

IBMBB

Institute of Biochemistry, Molecular Biology and Biotechnology

University of Colombo

Proceedings of the 14th Annual Scientific Sessions of the IBMBB

16th October 2026

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NATURE'S SCIENCE

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University of Colombo

Our Vision

"To be an International Centre of Excellence In Molecular Life Sciences "

14th Annual Scientific Session

16th October 2026

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    Abstract of the Prof. Stanley Wijesundera Memorial Lecture "Unveiling Three Decades of Flavonoid Metabolomics in *Camellia sinensis*: Deciphering Biosynthesis, Disease Resistance, and Quality Traits in Sri Lankan Tea Germplasm" by Former Prof. Nimal Punyasiri.
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Integrated enhancement of Life Sciences towards inclusive future

16th October 2026 at IBMBB University of Colombo

PROGRAMME

8.30 a.m. - 9.00 a.m.	Registration
9.00 a.m. - 9.05 a.m.	Inauguration
9.05 a.m. - 9.10 a.m.	Lighting the Traditional Oil Lamp
9.10 a.m. - 9.20 a.m.	Welcome Address by Director- IBMBB
9.20 a.m. - 9.30 a.m.	Address by Vice Chancellor- University of Colombo
9.30 a.m. - 9.40 a.m.	Best Teacher Award 2024/2025 & IBMBB Research Excellence Awards 2024/ 2025
9.40 a.m. -10.30 a.m.	Prof. Stanley Wijesundera Memorial Lecture- Former Prof. Nimal Punyasiri *"Unveiling Three Decades of Flavonoid Metabolomics in Camellia sinensis: Deciphering Biosynthesis, Disease Resistance, and Quality Traits in Sri Lankan Tea Germplasm"*
10.30 a.m. - 10.40 a.m.	Address by a Member of Professor Wijesundera family
10.40 a.m. - 10. 45 a.m.	Vote of Thanks
10.45 a.m. - 11.30 a.m.	Tea
11.30 a.m. -12.00 p.m.	Oral Presentations Session 1 - Genetics, genomics and bioinformatics
11.30 a.m. - 12.20 p.m.	Poster Presentations Session I
12.00 p.m. - 1.00 p.m.	Oral Presentations Session 2 - Biochemistry, Immunology and cell biology
12.20 p.m. - 1.10 p.m.	Poster Presentations Session 2
1.00 p.m. - 2.00 p.m.	Break
2.00 p.m. - 3.00 p.m.	Oral Presentations Session 3 - Nutrition, natural products and drug discovery
2.00 p.m. - 2.45 p.m.	Poster Presentations Session 3
3.00 p.m. - 3.45 p.m.	Oral Presentations Session 4 - Molecular Biology and Biotechnology
2.45 p.m. - 4.00 p.m.	Poster Presentations Session 4
3.45 p.m. - 4.15 p.m.	Tea Break
4.15 p.m. - 4.30 p.m.	Award Ceremony & Closing Remarks

Director's Message – 14th Annual Scientific Sessions, IBMBB, UOC



On behalf of the Institute of Biochemistry, Molecular Biology and Biotechnology (IBMBB), University of Colombo, I warmly welcome the Orator of the Prof. Stanley Wijesundera Memorial Lecture, delegates, researchers, academics, presenters and students to the 14th Annual Scientific Sessions of the IBMBB, UOC, 2026.

The Annual Scientific Sessions are an important annual event at the IBMBB, UOC, providing a platform for interaction, networking, collaboration, and new start-ups among all communities that directly or indirectly engage with the IBMBB. It also offers young researchers and students a valuable opportunity to interact with experienced academics and professionals.

It is with great pleasure that I acknowledge the contributions of the Orator, all presenters, reviewers, researchers, sponsors, and others who have been directly or indirectly involved in the session. I also greatly appreciate the dedication of the organizing committee and the IBMBB staff in making this event possible.

I wish everyone a productive, enjoyable and successful Scientific Session.

Professor Prasanna Galhena
Professor in Biochemistry and Clinical Chemistry
Director
Institute of Biochemistry, Molecular Biology and Biotechnology
University of Colombo

Message from the Co-Chairpersons





Prof. S.S.R. Samarakoon
Co-Chairperson
14th Annual Scientific Sessions – 2026
IBMBB, University of Colombo

Dr. A.S. Hewage
Co-Chairperson
14th Annual Scientific Sessions –2026
IBMBB, University of Colombo

It is with great pleasure that we welcome you to the 14th Annual Scientific Sessions of the Institute of Biochemistry, Molecular Biology and Biotechnology (IBMBB), University of Colombo**,** on 16th October 2026**.** The Annual Scientific Sessions of IBMBB provide a valuable platform for researchers, academics, students, and professionals to share their latest scientific findings and exchange ideas. Over the years, these sessions have contributed significantly to promoting research excellence and strengthening the scientific community in Sri Lanka and beyond.

This year's scientific programme brings together a diverse range of research spanning Biochemistry, Molecular Biology, Immunology, Bioinformatics, Natural Products and Drug Discovery, and related disciplines. The abstracts included in these proceedings reflect the enthusiasm, creativity, and commitment of researchers at different stages of their scientific careers.

As Co-Chairpersons, we are honoured to be part of this important scientific event. We extend our sincere appreciation to all researchers and authors who have contributed their work, as well as to the reviewers, organizing committee members, session chairs, invited speakers, sponsors and all those who have worked tirelessly to make these sessions a success.

We are particularly pleased to welcome young researchers and postgraduate students, whose participation brings fresh perspectives and new ideas to the scientific community.

We warmly welcome all participants to the 14th Annual Scientific Sessions of IBMBB and wish you an intellectually stimulating, productive, and memorable scientific experience.

Organizing Committee of the ARS 2026

Main Committee Appointments

Position	Name
Co-Chairpersons	Prof. Sameera Samarakoon
	Dr. Sudeshini Hewage
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Assistant Secretary	Dr. Anjana Welikala
Chief Editor	Dr. Visula Abeysuriya
Advisors	Prof. Prasana Galhena
	Prof. Kamani Tennekoon
	Prof. Nimal Punyasiri

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Ms. S.A.S.S. Samarasundara

Oral Presentations

Session 1 – Genetics, Genomics and Bioinformatics

OP1	Structural Bioinformatics of Ferric Uptake Regulator (Fur) across Siderophore-producing Plant Growth Promoting Bacteria (PGPB): Implication for Iron Acquisition.	**Jayamanna PS**, Mauran S, Dehiwalage DDH, Jayasinghe DDG
OP2	Detection of selected disease-associated variants in the SHANK3 gene in a cohort of Sri Lankan children with autism spectrum disorder	**Perera DNN**, De Silva S, Hewage AS, Fous SL, Abeysuriya V
OP3	Identification of a novel potentially pathogenic MSH6 protein variant in an endometrial cancer patient suggestive of lynch syndrome	**Azim S**, Abeysuriya V, De Silva S, Piyadigama I

Session 2 – Biochemistry, Immunology and Cell Biology

OP4	In vitro immunomodulatory effect of *Mikania cordata* aqueous leaf extract on leucocytes from type 2 diabetes mellitus patients	**Madusanka TRM**, Handunnetti SM, Katulanda P, Pathirana SL
OP5	Neodymium-induced alterations in human hemoglobin: analysis of methemoglobin formation and functional group binding interactions	**Nireshani MAMK**, Samarasekere PW, Rajapaksa G.
OP6	Do NS1 and anti-dengue IgG affect endothelial monolayer integrity? Evidence from *in vitro* study	**Wanigarathna GUS**, Rockwood N, Weeratunga PN, Pathirana SL, Perera IC, Nitsche A, Rajapakse S, Fernando N
OP7	Serum oxidative markers in patients with HER2-positive and HER2-negative breast cancer: A Pilot study	**Gamage HHM,** Rathnayake W, Fernando W, Fernando N
OP8	Effects of *Andrographis paniculata* on viability and monolayer integrity of DENV-2 NS1-exposed endothelial cells	**Jayarathna PMA**, Rodrigo J, Fernando N
OP18	Immunoinformatic Design of a Multi-Epitope Vaccine Targeting Co-Circulating Dengue and Zika Viruses in Sri Lanka and South-East Asia	**Sathsara WAS,** Gunasekara P, Senanayake K, Hapugoda M

Session 3 - Nutrition, Natural Products and Drug Discovery

OP9	Bioactivity assessment and micro-encapsulation of omega-3 rich fish oil from *Rastrelliger kanagurta* for nutraceutical capsule development	**Gunarathne GMRSB,** Indrajith CMC, Yasarathna KWGKP, Karunanayaka KDSV
OP10	Exploration of antibacterial properties of titanium-based species, incorporated in Seaweed extract, *Dictyota* sp.	**F. N. Rizvy,** A. M. Stevon and N. D. Wikramasinghe
OP11	Integrative Machine Learning, Molecular Simulation, for the Discovery of Small-Molecule Acetylcholinesterase Inhibitors.	**Rathnayake RMAS**, Senethilake SS, Samarakoon S, Adhikari A
OP12	Evaluation of immunomodulatory effects of *Camellia sinensis* (Ceylon black tea) brew in rats	**K.J. Kodikara Arachchige**, Abeysuriya V, Punyasiri PAN, Galhena P
OP13	Sub-acute toxicity evaluation of 6β-Cinnamoyl-7α-hydroxyvouacapan-5α-ol following intraperitoneal administration in female Wistar rats	**Oshadi EA,** Gunawardane SDV, Wijerathne PKS, Senathilake KS, Samarakoon SR, Punyasiri PAN
OP19	Cytotoxicity, developmental toxicity and phytochemical profiling of marine sponges: BSLT–ZFET concordance and isothiocyanate-rich bioactive chemistry	**Indurangi AMSK,** Edirisinghe EMRKB

Session 4 – Molecular Biology and Biotechnology

OP14	Molecular characterization and phylogenetic relationships of black gram (*Vigna mungo* L. Hepper) genotypes using ITS sequence analysis.	**Herath HMMN,** Terensan S, and Thirukkumaran G
OP15	A high-throughput method for quantifying transcription elongation rate	**Perera KCU**, Strobel EJ
OP16	Genome Mining and Biocatalytic Desulfation of Algal Biomass Using Marine Bacterial Sulfatases	**Nimansa DHS**
OP17	Development of a Real-time PCR-based approach for the early identification of latent tuberculosis infection	**Rathwita R**, Bandara T, Chiranthika D, Madegedara D, Magana Arachchi DN

Poster Presentations

PP1	Preliminary analysis of skin Pigmentation Gene variants, SLC24A5 (rs 1426654) and SLC45A2 (rs 16891982) among Sinhalese, Sri Lankan Tamil and Indigenous Adivasi Vedda Populations	**Jayakody A,** Ranasinghe R, Welikala A, Tennekoon KH
PP2	Association of FTO rs9939609 Variant with Obesity in different Vedda clans of Sri Lanka: A Preliminary Genetic Analysis	**Jani MGU**, Ranasinghe R, Welikala A, Tennekoon KH
PP3	Exploring the impact of *Camellia sinensis* (Ceylon black tea) consumption on theaflavin as a tea-derived metabolite and potential toxicological effects in rats	**Jayasinghe SM**, Abeysuriya V, Punyasiri PAN
PP4	Anticancer potential of flavones and flavanols in leaves of selected fruit plants focus on apigenin, luteolin, quercetin, myricetin, and kaempferol.	**Wickramawardana TGAI**, Muhinudeen FT, Chamuditha EAOV, Samarathunga LDTC, Punyasiri PAN, Rajagopalan U
PP5	Pretreatment with fucoidan-rich fractions from selected Sri Lankan Sargassum species modulates nitrite production and oxidative burst activity in activated RAW 264.7 macrophages	**Fernando KHE**, Gangani PD, Keerthi AAP, Dasanayaka BP
PP6	In vitro anti-inflammatory activity of aqueous and ethanolic leaf extracts of *Aporosa lanceolata* Thw.	**Devagiri DHN**, Senanayake P, Handunnetti S, Pathirana S
PP7	Comparison of Chloroplast Genomes of Six Cryptocoryne Species: In silico analysis	**Sugejan S**, Sirimalwatta VNS
PP8	DUOX2-related congenital hypothyroidism: Intrafamilial Phenotypic Variability in a Sri Lankan Family	**Bandarigoda J,** Gunawardhana KAPS, Liyanapathiranage DA, Kankananarachchi I, Padeniya P, Hettiarachchi M
PP9	Identification and Phylogeography of Dominant Hermit Crab species in Selected Locations from Matara District, Sri Lanka	**Weligamage UR,** Munasinghe DHN
PP10	Prevalence of GCKR rs1260326 and GCKR rs780094 variants in subjects with non-alcoholic steatohepatitis (NASH)-related hepatocellular carcinoma (HCC) in Sri Lanka	**Botheju IE**, Hewage AS, De Silva S, Tennekoon KH, Niriella MA, Siriwardana RC, Abeysuriya V, Samarasinghe SASM
PP11	Preliminary genetic analysis of a cohort of nasopharyngeal cancer patients in Sri Lanka	**Omede CE**, Hewage AS, De Silva S, Dissanayake S, Milhan B

PP12	Detection of chromosome 22q11.2 deletion in patients clinically suspected of DiGeorge syndrome attending an immunology clinic at Medical Research Institute, Sri Lanka.	**Lakshani PHPC,** Dasanayaka Dhanushka, de Silva Rajiva
PP13	Optimization of DNA extraction from Paraffin-Embedded tissues and preliminary analysis of NRAS and KRAS mutations in Well-Differentiated Thyroid Cancer	**Kugaperumal SD**, De Silva S, Abeysuriya V, Galhena P
PP14	Genomic characterization and phylogenetic analysis of Pseudomonas sp. isolated from a transplant unit of a national hospital	**Withanachchi S.U.**, Muthugala M.A.R.V.
PP15	Characterization of the forehead skin microbiome and antibiotic susceptibility patterns among healthy adults in Colombo District, Sri Lanka – A preliminary study	**Semindi LK,** de Zoysa MN, Kazmi AZ, Wijekoon RU, Sandamini HKN, Zakariya FZ
PP16	Antibacterial activity and melissopalynological characteristics of bee box honey and wild honey from Uva Province, Sri Lanka.	**Gunawardana SS**, Hewadikaram M, Dharmadasa RM
PP17	Evaluation of synergistic antibacterial potential of *Hemidesmus indicus* and *Terminalia chebula* against selected multi-drug resistance waterborne pathogens	**Ahamed MRR**, De Silva MSU, Jayathilaka LPTT, Nanayakkara NWERM, Upathissa ALM, Dissanayake CTN
PP18	Serotype predominance and molecular characterization of circulating dengue virus strains in Colombo District, Sri Lanka (2025)	**Dharmapriya HKSA**, Silva GN, Muthugala MARV
PP19	Microbiological identification and molecular characterisation of bacterial populations associated with black rot-like symptoms in *Brassica* crops in Sri Lanka	**Uthayakumar S,** Rajan K, Ranaweera D
PP20	Mapping bond strength in drug-like chemical space using the QM40 dataset: structural correlations and chemical insights	**Weerasuriya PS**, Dharmakeerthi R, Somasiri A, Kariyawasam S, Jayarathne NB, Kraka E, Madushanka A
PP21	Characterisation of Antimicrobial-Resistant Aquatic Biofilm-Forming Bacteria and Evaluation of Biosynthesised Silver Nanoparticles as Antibiofilm Agents	**Maddevithana HNMSN**, Rodrigo BKIS, Samarasinghe MHDTS, Silva KDT, Thathsarani KMT, Narawitage TCS, Attanayake DPSTG
PP22	Machine Learning-Based Radiomic Classification of Small Lymphocytes and Lymphoblasts in Smartphone-Aquired Cytology Images: A Step Toward Canine Lymphoma Diagnosis	**Kotawalagedara NNT,** Dissanayake D, Jayatilake ML, Ariyarathna H
PP23	Investigation of phytochemical and anti-inflammatory property of Leucas zeylanica	**Manthila KDM**, Diwyanjalee HK, Kulathunga MMSTCM,

