samples. **Conclusion:** Towards this, the vaccine formulation mimics a natural infection and has the potential to protect against ETEC infection by neutralizing the heat-labile toxin. Nonetheless, the cross-protection study should be further investigated in animal models.

Keywords: Live, Vaccine, *Vibrio cholerae*, LPS, ELISA, Antibodies

P25

Evaluation of Co-aggregation between Live Cholera Vaccine Candidates VCUSM14P with Enterotoxigenic Escherichia coli towards to the Biofilm Formation

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Abstract: Background: Cholera is a life threatening secretory diarrhea caused by infection of *Vibrio cholerae* of O1 and O139 serogroups. *Vibrio cholerae* is able to form a biofilm that confers protection against harsh environmental conditions and as part of the colonization process during infection. A live oral cholera vaccine candidate VCUSM14P was developed by AIMST University with USM University which eliminates repetitive dosing in contrast to all the existing WHO/FDA licensed whole-cell killed or live oral cholera vaccines. In a preliminary study, the coaggregation between *V. cholerae* with *Escherichia coli* (ETEC) has facilitated the formation of biofilm and increase the rate of colonization in the intestine of animals. In this direction, the present study is focused to evaluate the coaggregation of vaccine candidate VCUSM14P with Enterotoxigenic *Escherichia coli* and the formation of biofilm. **Methods:** In this study, the purity of the VCUSM14P and ETEC strains was assessed by Gram staining, selective media, PCR, and biochemical tests. The aggregation test was carried out to determine the percentage of self-aggregation and co-aggregation among *V. cholerae* and ETEC. The formation of biofilm was evaluated by crystal violet assay. **Results:** The strains VCUSM14P and ETEC show better aggregation because the percentage of co-aggregation is about 97.3% which is nearly 100%. This aggregation leads to the formation of a slimy layer of biofilm at the bottom of the 96-well plate. The Absorbance rate of biofilm formation is higher in the co-aggregation well of VCUSM14P and ETEC strains. The absorbance for their co-aggregation is about 1.7566 at 620nm. **Conclusion:** Towards this, the aggregation and biofilm formation playing an important role in gut colonization and diarrheal disease thus, this study will be helpful to develop a better vaccine that could protect against ETEC infection. Nonetheless, the colonization study would be further investigated in animal models.

Keywords: Cholera, *Vibrio cholera*, Vaccine, biofilm formation

P26

Ficus religiosa in Mitigating Hyperandrogenism in PCOS induced rats: A Phytotherapeutic Approach

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Abstract: Background: There are a multitude of female infertility based disorders like ovulatory dysfunction, endometriosis, uterine fibroids, tubal blockage, acquired infections in reproductive tracts etc. Polycystic Ovary Syndrome familiarly known as PCOS is a common malady of the endocrine function in women during their reproductive span of life. Based on the Rotterdam criteria, excess levels of androgens are still considered as the hallmark symptom of PCOS. At present, there is no prescribed treatment for PCOS. The treatments or interventions based on symptoms have some adverse effects. Hence, phytotherapy can be a judicious alternative to mitigate PCOS. As *Ficus religiosa* holds a significant position in traditional medicine, the study was aimed to examine the efficacy of *F.religiosa* fruits in reducing hyperandrogenism. **Methods:** In the present investigation, letrozole induced PCOS rat model was employed to analyze the effectiveness of *Ficus religiosa* fruit extracts in attenuating hyperandrogenism. **Results:** From the results, it was found that the fresh and dry fruits of *F. religiosa* had the ability to regularize the estrous cycle rhythm in letrozole administered PCOS rats. The PCOS induced rats exhibited significantly elevated levels of testosterone compared to that of intact rats, and the fruit extract administered groups showed a remarkable reduction in the androgen level than that of their PCOS counterparts A similar positive trend was observed in the levels of antioxidant status of the ovary and uterine tissues. **Conclusion:** Further, we are affirmative that the dried fruit extract of *F. religiosa* has comparatively better efficacy in reducing hyperandrogenism and estrous cycle compared to that of fresh fruit extract.

Keywords: *Ficus religiosa*; PCOS; hyperandrogenism; estrous cycle; letrozole

P27

Comparative studies on maternal and prenatal exposure to *Piliostigma thonningii* extract on serum lipid profile following acetaminophen induced toxicity on female Wistar rats

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Abstract. Background: The establishment of pregnancy requires a receptive uterus able to respond to a variety of biochemical and molecular signals produced by the developing conceptus, as well as specific interactions between the uterine endometrium and the extra-embryonic membranes. Pregnancy does not only demand the use of more metabolic fuels but causes hormonal imbalance, which may affect the lipid profile. **Method:** This research investigated the effect of maternal and prenatal exposure to ethanol leaf extract of *Piliostigma thonningii* on the lipid profile following acetaminophen induced toxicity in Wistar rats. The leaves of *P. thonningii* were collected and air dried for 14 days until constant weight was obtained. Twenty-five (25) pregnant female Wistar rats (180-200 g) were assigned based on their weight to groups labeled A-E and treated thus: animals in groups B-E were orally administered 200 mg/ kg bwt acetaminophen, 200 mg/kg b. wt *P. thonningii*, 100 mg/ kgb. wt *P. thonningii* +200 mg/ kg b .wt acetaminophen and 200mg/kg *P. thonningii* +200mg/kg b. wt acetaminophen respectively, while group A which served as the control received distilled water. The extract administration was done for 28 days consecutively until the dams underwent parturition. Thereafter, the animals were sacrificed and blood collected via cardiac puncture and tissues inclusive for assessment of the lipid profile. **Results:** It was observed that prenatal triacylglycerol (TAG) was not altered in all the test groups but the maternal TAG concentration of acetaminophen (Acet.) group was significantly ($p< 0.001$) higher than the control, and the test groups. This scenario was reversed for maternal HDL where that of Acet. group was significantly ($p<0.001$) lowered than the control and the test groups. The *P. thonningii* extract was able to reverse the effect of acetaminophen toxicity on HDL to normal both in the prenatal and maternal states. The maternal total cholesterol (TC) concentration of acetaminophen group was significantly ($p<0.05$) reduced to normal by the *P. thonningii* extract both at low and high doses. This was also reflected in the maternal LDL of acetaminophen group which was reduced significantly by low ($p<0.01$) and high ($p<0.05$) doses of *P. thonningii* extract. The prenatal TC and LDL were not affected by acetaminophen as there was no significant ($p>0.05$) difference between it and control or test groups. **Conclusion:** It can be inferred from this result that the extract of *P. thonningii* leaf reverses the effect of acetaminophen in pregnancy which includes hyperglyceridemia, hypercholesterolemia, with the possible reduction of the risk of preeclampsia.

***Keywords**:* Acetaminophen; Dams; Maternal; Prenatal; Preeclampsia; Serum lipid profile