		Sifaniya MNF, Shavindi WAA, Premarathna MGHM, Samarakoon DNAW
PP24	Potential of Garcinia quaesita Pierre extract to enhance meropenem activity against carbapenem-resistant Gram-negative bacteria	**Jayamangala DND**, Abeyrathne SGAM, Senarathna RMDR, Jayathilaka AWGSN, Pananwala KPD, Chandrasiri KG, Basnayake BMDT, Senaratne T, Weerasooriya BWMSB, Palihawadana HD, Jayasooriya RGBV, Tennakoon TMIUK, Mendis BCG
PP25	Phytochemical composition, antioxidant potential, and antimicrobial activity of selected Phaseolus leaves in Sri Lanka	**Nimansa DHS**
PP26	Evaluation of the Antimicrobial Potential of *Catharanthus roseus* (Madagascar Periwinkle) Leaf Extracts Against *Vibrio parahaemolyticus* Under In Vitro Conditions	**Pathirana WPDS** , Rathnapala JMSN , Bandara AMKA
PP27	Novel approach in natural cosmetics: Formulating and assessing the potential of *Ulva lactuca* extract in a cosmetic cream	**Wijerathna IA**, Nayomi HMD
PP28	Screening and Preliminary Identification of Oxytetracycline Residues in Commercial Milk Samples by TLC and HPLC	**Amaya WHO**, Nishshanka OKDUP, Abeysinghe DT
PP29	Evaluation of Antibacterial, Anti-inflammatory and Cytotoxic Activities of *Semecarpus subpeltata* (Kabara Badulla) Leaf Extract	**Pramodya DKGP**, Rathnayaka KGLNS, Kawishka PAR, Jayasuriya KAGM, Wikramasinghe MGTC, Kodikara VS, Jayamaha AR
PP30	Phytochemical and Bioactivity Assessment of an Endemic Medicinal Plant of Sri Lanka	**Karunathilaka WDR**, Mahesh SGDC, Pathmalojany P, Senadeera SPNN, Ranaweera CB, Kuruppu AI
PP31	Assessment of total phenolic content and total flavonoid content of three selected medicinal plants; *Artocarpus nobilis*, *Vernonia zeylanica* and *Bacopa monnieri*	**Jayabal FJ,** Rukshala BAD, Handunnetti SMH, Jagoda D
PP32	In silico molecular docking and ADMET profiling of *Borreria verticillata* bioactive compounds against endometrial inflammatory receptors; identifying lead candidates for endometriosis therapy	**Gamage JV**, Kawshalya I
PP33	In vivo liver protective effects and toxicity studies of a commercially available nutraceutical (LiverU) capsule	**Gunawardhana KWRD**, Wijerathna SK, Senathilaka K,

		Ranaweera G, Murugananthan A, Samarakoon SR
PP34	Evaluation of antioxidant and antimicrobial properties of plant-derived silver nanoparticles from Peanut Butter Fruit (Bunchosia sp.)	**Desmond DA,** Gunaratne B, Perera O, Kandiah M
PP35	Antibacterial screening of local medicinal plants *Mimosa pudica*, *Ocium tenuiflorum* and *Vernonia cinera*	**Dalsika KMTN**, Gamage HGSD, Rathnapala HC, Muthunayake NS
PP36	Antibacterial effects of fungal endophytes isolated from seaweeds likely belonging to Gracilaria spp. and Sargassum sp. collected from Pamunugama, Sri Lanka	**Fernando RAAS**, Asmone JV, De Silva MDS, Udalamaththa AVLK
PP37	Synergism of *Andrographis paniculata* and *Datura metel* Extracts on the Metastatic Ability of the Human Glioblastoma Cells	**Gamage NS**, Rajagopalan U, Samarakoon SR
PP38	Probiotic Pre-feeding Enhances the Protective Efficacy of a Streptococcus agalactiae Biofilm Vaccine in Nile Tilapia (*Oreochromis niloticus*)	**Shayanutha JS**, Guha R, Elumalai P
PP39	Isolation, Characterization and assessing Degradation kinetics of Fluorene degrading bacteria from marine water – A bioremediation approach	**Theekshana GPG**, Adhikari PAAS, Meddage AKMM, Bandara KRV
PP40	Isolation and characterization of indigenous potassium-solubilizing bacteria for biofertilizer development	**Prabaharan M**, Gunaratna LNR, Weerasena OVDSJ, Premanandarajah P
PP41	In silico screening and in vitro validation of anticancer properties of synthetic compound libraries	**Samarathunga LDTC,** Wickramawardana TGAI, Gunawardana SDV, Adhikaram AJSN, Rajagopalan U, Senathilake K. S, Adhikari A, Samarakoon SR
PP42	Large-scale structure-based virtual screening of natural products for the discovery of CDK2 and CDK4 inhibitors	**Perera WMR,** Indurangi AMSK, Darshani AMI, Sewwandi RMNM, Dissanayake HMNS, Edirisinghe EMRKB, Kraka E, Madushanka A
PP43	Electronic origin of the divergent bioactivities of eugenol and cinnamaldehyde in *Cinnamomum zeylanicum* leaf and bark: an integrated DFT, DPPH and GC-MS study	**Perera WMR**, Edirisinghe EMRKB

PP44	Synergistic antibacterial and anti-biofilm effect on *Phyllanthus niruri* extract and gentamicin against biofilm-forming *Pseudomonas aeruginosa* ATCC 27853	**Sachinthani SDD,** Shimra UF, Sandamali SP, Dulanjalee GR, Peiris WWDM, Rasanjanee DDY, Senanayake RASP
PP45	Genome-wide in silico analysis of iron-tolerant bacteria in paddy soils: unveiling genetic mechanisms for bioremediation	**Ranawaka TP**, Kariyawasam IU, Fernando PC

Professor Stanley Wijesundera Memorial Lecture

Introduction

Professor Stanley Wijesundera Memorial Lecture is an annual event of the IBMBB held to commemorate the late Professor Stanley Wijesundera, who served as Professor of Biochemistry and as First Vice Chancellor, University of Colombo from 1978-1987. Professor Wijesundera was a visionary leader during whose tenure, infrastructure development and academic progress at the University of Colombo were at their peak. He played a key role in the development of the discipline of Molecular Biology in the University of Colombo.

Previous Professor Stanley Wijesundera Memorial Lectures were delivered by Professor Rune Liminga, Former Director, International Programme in Chemical Sciences, University of Uppsala, Sweden; Professor W D Lakshman, Former Vice Chancellor, University of Colombo; Vidyajyothi Professor Eric Karunanayake, Founder Director, IBMBB & Emeritus Professor of Biochemistry, University of Colombo; Professor Lal Chandrasena, Senior Professor of Biochemistry, University of Kelaniya and Professor E Dilip de Silva, Senior Professor of Organic Chemistry, University of Colombo; Professor Kamani Tennekoon, Senior Professor of Molecular Life Sciences, IBMBB, University of Colombo, Former Director, IBMBB & former Professor of Physiology, Faculty of Medicine, University of Colombo; Vidyajyothi Professor Rezvi Sheriff, Senior Professor of Medicine, Kotelawala Defense University, Sri Lanka and Former Senior Professor of Medicine, Faculty of Medicine, University of Colombo; Dr Rajiva de Silva, Consultant Immunologist & President-Allergy and Immunology Society of Sri Lanka; Vidyajyothi Professor Harendra de Silva, Emeritus Professor of Paediatrics at the University of Colombo, Honorary Fellow of the Royal College of Paediatrics and Child Health; Senior Professor Sagarika Ekanayake, Professor in Department of Biochemistry, Faculty of Medical Sciences, University of Sri Jayewardenepura; Vidyajyothi Professor Vajira H. W. Dissanayake, Dean, Faculty of Medicine; Chair and Senior Professor Department of Anatomy, Genetics and Biomedical Informatics University of Colombo.

Last year, the Professor Stanley Wijesundera Memorial Lecture was delivered by Professor Dileep De Silva, Chair Professor and Board-Certified Specialist in Community Dentistry, Faculty of Dental Sciences, University of Peradeniya.

This year, at the 14th Annual Scientific Sessions, the Professor Stanley Wijesundera Memorial Lecture will be delivered by Former Professor Nimal Punyasiri, titled “Unveiling Three Decades of Flavonoid Metabolomics in *Camellia sinensis*: Deciphering Biosynthesis, Disease Resistance, and Quality Traits in Sri Lankan Tea Germplasm”.

Professor Stanley Wijesundera Memorial Lecture

Introduction to the Orator



Former Chair & Professor of Biochemistry, Institute of Biochemistry, Molecular Biology and Biotechnology (IBMBB), University of Colombo

Professor P.A. Nimal Punyasiri is an exceptionally distinguished biochemist, natural products chemist, and academic leader who has seamlessly integrated the three pillars of science—Research, Industry, and Academia—over a prolific career spanning more than four decades. He currently holds the prestigious position of Chair and Professor of Biochemistry at the Institute of Biochemistry, Molecular Biology and Biotechnology (IBMBB), University of Colombo, and serves honorably as the Deputy Director (Research) at the Neurophysiology Research Center, Faculty of Medicine, University of Colombo.

Professor Punyasiri's academic foundation began with the Institute of Chemistry, Sri Lanka, and culminated in a PhD in Biochemistry from the Postgraduate Institute of Science, University of Peradeniya in 2006. His global research footprint includes extensive postdoctoral fellowships at the prestigious Technical University of Braunschweig in Germany (spanning 2022 to 2025), the Swedish University of Agricultural Sciences, and the IBMBB. A scientist of the highest international caliber, he is a Chartered Chemist, Chartered Biologist, and holds prestigious Fellowships with the Royal Society of Chemistry (UK), the Institute of Chemistry, Sri Lanka, and the Institute of Biology, Sri Lanka.

Beginning his journey as a Technical Assistant at the Tea Research Institute (TRI) of Sri Lanka in 1981, Professor Punyasiri rose through the ranks to become a Senior Research Officer, dedicating decades to pioneering tea biochemistry. His breakthrough research on the *Exobasidium vexans* (blister blight) infection fundamentally advanced our understanding of the preformed and induced chemical resistance mechanisms in the tea plant. His work later bridged directly into the corporate sphere, where he served as the Director of Research & Development and Head of the Plant Research Centre for Nature's Beauty Creations Ltd. Today, his research focuses heavily on cutting-edge clinical and plant metabolomics.

An innovator at heart, Professor Punyasiri has successfully translated laboratory science into commercial enterprise. His notable innovations include the development of a commercialized anti-aging cosmetic ingredient and a skin-lightening ingredient derived from Sri Lankan flora, and an antifungal biocide targeting blister blight leaf disease.

His profound contributions have been recognized with numerous accolades, including eight Presidential Awards for Research Excellence, the National Awards for Excellence in Agricultural Research (First Prize in 2010 and 2017), the Professor Kandiah Memorial Award, and the Dr. C.L. De Silva Gold Medal from the Institute of Chemistry, Sri Lanka. His commitment to institutional excellence has also earned him multiple Senate Commendation Awards from the University of Colombo.

Professor Punyasiri is also a deeply committed educator and mentor, guiding generations of students with his personal motto: *"Help others" and "Teaching with a Personal Touch"*. He has shaped national curricula in Tea Biochemistry and Cosmetic Science and has served the scientific community as the President of the Cosmetic Manufacturers Association of Sri Lanka and a longtime Council Member of the Institute of Chemistry, Sri Lanka.

With an extensive, peer-reviewed publication record across top-tier international journals in chromatography, food composition, and chemical ecology, he stands as a vanguard of modern biochemical research.

Synopsis of the Orator

Unveiling Three Decades of Flavonoid Metabolomics in *Camellia sinensis*: Deciphering Biosynthesis, Disease Resistance, and Quality Traits in Sri Lankan Tea Germplasm

P. A Nimal Punyasiri

Abstract

Background: Flavonoids are ubiquitous secondary metabolites in the tea plant (*Camellia sinensis* L.) that critically dictate product quality, taste, color, and resistance to environmental stresses. Over the past two decades, a systematic metabolic and biosynthetic profiling approach was deployed to unleash the chemical potential of the Sri Lankan tea germplasm.

Methodology: Comprehensive metabolite profiling of over 90 beverage and non-beverage tea accessions was performed utilizing high-performance liquid chromatography (HPLC), liquid chromatography-tandem mass spectrometry (LC-MS/MS), enzyme assays, and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS).

Significant Findings:

- **Biosynthetic Elucidation:** The core flavonoid biosynthetic pathway in *C. sinensis* was successfully mapped, revealing the activity of seven cytosolic enzymes and documenting the presence of anthocyanidin reductase (ANR) for the first time. This confirmed that 2,3-*trans*-catechins are produced via leucoanthocyanidin reductase (LAR) whereas 2,3-*cis*-catechins are synthesized via ANR.
- **Biochemical Disease Markers & Defense Mechanisms:** In probing blister blight leaf disease caused by the biotrophic fungus *Exobasidium vexans*, preformed levels of $(-)$-epicatechin (EC) were established as a reliable biochemical marker for disease resistance. Fungal infection induced a pronounced host defense response, characterized by a 10-fold increase in proanthocyanidins coupled with a metabolic shift favoring 2,3-*cis* stereochemistry and elevated gallate esterification.
- **Tea Quality Prediction:** Quality indexing revealed that accessions suited for premium black tea manufacture possess elevated levels of dihydroxylated catechins (EC and ECg), higher dihydroxylated-to-trihydroxylated catechin ratios, and lower gallated-to-non-gallated catechin ratios.
- **Germplasm Diversification & Novel Cultivars:** Extensive screening mapped the distributions of major flavonols (quercetin, kaempferol, and myricetin) to determine the exotic origins and taxonomic affinities of the germplasm, establishing that *C. sinensis* ssp. *lasiocalyx* predominates in Sri Lanka. Furthermore, six distinct anthocyanin species—including novel delphinidin- and cyanidin-galactosides and their coumaroyl derivatives—were isolated and structurally characterized from the unique purple tea cultivar (TRI 2043) for the first time.

Conclusion: These collective milestones provide robust chemodiverse footprints that skip traditional long-term field processing trials, enabling early molecular-assisted selection and targeted breeding strategies for high-quality, disease-resistant tea cultivars.

Keywords: *Camellia sinensis, Catechin, Flavonoids, Anthocyanidin Reductase, Exobasidium vexans, Blister Blight, Purple Tea, Metabolite Profiling*

Abstract No: OP1

Structural Bioinformatics of Ferric Uptake Regulator (Fur) across Siderophore-producing Plant Growth Promoting Bacteria (PGPB): Implication for Iron Acquisition

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Promoting beneficial plant growth in a bio-friendly manner is a major concern in agriculture, where Plant Growth Promoting Bacteria (PGPB) play a vital role. Micronutrients such as iron are important for plant growth and productivity, which target various physiological processes, including photosynthetic pathways. Siderophore-producing PGPB enhance chelation of Fe^{3+}, thereby stimulating plant growth and iron acquisition under stress conditions. This study targets molecular screening of the Ferric Uptake Regulator (Fur) gene, which is responsible for transcriptional regulation of siderophore biosynthesis and iron transportation. Twelve bacterial PGPB strains, belonging to *Bacillus* spp., *Enterobacter* spp., and *Pseudomonas* spp., were selected based on the siderophore-iron acquisition mechanism. Using an integrated bioinformatics pipeline, the protein sequences retrieved from the STRING database were aligned with MUSCLE, and a phylogenetic tree was constructed using Maximum-Likelihood using Mega 12.1.2. Protein structures were retrieved/predicted via the Protein Data Bank/Swiss-Model; physicochemical parameters, functional annotation, and domain localization were predicted using ProtParam and InterProScan, respectively. Molecular docking of Fe^{2+}/Fe^{3+} ions towards the predicted pocket of the regulatory protein using PyRx-0.8. Furthermore, metal-binding sites of the strains were evaluated to determine the protein's target region, which could regulate iron uptake. *In silico* analysis revealed that the Iron-binding sites of *Bacillus* spp., *Enterobacter* spp., and *Pseudomonas* spp. reside in between the dimerization domain (Pro41-Val46: Glu41-Leu46), α2 (Leu26-His32), and α5 (Met102-Lys108), respectively. These regulatory proteins are stable with a slightly acidic pI, and possess a DNA-binding domain for transcriptional regulation. In conclusion, the regulation by the Fur protein in PGPB ultimately governs the iron uptake of associated plants via siderophore production.

Keywords: S*iderophore, Plant Growth Promoting Bacteria, Molecular docking, Ferric Uptake Regulator*

Abstract No: OP2

Detection of selected disease-associated variants in the *SHANK3* gene in a cohort of Sri Lankan children with autism spectrum disorder

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Autism spectrum disorder (ASD) is a complex, heterogeneous neurodevelopmental condition with increasing prevalence; however, its genetic basis remains largely unexplored in Sri Lanka. SH3 and multiple ankyrin repeat domains 3 (*SHANK3*) is a high-confidence autism-risk gene that encodes a central scaffolding protein essential for neuronal signalling and synaptic function. This study investigated the association of two selected *SHANK3* variants, rs9616915 (c.959T>C) and rs762292772 (c.3904dup), in Sri Lankan children with ASD. Twenty children with clinically diagnosed ASD (4–14 years) and five healthy controls (8–14 years) were recruited. Genomic DNA extracted from peripheral blood was amplified using exon-specific primers and analysed by Sanger sequencing. Detected variants were evaluated using *in silico* tools, including Mutation Surveyor, SIFT, PolyPhen-2, and MutationTaster. Maternal and paternal ages at childbirth were significantly higher in the ASD group than in the controls, whereas birth weight did not differ significantly. The rs9616915 variant was identified in 12/20 ASD cases (three CC and nine TC genotypes), while all controls were heterozygous (TC). However, genotype distribution did not differ significantly between groups (p=0.0864). The rs762292772 variant was absent in both groups. Additional variants identified in exon 22 of ASD patients were c.3903G>T (rs772120494), c.3830C>G (rs940248882), and a novel missense variant, c.3815G>C. These variants were absent in controls. *In silico* analysis predicted c.3830C>G and c.3815G>C variants to be possibly damaging and deleterious, suggesting a potential association with ASD. No statistically significant association was observed between ASD and the selected *SHANK3* variants. However, detection of rare variants, including a novel potentially deleterious missense variant, supports the need for larger, adequately powered studies to clarify the contribution of SHANK3 to ASD in Sri Lankan paediatric populations.

Keywords: *Autism spectrum disorder (ASD), SHANK3 gene, Exonic variants, Single Nucleotide Polymorphism (SNP), Sri Lanka*

Abstract No: OP3

Identification of a novel potentially pathogenic MSH6 protein variant in an endometrial cancer patient suggestive of lynch syndrome

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Hereditary endometrial cancer (EC) is an important gynaecological malignancy associated with Lynch syndrome (LS), an autosomal dominant hereditary cancer syndrome caused by pathogenic variants in DNA mismatch repair genes, including *MSH2, MSH6, MLH1*, and *PMS2*. Defective mismatch repair promotes genomic instability and contributes to carcinogenesis. In Sri Lanka, molecular data and standardized protocols for hereditary EC management remain limited. This study aimed to genetically characterise pathogenic mutations in the *MSH6* gene in EC patients clinically suggestive of LS, and model the mutation specific protein to identify changes to the conserved MSH6 structure. A descriptive study was conducted among six EC patients (n=6) diagnosed <50 years, with a significant family history of cancer. Patient DNA was sequenced using custom-designed primers specific for exon 5 of *MSH6* gene. The amino acid sequence corresponding to this novel frameshift deleterious c.3252_3253delTA *MSH6* mutation detected in one EC patient was formulated using LUMC Mutalyzer-3. The protein sequences were extracted and used to model this mutant MSH6 protein with the SWISS-MODEL and ChimeraX bioinformatic tools. Model stability and biological plausibility were assessed using Ramachandran plot analysis and MolProbity scoring. This analysis showed an acceptable backbone geometry with a MolProbity score of 1.44 compared with 1.27 for the conserved MSH6 protein that signifies the stability of this protein, this mutant protein lacked a significant majority of the ATPase domain, essential for mismatch base recognition, excision and repair. This significantly underlies its pathogenic relevance associated with the potent disruption of mismatch repair during DNA replication, actively driving a cell towards tumorigenesis. These findings support further investigation of the hereditary EC mutation spectra in Sri Lanka and associated development of evidence-based genetic testing and cancer management strategies. This work provides an initial molecular basis for strengthening local LS screening pathways and clinical counselling services.

Keywords: *Lynch Syndrome, Endometrial cancer, MSH6 mutation, Bioinformatics protein modelling, Sri Lanka*

Abstract No: OP4

In vitro immunomodulatory effect of *Mikania cordata* aqueous leaf extract on leucocytes from type 2 diabetes mellitus patients

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Type 2 diabetes mellitus (T2DM) is a chronic metabolic condition that significantly impairs phagocyte function, leading to increased infection susceptibility and complications such as delayed wound healing. *Mikania cordata*, a medicinal plant used to treat anti-inflammatory and antioxidant properties in traditional medicine, has not been tested for phagocytic functions in diabetic patients. Twenty T2DM patients were recruited from a diabetic clinic, and six healthy individuals were selected from university staff and students through convenience sampling. Clinical information of the patients, including HbA1c, lipid, hormonal, renal, and hepatic parameters, was recorded. Based on glycaemic control, patients were categorized into three subgroups: well-controlled (HbA1c 6.5–7.0%), moderately controlled (HbA1c 7.1–9.0%), and poorly controlled (HbA1c ≥9.0%). Five mL of blood was collected from each participant, and total leucocytes were isolated using dextran sedimentation. To assess the immunomodulatory potential of the *M. cordata* aqueous leaf extract (ALE), phagocytic activity was evaluated using a phagocytic assay, while reactive oxygen species and reactive nitrogen species production were quantified using the NBT and Griess assay, respectively. Phagocytes from T2DM patients had a significantly lower overall phagocytic index (OPI) compared to healthy controls ($p=0.0026$), which improved significantly following ALE treatment ($p=0.0153$). Patients with well-controlled glycaemia (HbA1c 6.5–7.0%) achieved complete restoration of phagocytic activity after ALE treatment, a level that was comparable to healthy controls. Resting superoxide production was significantly higher in T2DM patients relative to healthy controls, indicating chronic baseline oxidative stress ($p=0.0087$). Nitric oxide production was comparable among T2DM patients. Partial correlation analysis identified HbA1c, triglycerides, and LDL-cholesterol as negatively associated with phagocytic activity and superoxide production. The ALE of *M. cordata* exhibited an immunomodulatory effect that diminished with poorer glycemic control. These findings provide the first scientific evidence of *M. cordata* ALE-mediated immunomodulation in human leucocytes from T2DM patients, supporting its potential as an adjunctive agent in diabetic wound management.

Keywords: *Mikania cordata, type 2 diabetes mellitus, phagocytic activity, immunomodulation, superoxide production*

Abstract No: OP5

Neodymium-induced alterations in human hemoglobin: analysis of methemoglobin formation and functional group binding interactions

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Neodymium, a widely used rare earth element in emerging technological applications, has increasingly being recognized as an "emerging contaminant" owing to its presence in ecosystems and living organisms. The presence of rare earth elements in the human circulation have been reported to cause potential toxicity to erythrocytes. However, the exact molecular effects of Neodymium on erythrocytes are infrequently investigated. Therefore, this study aimed at exploring the impact of Neodymium on human hemoglobin structure and function in vitro. Neodymium-mediated binding and oxidation of hemoglobin were assessed using vitro assays. Following informed consent, 5ml of venous blood was collected from ten female participants and a 5% hematocrit was prepared. Erythrocytes were incubated with three different concentrations (10, 50 and 100 µmol/L) of $Nd(NO_3)_3$ for 24 hours. Hemoglobin oxidation induced by Neodymium was assessed by analysing methemoglobin levels. Interactions of Neodymium with peptide, aromatic, and heme groups of hemoglobin were analysed using UV-spectroscopy. All three concentrations have significantly increased methemoglobin production compared to the control (One-way ANOVA; $p < 0.05$). An increasing concentration of Neodymium has shown to increase the methemoglobin production, indicating a possible metal-hemoglobin interaction that could impair its oxygen binding capacity. Neodymium at 100 µmol/L was shown to interact with all the three functional groups. However, the concentrations of 10 and 50µmol/L) interacted with heme and aromatic groups of hemoglobin only. In conclusion, Neodymium exposure leads to increased methemoglobin production possibly due to disturbed hemoglobin integrity through the metal interaction with peptide, heme, and aromatic groups of hemoglobin. Findings from this preliminary study encourages more mechanistic studies and emphasize the importance of regulatory measures to reduce the low levels of Neodymium exposure in humans.

Keywords: *Neodymium, Erythrocytes, Hemoglobin, Methemoglobin, Metal-Hemoglobin Interactions*

Abstract No: OP6

Do NS1 and anti-dengue IgG affect endothelial monolayer integrity? Evidence from *in vitro* study

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Dengue is a major global health concern. Severe disease is characterized by endothelial barrier disruption and vascular leakage. This study investigated the *in vitro* effect of dengue NS1 and anti-dengue IgG, on endothelial barrier disruption between primary and secondary dengue infections. Serum samples were collected from 80 qPCR-confirmed dengue patients, comprising 44 patients with secondary infection. Among secondary infections, 28 patients had ultrasound-confirmed plasma leakage, while 16 had no evidence of leakage. The median day of fever at sample collection was similar between the secondary and primary infection groups ($p = 0.76$). Human macrovascular endothelial cells (EA.hy 926) were incubated with patient sera for 45 minutes. Endothelial monolayer disruption was quantified using ImageJ-based image analysis and expressed as the relative gap compared with controls. Secondary infections had significantly higher IgG levels, lower NS1 levels compared to primary infections ($p < 0.001$) and greater endothelial disruption than primary infections, with higher relative gap values (1.36 [1.17–1.59] vs. 1.26 [1.08–1.46], $p = 0.026$). However, NS1 had no association with endothelial monolayer disruption in either primary or secondary infections. In contrast, IgG levels showed a significant positive association with relative gap formation in secondary dengue infection ($r = 0.387$, $p = 0.005$) and remained independently associated in multiple linear regression analysis ($\beta = 0.411$, $p = 0.017$), whereas no such association was observed in primary infection. IgG distinguished secondary dengue patients with plasma leakage from those without (AUC 0.705, 95% CI: 0.529–0.882, $p = 0.025$; cut-off 131.6 RU/ml, sensitivity 96.4%, specificity 50.0%. Elevated anti-dengue IgG levels were associated with increased endothelial barrier disruption in secondary dengue infection and demonstrated moderate discriminatory ability for identifying patients with plasma leakage, with a sensitivity of 96.4% and specificity of 50.0%.

Keywords: *Dengue, Monolayer Disruption, Anti-Dengue IgG, NS1, Secondary Infection*

Acknowledgements: *This work was financially supported by the Robert Koch Institute (RKI), Germany*

Abstract No: OP7

Serum oxidative markers in patients with HER2-positive and HER2-negative breast cancer: A Pilot study

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Breast cancer is the most commonly occurring cancer among women worldwide. Breast cancer has different subtypes, including human epidermal growth factor receptor 2 (HER2) positive and negative tumors. Recent studies have increasingly focused on the role of Reactive nitrogen species (RNS) and lipid hydroperoxides (LP) in breast cancer biology. RNS is known to have both pro-tumor and anti-tumor effects in many cancer types. LP have been widely studied as potential biomarkers, as their concentration can vary significantly in different clinical outcomes of breast cancer. However, the relationship between distinct molecular subtypes of breast cancer and systemic oxidative markers remains poorly characterized. Therefore, this study aimed to determine systemic oxidative stress levels in terms of RNS and LP in HER2-positive and HER2-negative breast cancer patients compared to age and gender-matched healthy controls. A cross-sectional study was conducted using treatment naïve twenty-two HER2-negative and eleven HER2-positive patients, and six healthy controls. Individuals with uncontrolled comorbidities, systemic inflammatory conditions, and autoimmune conditions were excluded from the study. RNS and LP levels were measured by performing the modified Griess assay and the ferrous oxidation xylenol orange assay, respectively, in serum samples. Statistical comparisons were performed using the Kruskal-Wallis test and the Mann-Whitney U test. In this study, the serum total RNS levels were significantly higher in both cancer groups [HER2-positive ($p=0.018$), HER2-negative ($p=0.003$)] than in healthy controls. While no significant difference was observed in serum LP levels among the three study groups, higher serum LP levels were observed in patients with grade 3 tumors compared to those with tumor grades 1 ($p = 0.024$) and 2 ($p = 0.010$). No significant difference in systemic oxidative markers was observed between HER2-positive and HER2-negative breast cancer patients ($p>0.05$). These findings indicate that total RNS and LP may serve as meaningful biomarkers in high-grade breast cancer types.

Keywords: *Breast cancer, Molecular subtypes, Serum total RNS, Lipid hydroperoxides*

Abstract No: OP8

Effects of *Andrographis paniculata* on viability and monolayer integrity of DENV-2 NS1-exposed endothelial cells

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Dengue virus serotype 2 non-structural protein 1 (DENV-2 NS1) induces endothelial damage, leading to vascular leakage in dengue. *Andrographis paniculata* is a native medicinal plant with evidence of potential therapeutic effects against DENV. However, its effects on NS1-induced endothelial damage have not yet been evaluated. Therefore, this study evaluated the effect of *A. paniculata* extract on endothelial cell viability and monolayer integrity following DENV-2 NS1 exposure. EA.hy926 cells were treated with freeze-dried aqueous *A. paniculata* extract at 1000 µg/mL for 6 h either before (pre-treatment) or after (post-treatment) exposure to DENV-2 NS1 at 2 µg/mL for 12 h. Cell viability was assessed using the Sulforhodamine B assay, and monolayer integrity was evaluated by quantifying endothelial gap formation using ImageJ. Exposure to NS1 reduced cell viability to 88.17 ± 1.48% (~12% reduction) relative to control and increased endothelial gap formation to 2.78 ± 0.05 relative to control. Both treatment approaches significantly increased endothelial monolayer integrity, reducing NS1-induced gap formation to 0.94 ± 0.06 (pre-) and 0.89 ± 0.07 (post-) ($p < 0.001$). Pre-treatment partially increased cell viability (90.39 ± 1.10%), whereas post-treatment significantly restored viability relative to control (98.62 ± 0.37%, $p < 0.001$). These findings demonstrate that *A. paniculata* effectively reduces DENV-2 NS1-induced endothelial damage by increasing cell viability and monolayer integrity, with post-treatment showing greater restorative effects. This study supports further evaluation of *A. paniculata* as a potential plant-derived therapeutic candidate for dengue-associated endothelial dysfunction.

Keywords: *Andrographis paniculata, DENV-2 NS1, cell viability, monolayer integrity, endothelial cells*

Acknowledgements: *This work was supported by IBMBB and constitutes part of the MSC studies of PMAJ*

Abstract No: OP9

Bioactivity assessment and micro-encapsulation of omega-3 rich fish oil from *Rastrelliger kanagurta* for nutraceutical capsule development

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Omega-3 polyunsaturated fatty acids (PUFAs) are essential nutrients, especially in preventing neuroinflammation and coronary heart diseases. Although PUFAs offer many health benefits, they are highly susceptible to oxidation, which can reduce their nutritional value. This study aimed to evaluate the anti-inflammatory activity of Indian mackerel (*Rastrelliger kanagurta*) oil and formulate and assess micro-encapsulated hard gelatin capsules. In this laboratory-based study, fish oil was extracted from authenticated fish samples using Soxhlet extraction with hexane as the solvent. The anti-inflammatory activity of the oil was evaluated by conducting an egg albumin denaturation assay. Oil was micro-encapsulated by combining it with maltodextrin and gum acacia matrix, followed by freeze-drying, to reduce the oxidation of oil. The obtained powder was blended with excipients, including microcrystalline cellulose (MCC) (25% w/w), maize starch (10% w/w), polysorbate (2% w/w), and tocopherol (vitamin E) (0.5 w/w), followed by wet granulation to form beads, which were then manually filled into size number 0 hard gelatin capsules. Then, the final formulation underwent standard quality assessments to confirm that all quality attributes complied with pharmacopeial standards. The results of the study show that Indian mackerel oil has considerable anti-inflammatory activity with an IC_{50}= 1188 µg mL^{-1} ($p < 0.0001$), compared to diclofenac sodium (positive control) at 384.40 µg mL^{-1}. Importantly, formulated omega-3 hard capsules showed promising quality parameters, including complete disintegration within 4 minutes and 50 seconds, and a dissolution rate of 87.69%, which fully complies with pharmacopeial acceptable limits. Furthermore, all capsules complied with weight variation standards (370 mg- 430 mg), pH remained in a stable range (6.59-6.54) within one week, and no microbial contamination (TAMC≤ 10^3 CFU g^{-1}) was exhibited, and they were physically stable. Overall, these results strongly support that the formulated omega-3 hard capsules from Indian Mackerel oil are stable and pharmaceutically suitable as a nutraceutical for health concerns.

Keywords: *Anti-inflammatory, Hard gelatin capsule, Micro-encapsulation, Omega-3, Wetgranulation*

Abstract No: OP10

Exploration of antibacterial properties of titanium-based species, incorporated in Seaweed extract, *Dictyota sp.*

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Metatitanic acid (MTA) is a titanium-based intermediate which exhibits promising antimicrobial and photocatalytic properties. In the present study, MTA was synthesized via a modified sulfate extraction process followed by thermal aging. Subsequently, a novel MTA–*Dictyota* composite was developed through the incorporation of *Dictyota* extract into the synthesized material. The prepared materials were characterized using Fourier Transform Infrared Spectroscopy (FTIR), Scanning Electron Microscopy (SEM), UV–Visible spectroscopy, and X-ray Diffraction (XRD) analyses. Characterization results confirmed the successful synthesis of crystalline MTA, exhibiting characteristic Ti–O, sulfate, and hydroxyl functional groups. SEM analysis revealed well-defined, non-agglomerated particles with rod-like and rectangular morphologies. The antibacterial activities of MTA, MTA supernatant, and the MTA–*Dictyota* composite were evaluated using the agar diffusion method, while photocatalytic performance was assessed under varying experimental conditions. Key operational parameters, including catalyst concentration, solution pH, and light dependency, were systematically investigated. Statistical analyses were performed using analysis of variance (ANOVA) followed by Tukey's Honestly Significant Difference (HSD) multiple comparison test. Among the antibacterial treatments evaluated, the highest antibacterial activity was observed for the MTA supernatant against *Escherichia coli*, producing a mean inhibition zone of 20.67 ± 0.37 mm. Significant differences among treatments were observed ($p < 0.05$). Photocatalytic studies similarly revealed significant treatment effects ($p < 0.05$), with pure MTA demonstrating slightly higher degradation efficiency than the MTA–*Dictyota* composite under the tested conditions. Overall, the findings highlight the potential of MTA as an effective antibacterial and photocatalytic material, while the incorporation of *Dictyota* extract introduces a novel bio-based composite with promising applications in environmental remediation and antimicrobial technologies.

Keywords: *Antibacterial activity, Dictyota extract, Meta titanic acid (MTA), Photocatalytic activity*

Abstract No: OP11

Integrative Machine Learning, Molecular Simulation, for the Discovery of Small-Molecule Acetylcholinesterase Inhibitors

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Alzheimer's disease (AD), accounting for over 60% of dementia cases globally, is highly significant in Sri Lanka due to its rapidly ageing population. Characterized by cognitive decline, its hallmarks include amyloid-beta plaques and neurofibrillary tangles. Current symptomatic treatments target acetylcholinesterase's (AChE) catalytic active site but cannot halt disease progression. Because AChE's peripheral anionic site (PAS) promotes amyloid aggregation, developing dual-site inhibitors targeting both domains is a promising strategy. This study aimed to identify novel acetylcholinesterase inhibitors for the management of Alzheimer's disease by evaluating 54 molecular derivatives based on bioactive coumarin and isatin scaffolds. The pipeline included 2D multiple-linear-regression (MLR) and ridge-stacked ensemble, quantitative-structure-activity-relationship (QSAR) models to predict inhibitory activity. Molecular docking protocols were validated using four AChE structures against active and decoy compounds from the DUD-E database; performance was assessed via Receiver Operating Characteristic (ROC) curves and enrichment analysis, while redocking yielded root-mean-square deviation (RMSD) values <2 Å. Lead candidates were identified through consensus scoring, with coumarin-A17 selected for advanced evaluation. Molecular dynamics (MD), MMP-BSA, and umbrella sampling characterized binding stability and thermodynamics. The constructed 2D-MLR and ensemble QSAR models identified 14 compounds in total with predicted IC_{50} values lower than those of galantamine. A17 exhibited stable binding (mean RMSD: 0.32 nm), consistent hydrogen bonding, and a compact conformation. Free energy calculations yielded binding energies of -99.29 kJ/mol (MMP-BSA) and -17.27 kJ/mol (umbrella sampling), outperforming galantamine. Further in vitro, in vivo, and clinical investigations are required to validate A17 as an AD drug lead.

Keywords: *Alzheimer's disease, quantitative structure-activity relationship (QSAR) modelling, stacked ensemble, molecular dynamics, Umbrella sampling*

Abstract No: OP12

Evaluation of immunomodulatory effects of Camellia sinensis (Ceylon black tea) brew in rats

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Ceylon black tea (*Camellia sinensis*) is among the most widely consumed beverages in the world, but its immunomodulatory effects *in vivo* remain poorly characterized, particularly when sugar is added as is typical in everyday consumption. This study evaluated the dose-dependent immunomodulatory effects of Ceylon black tea, with and without sugar, in a carrageenan-challenged Wistar rat model. Tea was brewed according to ISO 3103 specifications, and human-equivalent doses of one, two, and three cups were converted to rat doses using body-surface-area (Km) scaling. In a Phase 1 dose-optimization study, rats received tea orally before an intraperitoneal carrageenan challenge, and nitric oxide production (Griess assay) and peritoneal phagocytic-cell migration were assessed. Black tea suppressed both endpoints in a graded, dose-dependent manner, with the three-cup-equivalent dose producing the greatest effect, nitrite fell from 23.47 µM to 3.69 µM and phagocytic cell migration index from 914.83 to 393.00 AU (both $p < 0.0001$). This dose was carried into a 28-day Phase 2 study comparing water, tea, and tea with sugar groups ($n = 6$ per group) across four endpoints: nitrite (Griess), superoxide (NBT), TNF-α gene expression (qPCR), and peritoneal cell recruitment. Tea alone produced the most consistent anti-inflammatory profile, reducing nitrite to 3.67 µM (~85%), superoxide to 290.17 µM (~41%), TNF-α expression to 0.07-fold, and migration index to 357.33 AU (~60%) relative to water (all $p < 0.0001$). Added sugar retained significant suppression of nitrite, superoxide, and TNF-α but these effects were attenuated with values consistently higher than tea alone, and phagocytic cell recruitment was partially restored. These findings demonstrate measurable, multi-endpoint anti-inflammatory activity of Ceylon black tea in acute inflammation and indicate that added sugar partially modifies this immunomodulatory profile, supporting further mechanistic and translational investigation.

Keywords: *Ceylon black tea, Camellia sinensis, immunomodulation, inflammation, nitric oxideTNF-α*

Abstract No: OP13

Sub-acute toxicity evaluation of 6β-Cinnamoyl-7α-hydroxyvouacapan-5α-ol following intraperitoneal administration in female Wistar rats

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A cassane diterpene, 6β-Cinnamoyl-7α-hydroxyvouacapan-5α-ol (6βCHV) isolated from the root bark of *Caesalpinia pulcherrima*, has demonstrated promising anticancer activity *in vitro*. *In vivo* safety of 6βCHV following oral administration has been established by previous studies. However, pharmacokinetic and tissue distribution studies revealed low systemic exposure, indicating poor absorption and limited bioavailability. Therefore, intraperitoneal administration has been proposed for further evaluation in preclinical efficacy studies using chemically induced rat mammary tumor models. The present study evaluated the sub-acute toxicity profile of 6βCHV following repeated intraperitoneal administration in female Wistar rats. Pure 6βCHV (7.3 g) was isolated from 3kg of dried root bark using the solvent extraction method, normal phase column chromatography, and recrystallization. The dose was prepared by dissolving 6βCHV in sesame oil at a final dosing volume of 5 mL/kg body weight. Twenty healthy female Wistar rats (8-12 weeks) were randomly divided into four groups (n = 5 per group). Daily intraperitoneal doses of 15,30 and 60 mg/kg were administered for 28 consecutive days. The control group was given the vehicle. Clinical observations, body weight, hematological parameters, relative organ weights, and histopathological changes in the kidneys, liver, and heart were evaluated. Mortality or treatment-related signs were not observed throughout the study period. Furthermore, no significant alterations were detected in hematological or biochemical parameters, organ weights, or gross pathological findings. Treatment-related pathological lesions or changes in the normal tissue architecture were not observed following histopathological examination in the kidneys, liver, and heart. Repeated intraperitoneal administration of 6βCHV at doses up to 60 mg/kg/day for 28 consecutive days was well tolerated in female Wistar rats. No evidence of systemic toxicity was observed throughout the study. These findings establish the safety of intraperitoneally administered 6βCHV and support its further evaluation in preclinical efficacy studies using chemically induced mammary tumor models.

Keywords: *Cassane diterpene, Caesalpinia pulcherrima, Sub-acute toxicity, Intraperitoneal administration*

Abstract No: OP14

Molecular characterization and phylogenetic relationships of black gram (Vigna mungo L. Hepper) genotypes using ITS sequence analysis

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Black gram (*Vigna mungo* L. Hepper) is an important leguminous crop in Sri Lanka, valued for its nutritional significance and contribution to sustainable agriculture. However, information on the genetic relationships among locally cultivated black gram germplasm remains limited, constraining effective germplasm conservation, parent selection, and crop improvement programs. As morphological traits are influenced by environmental conditions and may not reliably reflect genetic variation, this study employed ITS sequence analysis to evaluate genetic diversity and phylogenetic relationships among 12 selected black gram genotypes cultivated in Sri Lanka. Genomic DNA was extracted from young leaf tissues using the CTAB method, and amplified by PCR with ITS4 and ITS5 primers, followed by Sanger sequencing. Obtained sequences are quality checked, compared with NCBI GenBank records using BLAST, and submitted to GenBank to obtain accession numbers. Multiple sequence alignment with reference sequences was conducted in MEGA software using ClustalW, and phylogenetic relationships were inferred using Maximum Likelihood method with 1000 bootstrap replications. Sequence analysis followed by GenBank submission generated accession numbers PX486796-PX486804, providing publicly accessible molecular records for Sri Lankan black gram germplasm. Phylogenetic analysis revealed substantial genetic differentiation among the studied genotypes, forming two major clusters with bootstrap support ranging from 29% to 56%. Genotypes PX486800 and PX486801 clustered closely with the Indian accession MF322626.1, while PX486804 clustered with Indian accession CP144689.1 and the Chinese accession JX233500.1, indicating shared evolutionary relationships with regional germplasm. Genotypes PX486796, PX486797, PX486798, PX486799, and PX486803 formed related lineages within the principal cluster. In contrast, genotype PX486802 occupied an independent phylogenetic position supported by a bootstrap value of 53%, suggesting pronounced genetic divergence and the presence of potentially unique local variation within Sri Lankan black gram populations. The study confirmed that ITS – based molecular analysis is an effective approach for evaluating genetic diversity and phylogenetic relationships in black gram. The observed genetic variability among Sri Lankan genotypes, including the identification of distinct and potentially unique lines, provides valuable insight for germplasm conservation and breeding strategies.

Keywords: *Black gram, ITS markers, Molecular characterization, Phylogenetic relationships, Genetic diversity*

Abstract No: OP15

A high-throughput method for quantifying transcription elongation rate

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Transcription elongation is punctuated by frequent by RNA polymerase (RNAP) pause events that modify the average elongation rate (~30 nt/s). These transcriptional pauses play central roles in gene regulation, including nascent RNA folding, antitermination, and promoter-proximal pausing, while nascent RNA structures, and transcription elongation factors can further modulate RNAP pausing behavior. However, currently characterized regulatory pauses account for only a very small and biased subset of all possible pause sites across bacterial genomes. Although existing *in vitro* methods have provided important mechanistic insights, most methods assess only one DNA sequence at a time, limiting systematic analysis of pause determinants. Here, we develop a procedure for systematic quantification of relative transcription elongation rates across up to one million sequence variants simultaneously using our Transcription Elongation Complex display (TECdisplay) platform. In this assay, transcription rate is measured from time-dependent partitioning of variant DNA templates between the pellet and supernatant fractions. Actively transcribing transcription elongation complexes (TECs) that have reached a downstream biotin roadblock prevent binding of template DNA to streptavidin-coated beads (supernatant fraction), whereas variant templates on which the TEC has not reached the biotin roadblock remain bead-accessible (pellet fraction), upon transcription termination by EDTA. Pellet and supernatant fractions are subsequently barcoded and sequenced to assess the distribution of each variant DNA template between fractions over time. We have validated this partitioning strategy and are currently applying it to measure elongation rates across >65,000 systematically perturbed variants of the hairpin-stabilized bacterial *his* pause. By enabling large-scale combinatorial sequence perturbations, this approach will reveal how sequence motifs and nascent RNA structures govern pausing and ultimately transcription elongation.

Keywords: *Transcription elongation, RNA polymerase pausing, Cotranscriptional RNA folding, High-throughput sequencing, TECdisplay*

Abstract No: OP16

Genome Mining and Biocatalytic Desulfation of Algal Biomass Using Marine Bacterial Sulfatases

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Marine algae represent a promising renewable feedstock for biotechnology, yet their high levels of sulfated polysaccharides hinder downstream processing for biofuels, pharmaceuticals, and nutraceuticals. This study aimed to identify and characterize sulfatase genes from the genome of *Gimesia maris* with potential applications in algal polysaccharide desulfation. Bioinformatic mining revealed six distinct sulfatase genes with diverse domain architectures, including metallo-β-lactamase folds and conserved sulfatase motifs. Phylogenetic analysis clustered these enzymes with known bacterial alkyl/arylsulfatases, supporting their potential role in polysaccharide desulfation. Selected genes were cloned into *Escherichia coli* expression systems, and recombinant proteins were purified via Strep-Tactin affinity chromatography. Enzymatic assays demonstrated variable catalytic efficiencies: RB9650 exhibited inconsistent kinetic parameters, while SpAS2 showed a low Km and moderate Vmax, indicating high substrate affinity and effective catalytic turnover. These findings highlight SpAS2 as a promising candidate for biocatalytic desulfation of algal polysaccharides such as carrageenan and ulvan. The discovery of multi-modular sulfatases further suggests synergistic roles in polysaccharide degradation, opening avenues for engineering tailored biocatalysts. Overall, this work expands the repertoire of marine microbial sulfatases and underscores their potential in sustainable algal biorefinery technologies. By enhancing the usability of algal biomass, these enzymes could support eco-friendly production of biofuels and value-added bioproducts.

Keywords: *Genome mining, sulfatases, algal biomass, biocatalysis, sustainable biotechnology*

Abstract No: OP17

Development of a Real-time PCR-based approach for the early identification of latent tuberculosis infection

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Several studies have focused on the early identification of latent tuberculosis infection (LTBI) due to the absence of clinical symptoms and its potential to develop into active tuberculosis (ATB). However, early identification and accurate differentiation are more challenging with the available diagnostic methods. Host biomarkers provide a valuable insight into the host immune response and have the potential to improve early diagnosis and differentiation tuberculosis disease states. There are only a few studies that have explored the use of host biomarkers; therefore, this study aimed to fill this gap by accurately differentiating disease statuses for the early identification of LTBI using serum-based host biomarkers. Blood samples were collected from 93 participants: 20 with ATB, 54 with LTBI, and 19 in contact tracing. Serum was separated for the downstream RNA extraction. Complementary DNA was synthesized, and real-time qPCR was performed for the evaluation of gene expression of selected host genes (CXCL10, L6, CVIL, LIMD2, and ARSA1). The 2^−ΔΔCt method was used to analyze relative gene expression, with B2M as the reference gene. Appropriate parametric and nonparametric tests were used for the statistical analysis, with $p < 0.05$ as the significance level. Gene expression of CXCL10 ($p=0.004$), L6 ($p=0.001$), and CVIL ($p=0.001$) showed significant differences between the LTBI and ATB groups ($p < 0.05$). CXCL10, L6, and CVIL were significantly upregulated in LTBI compared with ATB. In contrast, LIMD2 and ARSA1 did not differ significantly among the groups. These findings suggest that selected biomarkers can effectively differentiate LTBI from ATB, and CXCL10, L6, and CVIL genes might be useful as potential biomarkers for early diagnosis of LTBI, which leads to the accurate differentiation of LTBI from ATB and prevents progression to ATB through early treatment, and this will also lead to achieving the World Health Organization's goal to end TB by 2035.

Keywords: *Latent tuberculosis, serum biomarkers, gene expression, RT-qPCR, CXCL10*

Acknowledgements: *This work was supported by the National Research Council, Sri Lanka (Investigator-driven Grant No. 22-027)*

Immunoinformatic Design of a Multi-Epitope Vaccine Targeting Co-Circulating Dengue and Zika Viruses in Sri Lanka and South-East Asia

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Dengue virus (DENV) and Zika virus (ZIKV) are mosquito-borne flaviviruses threatening public health mainly in Sri Lanka and South-East Asia. Their co-circulation, coupled with limitations of existing vaccines and the risk of Antibody-Dependent Enhancement (ADE), necessitates safer and broadly protective vaccine strategies. This study employed comparative genomics and immunoinformatic approaches to identify conserved immunogenic targets and design a Multi-Epitope Vaccine (MEV) against all four DENV serotypes and ZIKV. 1,928 high-quality, human-derived DENV and ZIKV polyprotein sequences from seventeen countries were retrieved from the NCBI Virus database following stringent quality control. Multiple Sequence Alignment using Fast Fourier Transform (MAFFT version 7) identified conserved regions across viral genomes, which were evaluated for antigenicity, allergenicity, toxicity, and immunogenic potential. B-cell, cytotoxic T lymphocyte (CTL), and helper T lymphocyte (HTL) epitopes were predicted and screened using immunoinformatic tools, and population coverage analysis assessed the global applicability of selected epitopes. Sequence analysis revealed 207 highly conserved regions among DENV serotypes and 51 shared with ZIKV, predominantly within the NS3 and NS5 proteins. Screening identified 27 B-cell, 15 high-confidence CTL, and 239 HTL epitopes with immunogenic potential, and the combined CTL–HTL set achieved an estimated 99.99% global population coverage. Five vaccine constructs (MEV1–MEV5) were designed using selected epitopes, linker sequences, and molecular adjuvants, and all were predicted to be antigenic, non-allergenic, and non-toxic, with favorable safety and immunogenicity profiles. *In silico* evaluation of physicochemical, structural, and immunostimulatory properties identified MEV4 and MEV5 as the most promising candidates, with superior stability and predicted immunogenic performance. These conserved epitopes enabled the rational design of a MEV with potential cross-protective efficacy against both co-circulating flaviviruses. These findings provide a foundation for developing broadly protective flavivirus vaccines. However, the immunogenicity, safety, and protective efficacy of the constructs require further validation through *in vitro* and *in vivo* studies.

Keywords: Dengue virus, Zika virus, multi-epitope vaccine, reverse vaccinology, immunoinformatics

Acknowledgements: *This study was financially supported by the Swedish International Development Cooperation Agency (SIDA) through the UNESCO-TWAS Research Grant Programme (Grant No. 24-091 RG/BIO/AS_G-FR 3240339171) awarded to SLIBTEC and forms part of the MSc research work of WASS. The views expressed herein do not necessarily represent those of UNESCO-TWAS, SIDA or its Board of Governors.*

Abstract No: OP19

Cytotoxicity, developmental toxicity and phytochemical profiling of marine sponges: BSLT–ZFET concordance and isothiocyanate-rich bioactive chemistry

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Marine sponges are a globally significant source of structurally novel bioactive natural products, yet integrated invertebrate–vertebrate cytotoxicity profiling of Sri Lankan coastal sponge fauna remains largely unreported. Five sponge specimens collected by SCUBA diving from waters off Kudawella on the Southern coast of Sri Lanka was identified to genus level by light-microscopic spicule morphology as *Suberites* sp. (S01), *Clathria* sp. (S02), two *Axinella* sp. (S04, S05), and *Halichondria* sp. (S06). Sequential solvent extraction with methanol, dichloromethane, and hexane yielded crude extracts that were characterised by the brine shrimp lethality test (BSLT), the zebrafish embryo toxicity test (ZFET, OECD TG 236), and GC–MS phytochemical profiling. Cytotoxicity was modelled by binomial generalised linear models with probit link. BSLT LC_{50} values were 397.4 ppm (S01), 28.9 ppm (S02), 61.6 ppm (S04), 19.3 ppm (S05), and 978.1 ppm (S06), classifying S02, S04, and S05 as highly toxic (≤100 ppm). ZFET LC_{50} values (S01: 330.2 ppm; S02: 16.3 ppm; S04: 45.1 ppm; S06: 399.8 ppm) were concordant with BSLT (ratio 0.41–0.83) for four specimens, while S05 exhibited a pronounced 78-fold discordance (ZFET LC_{50} 1501.3 ppm vs. BSLT LC_{50} 19.3 ppm). Morphological ZFET endpoints included enlarged yolk sac oedema in S05 at 200 ppm (sublethal LOAEL = 50 ppm) and absence of heartbeat in S06 at 50 ppm, with mortality NOAEL values of <12.5 ppm for S02, S04, and S05. GC–MS profiling of the combined methanol–dichloromethane–hexane extracts (102 chromatographic peaks) identified isothiocyanate-dominated relative-peak-area profiles in S02 (~29.5%) and S05 (~32.6% ITC plus ~38.9% ergosterol-derived sterols), providing a chemical rationale for their cytotoxicity and the mechanistically informative BSLT–ZFET discordance of S05. *Clathria* sp. S02 is identified as a priority candidate for bioassay-guided isolation of cytotoxic isothiocyanate constituents.

Keywords: *Marine sponges, BSLT, ZFET, Isothiocyanate cytotoxicity, GC–MS profiling*

Abstract No: PP1

Preliminary analysis of skin Pigmentation Gene variants, *SLC24A5* (rs 1426654) and *SLC45A2* (rs 16891982) among Sinhalese, Sri Lankan Tamil and Indigenous Adivasi Vedda Populations

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Human skin pigmentation is a polygenic trait which is significantly affected by natural selection, UV radiation and population history. While global allele frequency distributions of the genetic markers *SLC24A5* (rs 1426654) c.331A>G (p.Thr111Ala), where G is the ancestral dark pigmentation allele and *SLC45A2* (rs 16891982) c.1122C>G (p.Leu374Phe) where G is the ancestral dark pigmentation allele are well documented, ethnicity-specific data for Sri Lankan groups especially the Adivasi Vedda population which is one of the oldest indigenous communities in Sri Lanka considered have been notably absent. The objective of this study was to describe these allele frequencies in Sinhalese, Sri Lankan Tamils and Indigenous Adivasi Vedda population. The study used a cross-sectional population genetic framework, genomic DNA were extracted using salting-out and Silica-spin column methods from 10 subjects (Sinhalese, n= 4 and Adivasi Vedda, n= 6). The extracted DNA samples were subsequently subjected to Sanger sequencing for genotyping of the *SLC24A5* and *SLC45A2* variants. For the Sri Lankan Tamil population, genotype data from 20 individuals were obtained from the 1000 Genomes Project. Diversity and the genetic structure were analyzed using Principal Component Analysis (PCA) for all populations from 1000 Genomes Project and Hardy-Weinburg (HWE) test on Sri Lankan Tamil population. The results of the Sanger sequenced samples showed that all the Sinhalese and Adivasi Vedda samples appeared homozygous for the ancestral allele at both loci. Due to the limited number of successfully sequenced Sinhalese and Adivasi Vedda samples, population-level allele frequencies were not estimated for these groups. The Sri Lankan Tamil cohort showed intermediate derived allele frequencies of 0.40 and 0.025, respectively for the two variants and neither variant departed significantly from HWE. PCA analysis revealed that South Asian populations are placed between the European and East Asian clusters, reflecting complex historical admixture. The present study suggests that the genetic isolation of the Adivasi Vedda and strong UV-mediated selection near equatorial latitudes favor the dominance of dark pigmentation allele. However, further analysis with the large cohort of individuals will be required to made a solid conclusion.

Keywords: *Skin pigmentation, SLC24A5, SLC45A2, Allele-specific PCR, Sanger sequencing*

Acknowledgements: *This study was jointly supported by the MSc programme in Molecular Life Sciences, IBMBB and the IPICS Grant*

Abstract No: PP2

Association of *FTO* rs9939609 Variant with Obesity in different Vedda clans of Sri Lanka: A Preliminary Genetic Analysis

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Obesity is a complex metabolic disorder influenced by genetic and environmental factors. The fat mass and obesity-associated (*FTO*) gene variant rs9939609 (T>A) has been widely associated with adiposity and obesity susceptibility across populations. The indigenous Vedda population of Sri Lanka is a genetically distinct community undergoing rapid lifestyle and dietary transitions; however, their genetic susceptibility to obesity remains largely unexplored. This study investigates the *FTO* rs9939609 polymorphism among selected Vedda clans in Sri Lanka. Archived blood samples from individuals representing four Vedda clans (N=10): Rathugala, Pollebedda, Dambana, and Vakarei, along with normal BMI (N=5) and obese BMI (N=2) non-Vedda controls, were analysed. Genomic DNA was extracted using the QIAamp DNA Investigator Kit and the region flanking the rs9939609 SNP in the first intron of the *FTO* gene was amplified by polymerase chain reaction (PCR) and genotyped by Sanger sequencing. Principal component analysis (PCA) was conducted using global obesity-associated allele frequency data from the 1000 Genomes Project. Individuals with normal BMI and those classified as Obesity Class I according to WHO Asia-Pacific BMI classification carried the homozygous wild-type (TT) genotype, whereas, participants with Obesity Class II, including obese non-Vedda controls, carried the heterozygous (AT) genotype. No differences in genotype distribution among the four Vedda clans were assessed due to the limited sample size. No homozygous variant (AA) genotype was detected. Risk allele (A) carriers demonstrated elevated waist circumference and waist-to-hip ratio indicating central adiposity, despite normal blood glucose levels. PCA of global obesity-associated allele frequency data demonstrated population-specific clustering patterns, with South Asian populations occupying an intermediate position between European and East Asian populations. Within South Asians, Sri Lankan Tamils clustered more closely with Punjabi and Gujarati populations. These findings provide preliminary evidence that the *FTO* rs9939609 A allele may be associated with increased susceptibility to obesity in the studied Vedda population. Further characterization with larger sample sizes is required to demonstrate the association of *FTO* variants with obesity risk among indigenous Sri Lankan populations.

Keywords: *FTO rs9939609, Obesity, Vedda population, Genetic Polymorphism, Sanger sequencing*

Acknowledgements: *This study was jointly supported by the MSc programme in Molecular Life Sciences, IBMBB and IPICS Grant*

Abstract No: PP3

Exploring the impact of *Camellia sinensis* (Ceylon black tea) consumption on theaflavin as a tea-derived metabolite and potential toxicological effects in rats

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Ceylon black tea (*Camellia sinensis var. assamica*) is well-known for its remarkably high theaflavin content. However, a significant gap exists in pharmacokinetics and preclinical safety data for premium-grade Ceylon black tea. This study assesses the subacute oral toxicity and pharmacokinetic profile of theaflavin in male Wistar rats following a 28-day repeated-dose oral administration of Dilmah English breakfast tea, with and without sugar, at a human equivalent dose (319.56 mg/kg/day), following OECD guideline 407. Eighteen Wistar rats were assigned to three study groups: tea, tea with sugar (822.2 mg/kg/day sucrose), or distilled water (n=6 per group). Clinical signs, body weight, food and water intake, haematological parameters, biochemical markers of hepatic and renal function, organ weights, and histopathology were evaluated. The pharmacokinetic study was conducted using a validated reverse-phase HPLC-UV method developed in accordance with FDA 2022 bioanalytical guidelines (n=3 per time point). No significant differences were observed ($p > 0.05$) across groups for body weight, food intake, organ weights, haematological parameters, and blood urea nitrogen. Furthermore, no mortality or adverse clinical signs were observed. Water intake was significantly higher in the tea with sugar group ($P < 0.001$). Histopathology examination revealed no overt hepatotoxicity or nephrotoxicity. An excellent linearity (R^2=0.9998; LLOQ=10 ng/mL) was observed in the employed RP-HPLC method. Theaflavin peak plasma concentration was detected at Tmax = 1 hour with a concentration Cmax=123.6 ng/mL for the tea group. The elimination half-life was 1.07 hours. The tea with sugar group reached a Cmax of 73 ng/mL at a delayed Tmax of 1.5 hours. The delayed Tmax and attenuated Cmax suggest that sugar co-consumption reduces theaflavin bioavailability, potentially through osmotic delay of gastric emptying. The results of the study are foundational for further subchronic toxicity and bioavailability studies regarding premium-grade Ceylon black tea.

Keywords: *Theaflavin, Ceylon black tea, Pharmacokinetics, Subacute oral toxicity, Bioavailability*

Abstract No: PP4

Anticancer potential of flavones and flavanols in leaves of selected fruit plants focus on apigenin, luteolin, quercetin, myricetin, and kaempferol

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Cancer remains a major global health challenge, necessitating the development of safer and effective therapeutic agents. This study evaluated the flavonoid composition and anticancer potential of methanolic leaf extracts from selected fruit plants, namely *Annona muricata*, *Psidium guajava*, *Tamarindus indica*, *Punica granatum*, and *Phyllanthus emblica*. Particular attention was given to flavones apigenin and luteolin and flavanols quercetin, myricetin, and kaempferol, using HPLC profiling and SRB cytotoxicity assays on ER+ breast Carcinoma (MCF-7) and non-small cell lung carcinoma (NCI-H292) cell. HPLC analysis confirmed the presence of all five target flavonoids in all extracts, with significant species-dependent variation in concentration. Apigenin was the predominant flavonoid, highest in *A. muricata* (70.43 ± 1.10 mg/g DW) and *P. emblica* (69.60 ± 2.83 mg/g DW), while *T. indica* showed the lowest levels overall. *Punica granatum* exhibited strongest activity against MCF-7 cells (IC_{50} at 9.689 µg/mL at 48 h), whereas *P. emblica* showed highest cytotoxicity against NCI-H292 cells (IC_{50} 5.386 µg/mL). Extracts with higher flavonoid content showed stronger cytotoxic activity, indicating a correlation between apigenin, quercetin, kaempferol, myricetin levels and anti-proliferative effects. Apoptosis was confirmed by increased caspase-3/7 activity and DNA fragmentation. Overall, flavonoid-rich extracts from *A. muricata*, *P. emblica*, and *P. granatum* demonstrated prominent anticancer potential through inhibition of cancer cell proliferation and induction of apoptosis. The study provides an integrated evaluation of the flavonoid composition and in vitro anticancer activity of selected fruit plant leaf extracts using HPLC profiling, SRB cytotoxicity assays, caspase-3/7 activation, and DNA fragmentation analysis. Variations in flavonoid composition and biological activity were observed among the selected plant species, emphasizing the importance of plant selection in the investigation of plant-derived anticancer agents. The findings support the further evaluation of flavonoid-rich fruit plant leaves as sustainable sources of bioactive compounds for future anticancer research, nutraceutical development, and functional food applications.

Keywords: *Flavonoids, Anticancer activity, MCF-7, NCI-H292, Apoptosis*

Abstract No: PP5

Pretreatment with fucoidan-rich fractions from selected Sri Lankan *Sargassum* species modulates nitrite production and oxidative burst activity in activated RAW 264.7 macrophages

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Abstract withdrawn.

Abstract No: PP6

In vitro anti-inflammatory activity of aqueous and ethanolic leaf extracts of *Aporosa lanceolata* Thw.

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Aporosa lanceolata Thw. is a Sri Lankan endemic medicinal plant which is used in traditional medicine and Ayurvedic Medicine as a treatment of inflammatory conditions. However, its anti-inflammatory properties remain scientifically underexplored. This study investigated the *in vitro* anti-inflammatory activity of aqueous leaf extract (ALE) and ethanolic leaf extract (ELE) of *A. lanceolata* using carrageenan-induced rat peritoneal cell model. The non-toxic concentration range determined using Trypan Blue exclusion assay was used to assess anti-inflammatory activity by measuring the inhibition of nitric oxide (NO) production using the Griess assay and reactive oxygen species (ROS) production using the nitroblue tetrazolium (NBT) assay. Both ALE and ELE did not show significant cytotoxicity within the tested concentration range (15.63–1000 µg/mL), maintaining cell viability above 80%. Concentrations of 31.25–1000 µg/mL were used in subsequent assays. In the Griess assay, ELE demonstrated strong concentration-dependent inhibition of NO production ($r = 0.825$, $p < 0.001$), achieving approximately 80% inhibition at 1000 µg/mL. ALE also showed NO inhibitory activity, with comparatively higher inhibition at lower concentrations. In the NBT assay, ALE and ELE showed maximum ROS inhibition of 32.74 ± 6.03% and 35.63 ± 4.03%, respectively. The ethanol vehicle control for ELE showed negligible activity, confirming that the observed effects were due to the plant extracts. These findings suggest the anti-inflammatory potential of both ALE and ELE of *A. lanceolata* through the suppression of inflammatory mediators and oxidative stress. This study provides the first scientific evidence of the anti-inflammatory activity of *A. lanceolata*. These findings support its traditional medicinal use and highlight its potential as a source of natural anti-inflammatory agents.

Keywords: *Aporosa lanceolata, anti-inflammatory activity, nitric oxide, reactive oxygen species, medicinal plants*

Abstract No: PP7

Comparison of Chloroplast Genomes of Six *Cryptocoryne* Species: In silico analysis

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Cryptocoryne (commonly known as crypts) is a genus of aquatic plants exploited from natural populations to meet the demand in the aquarium trade. Species identification based on vegetative traits is challenging due to high morphological plasticity whereas molecular markers offer a more feasible and reliable route to high genetic resolution among species. However, comparative chloroplast genomic resources for identifying informative species-level markers in crypts remain limited. This study aimed to compare the six complete chloroplast genomes of *Cryptocoryne* species to identify informative chloroplast markers for species discrimination and phylogenetic inference. Chloroplast genomes were retrieved from GenBank and analyzed in silico using Geneious Prime software. All genomes displayed the typical quadripartite structure but substantial variation in inverted repeat (IR) region expansions and small single-copy contraction. Average GC content was tightly conserved, ranging between 33.08% and 34.62%. Nucleotide diversity analysis identified prominent hypervariable regions within the *petD* and *rpoC2* genes rather than *matK*, making *petD* and *rpoC2* as promising candidate barcode regions for future validation. Comparative analysis revealed highly diverse simple sequence repeat patterns dominated by A/T rich motifs, alongside varying configurations of long repeats. Pairwise alignment showed high genome-wide similarity, ranging from 96.24% to 99.03%, with *C. striolata* and *C. tirtadinatae* exhibiting the highest sequence identity. To facilitate downstream screening and target authentication of the core *matK*, *petD*, and *rpoC2* markers, optimized primer pair was designed using NCBI PrimerBLAST, yielding robust 700-800 bp amplicons with well-balanced melting temperatures. Overall, comparative chloroplast genome analysis revealed substantial structural variation among *Cryptocoryne* species, particularly in IR regions. Among the three markers, *petD* emerged as the most variable marker. These findings provide valuable genomic resources for species authentication, conservation management, and future phylogenetic studies of this taxonomically challenging aquatic plant genus.

Keywords: *Cryptocoryne, Chloroplast genome, species-level markers, Phylogenetic inference, Hypervariable regions*

Abstract No: PP8

DUOX2-related congenital hypothyroidism: Intrafamilial Phenotypic Variability in a Sri Lankan Family

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Congenital hypothyroidism (CH) is one of the most frequent endocrine disorders detected by newborn screening. Dual oxidase 2 (*DUOX2*) gene variants are known cause of thyroid dyshormonogenesis and can cause a significant variation in the phenotype, from transient congenital hypothyroidism to permanent congenital hypothyroidism and even to mild thyroid dysfunction in adults. The current study aimed to characterize the clinical and genetic features of two siblings with CH and assess the phenotypic variability within the family. Two male siblings (aged 8 and 4 years) diagnosed with CH by the national newborn screening program in 2017 and 2022 respectively were recruited. Both underwent clinical evaluation (including family history assessment), biochemical functional testing, and thyroid ultrasonography. Subsequently, whole exome sequencing was performed and potential thyroid dyshormonogenesis-causing variants were identified using ANNOVAR annotation. Both siblings demonstrated biochemical evidence of CH with elevated thyroid-stimulating hormone (TSH) levels and reduced thyroid hormone levels during infancy. The thyroid ultrasonography showed normally located thyroids without ectopy or agenesis, suggesting thyroid dyshormonogenesis. Both affected siblings were found to have compound heterozygous *DUOX2* mutations: c.1709A>T (p.Gln570Leu) and c.1264C>T (p.Arg422 Cys). Both variants were predicted to have damaging consequences for the protein structure and/or function by bioinformatic prediction tools. Family history included thyroid disease in the maternal line and late onset thyroid dysfunction in the paternal grandfather indicating inter-familial variability and incomplete penetrance. This incident underscores the clinical relevance of compound heterozygous variants of *DUOX2*, and the significant intrafamilial phenotypic diversity. These variants are not novel, but the increased familial clustering and multigenerational thyroid disorder extends the phenotypic spectrum of the *DUOX2* involvement in CH.

Keywords: *Congenital Hypothyroidism, DUOX2, Compound Heterozygous, Thyroid Dyshormonogenesis, Familial Thyroid Disease*

Abstract No: PP9

Identification and Phylogeography of Dominant Hermit Crab Species in Selected Locations from Matara District, Sri Lanka

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Hermit crabs are decapod crustaceans recognized for their soft abdomens and dependence on gastropod shells for protection. They exhibit remarkable diversity in morphology, anatomy, ecology, behavior, and habitat, occurring across subtropical and tropical regions in both marine and terrestrial environments. As omnivores, they serve important ecological functions as ecosystem engineers, scavengers, and decomposers. Of the five major hermit crab families, three are recorded in Sri Lanka. Despite its occurrence in Sri Lanka, molecular characterization of this species has not yet been reported, creating a significant gap in the existing scientific literature. The objective of this study was to identify the most abundant hermit crab species, to compare genetic divergence levels among samples, determine their phylogeographic and evolutionary relationships. This study focuses on the most abundant species at Nilwella, Kamburugamuwa, and Thotamuna in the Matara District, where the sites differ in topography and the intensity of anthropogenic pressure, providing contrasting environmental conditions for investigation. Ninety samples were collected using vertical line transects and observed morphologically. Six samples (two from each site) were sequenced for the ~650 bp region of the mitochondrial COI barcoding gene region. Resulting sequence data was compared with the data from GenBank for other geographical locations in the world. Pairwise comparisons, phylogeographic relationships among lineages, and haplotype network construction were performed. The identification of the abundant species as *Coenobita rugosus* was confirmed by molecular data. The results revealed the mean divergence level among Sri Lankan samples as 0.61% with the divergence ranging from 0.46% to 0.76%, and that the divergence levels between Sri Lanka and other geographical locations range from 0.6 3.1%. Molecular analyses indicate clear genetic affinity among populations and are consistent with the possibility% to of historical long-distance dispersal and recent divergence, along with possible ongoing gene flow across geographical barriers.

Key words: *Hermit Crab, Coenobita rugosus, COI, phylogeographic relationships*

Abstract No: PP10

Prevalence of *GCKR* rs1260326 and *GCKR* rs780094 variants in subjects with non-alcoholic steatohepatitis (NASH)-related hepatocellular carcinoma (HCC) in Sri Lanka

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Hepatocellular carcinoma (HCC) is becoming a challenging global health burden due to the rising prevalence in Asian and African countries. It is estimated that by 2030, the worldwide number of primary liver cancer patients will exceed one million annually. Non-alcoholic steatohepatitis (NASH) is an emerging cause of HCC, driven by unhealthy diets and sedentary lifestyles.Variants in the glucokinase regulator (*GCKR*) gene, rs1260326 and rs780094, influence glucose metabolism in the liver and may contribute to the development of HCC. This is the first study to evaluate the association of these single nucleotide polymorphisms (SNPs) in a cohort of Sri Lankan patients with NASH-related HCC. Conventional PCR was utilized to amplify the *GCKR* rs1260326 and rs780094 regions in 40 individuals, including a NASH-related HCC cohort (n = 10) and age-, body mass index (BMI)-, and gender-matched control groups comprising NASH-related cirrhosis (n = 10), fatty liver (n = 10), and healthy individuals (n = 10). The amplified products were subjected to Sanger sequencing for mutation detection. Statistical analysis was performed to evaluate the associations between SNPs and liver disease risk. The rs1260326 variant showed a strong positive association with liver disease ($\beta = 3.154$, odds ratio (OR) = 23.44, $p = 0.020$), indicating increased susceptibility. In contrast, the rs780094 variant showed a significant inverse association ($\beta = -1.147$, OR = 0.318, $p = 0.040$), suggesting a protective effect. A novel intronic variant, NC_000002.12 (NM_001486.4): c.1423-73_1423-72insC, was identified in the HCC cohort. The findings demonstrate a strong association of *GCKR* rs1260326 and rs780094 with NASH-related HCC. The identification of a novel intronic variant further suggests genetic heterogeneity among Sri Lankan patients, highlighting the need for larger studies in the future. These findings emphasize the importance of integrating genetic and molecular profiling into precision medicine approaches for NASH-related HCC, particularly in South Asian populations.

Keywords: *Non-alcoholic steatohepatitis, Hepatocellular carcinoma, Single nucleotide polymorphisms, GCKR, Sri Lankan population*

Abstract No: PP11

Preliminary genetic analysis of a cohort of nasopharyngeal cancer patients in Sri Lanka

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Nasopharyngeal carcinoma (NPC) is a multifactorial epithelial malignancy that arises from the nasopharyngeal mucosa. It is marked by a complex interrelation between host genetics, Epstein–Barr virus, and environmental factors. Among many molecular determinants, defects in DNA repair mechanisms, notably the nucleotide excision repair (NER), have been linked to genomic instability and carcinogenesis. The excision repair cross-complementation group 1 (*ERCC1*) gene, a critical component of NER, removes DNA adducts and bulky lesions caused by carcinogens. The c.*197G>T (rs3212986; C8092A) and c.354T>C (rs11615; C118T) polymorphisms have been broadly studied in many cancer types, however, the role they play in susceptibility to NPC among South Asian populations, has remained inconsistent. This study aims to evaluate the association between these gene variants and NPC risk in a Sri Lankan cohort. Also, their relationship with clinicopathological parameters was explored. A total of 24 participants, consisting of 19 NPC patients and 5 healthy controls were enrolled in a case-control study. Allele and genotype frequencies were assessed and analyzed under codominant, dominant, and recessive models. Case-only subgroup analysis was carried out to examine potential relationships with clinicopathological features. No statistically significant associations were observed between either polymorphism and NPC susceptibility at the allelic or genotypic level ($p > 0.05$). The T allele of c.*197G>T was more frequent in cases than controls (28.9% vs 20.0%; OR = 1.63) but did not reach significance. For c.354T>C, the C allele was marginally higher in cases (55.3% vs 50.0%; OR = 1.24), though not significant. Genotype analyses found no significant links across codominant, dominant, or recessive models. Nonetheless, the rs3212986 showed directional enrichment in metastatic and advanced-stage NPC. This puts forward that rs3212986 may influence tumor progression rather than disease initiation. Conversely, rs11615 exhibited a uniform distribution across clinical categories, indicating a limited role in disease stratification.

Keywords: *NPC, ERCC1, Genetic susceptibility, rs3212986, rs11615*

Acknowledgements: *This research was funded by IBMBB and the Association of Commonwealth Universities (UK)*

Abstract No: PP12

Detection of chromosome 22q11.2 deletion in patients clinically suspected of DiGeorge syndrome attending an immunology clinic at Medical Research Institute, Sri Lanka

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Chromosome 22q11.2 deletion syndrome (22q11.2DS), also known as DiGeorge syndrome, is one of the most common microdeletion syndromes in humans. It is characterized by marked phenotypic variability, affecting multiple organ systems, and commonly presents with congenital heart defects, recurrent infections, thymic abnormalities, hypocalcaemia, and craniofacial anomalies. To identify chromosome 22q11.2 deletions in patients clinically suspected of DiGeorge syndrome attending the Immunology Clinic at the Medical Research Institute (MRI), Sri Lanka, and to describe the clinical characteristics of affected individuals. A cross-sectional study was conducted involving five patients with clinical features suggestive of DiGeorge syndrome. Genomic DNA extracted from peripheral blood samples was analyzed using multiplex ligation-dependent probe amplification (MLPA) with the SALSAP250-025RB2DiGeorge probe mix. Clinical and demographic data were obtained from medical records. In addition, clinical features of previously diagnosed patients with 22q11.2 deletion syndrome attending the MRI clinic were reviewed. Among the five clinically suspected cases, two patients (40%) were positive for chromosome22q11.2 deletion, while three patients (60%) showed no detectable deletion by MLPA. Congenital heart disease and recurrent infections were present in all patients, whereas facial dysmorphism and thymic hypoplasia were observed in 80% and 60%, respectively. Analysis of previously diagnosed patients demonstrated congenital heart disease in 81.2%, recurrent infections in 87.5%, developmental delayin 62.5%, and facial dysmorphism in 43.8%. The clinical spectrum of 22q11.2DS is highly variable, and clinical findings alone are insufficient for diagnosis. MLPA is a useful and cost-effective method for detecting chromosome 22q11.2deletions in resource-limited settings.

Keywords: *22q11.2 deletion syndrome, DiGeorge syndrome, Immunodeficiency, MLPA*

Abstract No: PP13

Optimization of DNA extraction from Paraffin-Embedded tissues and preliminary analysis of *NRAS* and *KRAS* mutations in Well-Differentiated Thyroid Cancer

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Thyroid cancer, particularly well-differentiated forms such as papillary and follicular thyroid carcinomas, has shown a rising incidence worldwide, including in Sri Lanka. Mutations in the *NRAS* and *KRAS* oncogenes, are well-established contributors to thyroid tumourigenesis and hold promise for improving diagnosis and treatment through molecular profiling. However, the use of molecular diagnostics is often limited by the quality of available tissue samples. Formalin-fixed, paraffin-embedded (FFPE) tissues are widely available and suitable for retrospective studies, but DNA degradation can compromise mutation analysis. This challenge is especially relevant in resource-limited settings, where access to fresh tissue is restricted. Optimizing DNA extraction from FFPE tissues can enable cost-effective, ethically viable, and logistically feasible mutation screening. This study aimed to optimize DNA extraction from FFPE thyroid tumour tissues and adjacent healthy tissue samples and establish PCR conditions to detect clinically relevant *NRAS* (Q61K and Q61R) and *KRAS* (G12D and G13D) mutations. DNA was extracted using the QIAamp® DNA FFPE Tissue Kit and quantified spectrophotometrically. Target-specific primers were designed, and PCR conditions were optimized by adjusting $MgCl_2$ concentration and annealing temperature. Amplified products were verified by agarose gel electrophoresis and Sanger sequencing. Successful amplification and sequencing of the target regions demonstrated the feasibility of using FFPE-derived DNA for downstream mutation analysis. Optimization of whole-block tissue processing, annealing temperature, and $MgCl_2$ concentration improved DNA yield and PCR efficiency. Preliminary sequencing of healthy tissue samples validated the workflow and established a protocol suitable for future screening of *NRAS* and *KRAS* variants in well-differentiated thyroid cancer samples. These findings support the use of FFPE tissues for molecular studies in thyroid cancer and provide a foundation for retrospective genetic analyses and molecular diagnostic research in Sri Lanka. The optimized protocol offers a practical approach for mutation screening in resource-limited settings.

Keywords: *Thyroid cancer, Formalin-fixed paraffin-embedded (FFPE) tissue, NRAS, KRAS, PCR optimization*

Abstract No: PP14

Genomic characterization and phylogenetic analysis of Pseudomonas sp. isolated from a transplant unit of a national hospital

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Abstract withdrawn.

Abstract No: PP15

Characterization of the forehead skin microbiome and antibiotic susceptibility patterns among healthy adults in Colombo District, Sri Lanka – A preliminary study

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The skin microbiome is fundamental for host defense and barrier integrity, but region-specific preliminary data from tropical South Asia remains scarce. This pilot study investigated the culturable bacterial diversity of the forehead skin microbiome of healthy adults in the Colombo district of Sri Lanka, and assessed isolate susceptibility to vancomycin, ciprofloxacin, tetracycline, and erythromycin. A total of 5 healthy adults aged 18-65 were chosen based on strict inclusion and exclusion criteria. Forehead skin swab samples were collected using sterile cotton swabs from a 4×4 cm area in the forehead. Swabbed bacteria were enriched in nutrient broth, serially diluted, and cultured using standard microbiological techniques. Ten representative isolates were chosen from the 18 morphologically different colonies that were obtained. Antibiotic Susceptibility Testing (ABST) was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar. Molecular identification was conducted by amplifying the 16S rRNA gene via Polymerase Chain Reaction (PCR). Amplicons were sequenced using sanger sequencing and analyzed using NCBI Blast tool. Six different bacterial taxa, including *Bacillus pumilus*, *Bacillus safensis*., *Acinetobacter baumannii*, *Staphylococcus haemolyticus*, *Pantoea calida* and *Acinetobacter* sp. The abundance of *Bacillus* species suggested a significant environmental influence on the forehead microbiome. Ciprofloxacin and tetracycline isolates were susceptible to all isolates, whereas vancomycin and erythromycin presented 80% susceptibility with two isolates exhibiting resistance. The coexistence of commensal, opportunistic and environmentally derived microorganisms reflect the dynamic community of the forehead skin microbiome. Providing baseline data on forehead skin microbial diversity and patterns of antimicrobial susceptibility on the forehead skin of an urban Sri Lankan population. Combining molecular and culture-based methods increases accuracy and signifies the importance of ongoing monitoring of antibiotic resistance in commensal microbial communities. and provides a foundation for future microbiome studies and surveillance of antibiotic resistance in Sri Lanka.

Keywords: *Forehead skin microbiome, Molecular identification, Antibiotic susceptibility, Bacterial diversity, Colombo*

Abstract No: PP16

Antibacterial activity and melissopalynological characteristics of bee box honey and wild honey from Uva Province, Sri Lanka

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Honey is a natural substance produced by honey bees from floral nectar and is widely recognized for its nutritional, therapeutic, and antimicrobial properties. However, the influence of floral origin, pollen composition and moisture content on the antibacterial activity of Sri Lankan honey remains insufficiently studied. This study evaluated the antibacterial properties and pollen profiles of wild and bee box honeys collected from Uva Province, Sri Lanka. Seven wild honey samples from Kuda Oya and Ethiliwewa and two bee box honey samples from Welimada and Weherayaya were analyzed. Antibacterial activity against Staphylococcus epidermidis (ATCC 12228), Streptococcus pyogenes (ATCC 19615), and Staphylococcus aureus (ATCC 25923) was assessed using the agar well diffusion method. Pollen profiles were examined microscopically, Absolute Pollen Count (APC) was determined, and moisture content was measured using a refractometer according to Sri Lanka Standard 464:2016. All honey samples exhibited varying degrees of antibacterial activity, with Streptococcus pyogenes being the most susceptible bacterium. The highest inhibition zone (12.9 mm) was recorded for the Weherayaya bee box honey. Samples with higher pollen concentrations generally demonstrated stronger antibacterial effects, while elevated moisture content was associated with reduced activity. APC values ranged from 8.5×10^4 to 1.5×10^6 grains 10 g^{-1}, and moisture content ranged from 20.7% to 24.6%. The findings indicate that both wild and bee box honeys from Uva Province possess mild to moderate antibacterial properties influenced by pollen richness and moisture content. This study highlights the potential of melissopalynological analysis and antimicrobial screening as complementary tools for honey quality assessment and provides baseline information supporting future development of value-added therapeutic honey products in Sri Lanka.

Keywords: *Honey, melissopalynology, antibacterial properties, bee box, Sri Lanka*

Abstract No: PP17

Evaluation of synergistic antibacterial potential of *Hemidesmus indicus* and *Terminalia chebula* against selected multi-drug resistance waterborne pathogens

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New emerging multidrug-resistance (MDR) water-borne pathogens call for alternative antibacterial strategies. The use of traditional medicinal plants like *Hemidesmus indicus* and *Terminalia chebula* are reported but not studied with the combination against MDR *Escherichia coli* and *Klebsiella pneumoniae* from water sources. The study identified and evaluated the antibacterial activity of methanolic extract of *H. indicus* and *T. chebula* against MDR *E. coli* and *K. pneumoniae* in the presence and absence of each other and investigated the nature of their combination by FIC Index value. Previously confirmed MDR *E. coli* and *K. pneumoniae* isolates were obtained from the Biomedical Science Laboratory, Faculty of Health Science, KIU University, Sri Lanka. Dried plants were macerated in 98% methanol. The inhibition zone was determined by the agar well diffusion method and compared with the positive control, $p<0.05$ was considered significant. Broth macro-dilution was used for determining the Minimum Inhibitory Concentrations (MICs) and Minimum Bactericidal Concentrations (MBCs). The FICs and FICI values were calculated for combined extracts using checkerboard assay. In agar well diffusion, moderate amount of inhibition was observed, *T. chebula* (150-200mg/mL) showed 10.2-10.8mm against *E. coli* and 10.5-10.7mm against *K. pneumoniae* while for *H. indicus* 10.0-10.7mm was observed against both the strains. Ciprofloxacin (100µg/mL) showed significantly larger zones (*E. coli*: 29.6–30.4mm; *K. pneumoniae*: 30.7–37.3mm; $p<0.001$). MICs: *T. chebula*: *E. coli*: 12.5mg/mL; *K. pneumoniae* 25mg/mL; *H. indicus*: *E. coli* 25mg/mL; *K. pneumoniae* 25mg/mL. MBCs: *T. chebula*: 12.5mg/mL (*E. coli*), 25mg/mL (*K. pneumoniae*); *H. indicus*: 50 mg/mL for both. The checkerboard assay showed FICI=0.5 for *E. coli* (synergy) and FICI=1.0 for *K. pneumoniae* (additive). Both methanolic extracts were dose-dependent against MDR *E. coli* and *K. pneumoniae* and were synergistic against *E. coli* and additive against *K. pneumoniae*. The combined extracts are suggested to be characterized for phytochemicals and tested *in vivo* to be used as possible auxiliary agents in the control of MDR waterborne pathogens.

Keywords: *Hemidusmus indicus, Terminalia chebula, Multidrug resistance, waterborne pathogens, Synergistic antimicrobial activity*

Abstract No: PP18

Serotype predominance and molecular characterization of circulating dengue virus strains in Colombo District, Sri Lanka (2025)

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Dengue is a significant health concern in Sri Lanka, which requires continuous molecular surveillance to predict outbreaks, manage clinical risks and optimise treatments. This research aimed to determine the predominant dengue serotypes (DENV 1–4) circulated in Colombo District, and to characterize their respective genotypes during transmission season in 2025. Acute-phase serum samples (n=20) from dengue-confirmed patients (positive by Flavi PCR) were obtained from National Hospital Sri Lanka (NHSL) and Infectious Diseases Hospital (IDH) in 2025. Viral RNA was extracted using QIAGEN QIAamp Viral RNA Mini Kit (250). Serotyping was accomplished with multiplex real-time RT-PCR targeting the capsid-premembrane (C-prM) junction region. For genotyping, the prM-E junction into the 5' end of Envelope (E) gene fragment was amplified and sequenced using Oxford Nanopore Technology (MinION). Phylogenetic analysis was carried out using reference genomes via the Genome Detective Dengue Virus Typing Tool. Out of 20 samples, DENV-3 (70%; n=14) and DENV-2 (20%; n=4) dominated, having 90% of cases. DENV-1 and DENV-4 were absent. Two remaining samples (10%) could not be assigned to a specific serotype due to low viral loads yielding insufficient genetic material for multiplex real-time RT-PCR amplification. No co-infections were detected. Samples indicated at least >92% nucleotide identity to the matched serotype. DENV-2 samples were assigned to genotype II F.1.1 (Cosmopolitan lineage) which was dominant in Sri Lanka in the recent past. DENV-3 samples could not be categorized into any known genotype, suggesting potential structural divergence. In conclusion, this study continues the DENV-3 dominance that replaced DENV-2 in 2023 and indicated the dominance of particular genotype in Colombo during 2025. These molecular, genetic and epidemiological insights show the importance of active dengue surveillance, providing essential datasets required to enhance future public health outbreak forecasting, tailored treatment plans for more virulent strains, vaccine strategies and overall management of the dengue disease.

Keywords: *Dengue virus, Serotyping, Genotyping, Oxford Nanopore sequencing, Molecular epidemiology*

Acknowledgement: *This study was supported by the Medical Research Institute (Colombo), IDEA Project, Department of Zoology, University of Colombo, and the Robert Koch Institute, Germany*

Abstract No: PP19

Microbiological identification and molecular characterisation of bacterial populations associated with black rot-like symptoms in *Brassica* crops in Sri Lanka

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Black rot disease, caused by *Xanthomonas campestris* pv. *campestris* (Xcc), is among the most damaging bacterial diseases affecting *Brassica* crops, yet its molecular epidemiology and seed health significance in Sri Lanka remain poorly characterised. This study investigated bacterial populations associated with black rot-like symptoms in cabbage (*Brassica oleracea* var. *capitata*) and cauliflower (B. oleracea var. botrytis) through an integrated microbiological and molecular approach. Symptomatic and asymptomatic leaf and seed samples were collected from three agro-ecological zones spanning Colombo, Badulla, and Nuwara Eliya districts. Bacteria were isolated on nutrient agar (NA) and yeast dextrose calcium carbonate (YDC) agar, and yellow mucoid colonies were consistently recovered, indicating the presence of potentially phytopathogenic bacteria. Gram staining revealed Gram-negative, rod-shaped morphology, while biochemical profiling — including catalase, KOH, oxidase, and starch hydrolysis tests-confirmed metabolically active and phenotypically heterogeneous bacterial populations. Genomic DNA was successfully extracted and amplified by PCR using universal 16S rRNA gene primers (341F/785R), yielding discrete bands at approximately 480 bp. However, Sanger sequencing and phylogenetic analysis using MEGA 12.1 revealed that the dominant isolates belonged to the genus *Bacillus*, including *Bacillus pumilus* and *Bacillus cereus*, rather than the target pathogen Xcc. Phylogenetic clustering and genetic distance matrices confirmed clear divergence between the recovered isolates and Xcc reference sequences. These findings indicate that fast-growing, opportunistic *Bacillus* species present in symptomatic tissues and seed samples masked Xcc detection when using non-selective culture methods and universal primers. This highlights a critical limitation of conventional diagnostic approaches and underscores the need for Xcc-specific molecular tools and enhanced microbiological surveillance in plant pathology to ensure accurate epidemiological monitoring of black rot in Sri Lankan Brassica cultivation.

Keywords: *Bacillus spp*., *Brassica* crops, black rot disease, molecular epidemiology, *Xanthomonas campestris* pv. *campestris*

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Abstract No: PP20

Mapping bond strength in drug-like chemical space using the QM40 dataset: structural correlations and chemical insights

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The chemical space of drug-like molecules is vast, and elucidating how molecular structure governs bond strength is fundamental to rational molecular design. Mapping of the bond-strength landscape is presented using the QM40 dataset (freely available), comprising 163,000 molecules computed at the B3LYP/6-31G (2df, p) level and containing 7,760,216 bond-strength measurements. Local vibrational mode force constants, k^a, quantify a bond's resistance to stretching while minimizing vibrational coupling. Statistical analysis and machine learning (k-NN, random forests and SVM) reveal structure–property relationships that govern variations in bond strength across drug-like molecules. Bond-strength patterns are analyzed across 13 bond classes, including C–C, C–H, O–H, N–H, N–O, C–O, S–O, C–S, C–N, N–N, C–Cl, C–F, and S–N bonds. C–H bonds are the most abundant (3.5 M), followed by C–C and C–N. C–H bonds exhibit the narrowest distribution, whereas C–C and C–N bonds show broader bond-strength variability. Stronger C–H bonds occur in ring environments with greater steric crowding. N–H bond strength is strongly influenced by inductive effects from nearby heteroatoms, with stronger N–H bonds closer to electronegative atoms. In contrast, O–H bonds display sensitivity to steric hindrance, with stronger O–H bonds occurring in less crowded environments. Aromaticity enhances the strength of C–S, C–N, and N–N bonds, emphasizing the role of electron delocalization. S–N bonds exhibit high variability from resonance effects and sulfur oxidation state. Aromatic six-membered-ring C–C bonds show force constants of 6.1–6.8 mdyn/Å, whereas C≡C triple bonds exhibit substantially larger values of 16.3–17.2 mdyn/Å. This allows researchers to prioritize chemically stable, synthetically accessible, and pharmacologically promising molecules much earlier in the drug discovery pipeline, accelerating lead optimization while reducing computational cost and experimental effort.

Keywords: *QM40 dataset, Bond strength, Local vibrational mode force constant*

Acknowledgement: *Supercomputer resources provided by the O'Donnell Data Science and Research Computing Institute at SMU*

Abstract No: PP21

Characterisation of Antimicrobial-Resistant Aquatic Biofilm-Forming Bacteria and Evaluation of Biosynthesised Silver Nanoparticles as Antibiofilm Agents

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Aquatic biofilm-forming bacteria act as reservoirs of antimicrobial resistance, facilitating the persistence and dissemination of resistant microorganisms. This study characterised biofilm formation and antibiotic resistance in aquatic biofilm-forming bacteria and evaluated the antibiofilm activity of green-synthesised silver nanoparticles (AgNPs). Biofilm samples collected from five urban lake sites in Sri Lanka were cultured, and bacterial isolates were identified using Gram, acid-fast, and endospore staining, followed by biochemical tests including Triple Sugar Iron (TSI) agar, citrate utilisation, and catalase. Antibiotic susceptibility was assessed using the Kirby–Bauer method, while biofilm formation was quantified by the crystal violet assay using the criteria of Stepanović et al. AgNPs were biosynthesised using *Lactobacillus* spp. and preliminarily confirmed by UV–Visible spectroscopy. Antibacterial activity was evaluated using the agar well diffusion assay. Based on phenotypic and metabolic characteristics, isolates were presumptively identified as *Bacillus*, *Staphylococcus*, *Escherichia coli*, *Klebsiella*, and *Pseudomonas* spp. Biofilm formation varied among isolates: *E. coli* (OD_{630} = 0.179±0.031) and *Bacillus* spp. (0.151 ±0.053) were moderate biofilm formers, *Staphylococcus* spp. (0.080±0.015) showed weak formation, while *Pseudomonas* spp. (0.045±0.009) and *Klebsiella* spp. (0.056 ±0.017) were non-biofilm formers. Antibiotic susceptibility testing against ampicillin, gentamicin, vancomycin, cefotaxime, ceftazidime, and ciprofloxacin, interpreted according to CLSI criteria, revealed diverse resistance profiles, including multidrug resistance among *Pseudomonas* spp. and *E. coli* isolates, with both showing resistance to ampicillin and vancomycin. AgNPs exhibited antibacterial activity against most isolates, with the highest inhibition against *Pseudomonas* spp. (16.55±0.69 mm), followed by *Bacillus* spp. (13.92±1.50 mm), *Staphylococcus* spp. (12.62±0.17 mm), and *E. coli* (10.55±0.51 mm), while *Klebsiella* spp. showed no inhibition. Furthermore, AgNPs significantly reduced biofilm biomass in *Staphylococcus* spp. (78.6%), *Pseudomonas* spp. (74.54%), *E. coli* (58.9%) and *Bacillus* spp. (58.2%), whereas *Klebsiella* spp. showed no reduction (independent samples *t*-test, $p < 0.05$). Overall, biosynthesised AgNPs demonstrated strong antibacterial and antibiofilm activity, highlighting their potential for biofilm control.

Keywords: *Biofilms, Antimicrobial resistance, Silver nanoparticles, Antibiofilm efficacy*

Acknowledgements: *This study was jointly supported by the MSc programme in Molecular Life Sciences, IBMBB and the IPICS Grant*

Abstract No: PP22

Machine Learning-Based Radiomic Classification of Small Lymphocytes and Lymphoblasts in Smartphone-Aquired Cytology Images: A Step Toward Canine Lymphoma Diagnosis

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Lymphoma is one of the common malignancies in dogs. Early and accurate diagnosis is essential for timely treatment and favorable prognosis. Cytological diagnosis relies on identifying the proportion of lymphoblasts in a lymph node aspirate which may vary according to the level of pathologist's experience. In Sri Lanka, diagnostic delays frequently occur due to long transit time between clinics and the laboratories as in-house diagnosis of lymphoma is perform only occasionally. This study evaluated a machine learning-based radiomic framework using smartphone-acquired cytology images as a preliminary step toward a context-specific diagnostic tool for canine lymphoma. A retrospective dataset of 15 canine lymphadenomegaly cases, comprising 11 histopathologically confirmed lymphomas and 4 reactive lymph nodes, was used. Cytology images were captured through a microscope using a handheld smartphone camera to simulate a low-resource diagnostic setting. A total of 470 cells (254 lymphoblasts and 216 small lymphocytes) were manually annotated under the supervision of a pathologist. Fifty radiomic features describing cellular morphology, intensity, and texture were extracted, and the 10 most discriminative features were selected using the Kruskal–Wallis H test. Eleven machine learning classifiers were evaluated using Stratified Group K-Fold cross-validation to prevent patient-level data leakage. Performance was assessed on an independent test set. The Extra Trees classifier achieved the best performance, with 97.5% accuracy, precision, and recall, and an area under the receiver operating characteristic curve of 0.98. Texture-based features, particularly Local Binary Patterns, demonstrated the highest discriminatory power, reflecting chromatin heterogeneity used by veterinary pathologists to distinguish lymphoblasts from small lymphocytes. These findings demonstrate that radiomics combined with machine learning can potentially differentiate Small Lymphocytes and Lymphoblasts from smartphone-acquired images, highlighting its potential for AI-assisted cytological diagnosis in resource-limited settings. Further validation using larger, multicenter datasets is required before clinical implementation.

Keywords: *Clinical pathology, Lymph nodes, Immature lymphoid cells, Group K-fold, Extra-trees*

Abstract No: PP23

Investigation of Phytochemical and anti-inflammatory property of *Leucas zeylanica*

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Leucas zeylanica is a medicinal plant in the family Lamiaceae, a native plant used in a variety of Ayurvedic preparations to treat skin diseases, itches, and helminthic infections in Sri Lanka. The main objective of this study was to evaluate the phytochemical composition and the anti-inflammatory potency of *L. zeylanica* using the human red blood cell (HRBC) membrane stabilization method. The air-dried whole plant was powdered and subjected to sequential extraction using ethyl acetate, methanol, and aqueous solvents by the maceration technique. Phytochemical screening was performed using qualitative methods, which revealed the presence of alkaloids, saponins, flavonoids, tannins, polyphenols, and terpenoids. 1g of extracted powder was dissolved in 10 mL of distilled water to prepare the concentration dilution series (100mg/mL- 0.09 mg/mL). For the preparation of the RBC suspension, the blood was collected from healthy volunteer participants. A 40% (v/v) RBC suspension was prepared using phosphate-buffered saline (pH 7). Anti-inflammatory activity was assessed using the heat-induced hemolysis assay, using acetylsalicylic acid as the standard drug. Absorbance was measured at 540 nm with a spectrophotometer, percentage inhibition was calculated, and data were analyzed using GraphPad Prism 10. Phytochemical analysis demonstrated the presence of flavonoids, polyphenols, and terpenoids in all three extracts. All extracts showed anti-inflammatory activity in a concentration-dependent manner. The highest inhibition percentage was observed with the methanol extract (66 ± 0.60%), while the drug showed 81 ± 0.1% at the highest tested concentration. The One-way ANOVA results revealed the most significant effects for the methanol ($p < 0.0001$) and aqueous ($p < 0.0001$) extracts, while ethyl acetate did not show a statistically significant effect ($p > 0.3776$). These findings suggest that methanol (66.82 ± 0.60%) and aqueous (66.0 ± 0.33%) extracts possess good anti-inflammatory potential through stabilization of the erythrocyte membrane, whereas the ethyl acetate extract exhibited comparatively weaker activity. Although the active constituents were not identified in this study, the higher activity of the methanol and aqueous extracts may be associated with the presence of polar bioactive compounds, which have been widely reported to exhibit membrane-stabilizing and anti-inflammatory properties. The IC50 values of the methanol aqueous and ethyl acetate extracts were 2.73 mg/mL, 6.75mg/mL, and 0.4061 mg/mL, respectively. Based on the IC50 values, ethyl acetate exhibits the highest potency. However, its membrane-stabilizing activity is not statistically significant. Further *in vivo* studies are recommended to confirm their therapeutic approaches.

Keywords: *Heat-induced hemolysis, Leucas zeylanica, Preliminary phytochemical*

Abstract No: PP24

Potential of *Garcinia quaesita* Pierre extract to enhance meropenem activity against carbapenem-resistant Gram-negative bacteria

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Carbapenem-resistant Gram-negative bacteria (CR-GNB) have become a major global health problem. The World Health Organization has identified carbapenem-resistant *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and Enterobacterales as the most critical pathogens due to increasing morbidity, mortality, and limited treatment options. Therefore, the development of new alternative approaches, including plant-derived compounds in combination with existing antibiotics is needed to combat carbapenem resistance. This study evaluated the synergistic effect of *Garcinia quaesita* Pierre extract with meropenem against phenotypically and molecularly confirmed CR *Escherichia coli*, *Klebsiella pneumoniae*, *P. aeruginosa,* and *A. baumannii*. The plant extract was prepared using ethyl acetate and concentrated using a rotary evaporator. Antimicrobial activities of the extract and meropenem were evaluated against selected CR-GNB using standard methods. The disc diffusion assay demonstrated concentration-dependent antimicrobial activity of plant extract against all CR-GNB, with maximum inhibition zones ranging from 8.33 ± 0.58 mm to 10.33 ± 1.53 mm at 200 mg/mL. The minimum inhibitory concentration (MIC) was determined using the broth microdilution method. The MICs of plant extract were 3125 µg/mL against *E. coli*, *K. pneumoniae*, *A. baumannii*, and 1560 µg/mL against *P. aeruginosa*. Meropenem MICs were 16 µg/mL for *E. coli*, *A. baumannii*, 64 µg/mL for *K. pneumoniae*, and >256 µg/mL for *P. aeruginosa*, confirming carbapenem resistance. The combined activity of meropenem and the plant extract was tested using the checkerboard microdilution assay and interpreted by the Fractional Inhibitory Concentration Index (FICI). Synergistic tendency was observed against *P. aeruginosa* (FICI<0.625), and additive effects against *K. pneumoniae*, *A. baumannii* (FICI=1.00), and an indifferent effect against *E. coli* (FICI=1.50) were observed. Notably, no antagonistic interactions were observed. Overall, *G. quaesita* extract enhanced meropenem activity against selected CR-GNB, highlighting its potential as an antimicrobial adjuvant. Further investigations are required to identify the active phytochemical compounds of *G. quaesita* and validate the combination in vivo.

Keywords: *Carbapenem resistant Gram-negative bacteria, Meropenem, Garcinia quaesita Pierre, Checkerboard assay, Synergistic effect*

Abstract No: PP25

Phytochemical composition, antioxidant potential, and antimicrobial activity of selected Phaseolus leaves in Sri Lanka

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Plant-derived phytochemicals are increasingly recognized for their therapeutic potential in combating oxidative stress and microbial infections. This study investigated the phytochemical profile, antioxidant activity, and antimicrobial properties of leaves from five Phaseolus species (P. aureus, P. calcaratus, P. vulgaris, P. coccineus, and P. lunatus) collected in Sri Lanka. Leaf extracts were prepared using water and methanol solvents, and qualitative screening confirmed the presence of tannins, terpenoids, steroids, and alkaloids. Quantitative assays revealed significant variation in phytochemical yields depending on solvent choice: water extracts of P. coccineus exhibited the highest total phenolic content (530.51 mg GAE g^{-1}), while methanolic extracts of P. vulgaris showed the highest flavonoid content (29.69 mg QE g^{-1}). Antioxidant capacity, measured via phosphomolybdenum assay, was greatest in methanolic extracts of P. calcaratus (2190.11 mg AAE g^{-1}). Free radical scavenging assays demonstrated strong activity in water extracts, with P. aureus showing the lowest IC_{50} for DPPH (276.07 µg mL^{-1}) and P. vulgaris for ABTS (642.64 µg mL^{-1}). Antimicrobial testing revealed that methanolic extracts inhibited Escherichia coli growth, while water extracts showed negligible activity. Overall, water proved more effective for phenolic extraction and antioxidant activity, whereas methanol favoured flavonoid recovery and antibacterial effects. These findings highlight the potential of Phaseolus leaves as sustainable sources of natural antioxidants and antimicrobials, supporting their future application in nutraceutical and pharmaceutical development.

Keywords: *Phaseolus leaves, phenolic content, flavonoids, antioxidant activity, antimicrobial properties*

Abstract No: PP26

Evaluation of the Antimicrobial Potential of *Catharanthus roseus* (Madagascar Periwinkle) Leaf Extracts Against *Vibrio parahaemolyticus* Under In Vitro Conditions

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Antibiotic resistance has become a significant public health and therapeutic concern worldwide, highlighting the critical need for discovery of novel alternative antimicrobial agents. Consequently, there is an increasing global interest in medicinal plants as sources of novel bioactive compounds for drug discovery, owing to their unique chemical structures and diverse biological activities. The *Catharanthus roseus* leaf contains several alkaloids including vincristine, which is an important therapeutic compound that affects all rapidly proliferating cells. Laboratory experiment was performed to assess the antibacterial potential of *C. roseus* leaf extracts against fish pathogenic bacteria. 70% ethanol and hot water crude extracts were prepared from the plant material and subsequently tested against *Vibrio parahaemolyticus* to evaluate their antibacterial potential. The inhibitory effects of the extracts were assessed using Kirby- Bauer disc diffusion method with 50mg/mL, 100mg/mL, and 150mg/mL concentration series followed with Tetracycline (30 μg) as the positive control. To find out chemical compounds in crude, preliminary phytochemical tests and Fourier Transform Infrared Spectrometer (FTIR) analysis were conducted. The results of the phytochemical tests and FTIR showed the presence of alkaloid, flavonoid, phenol, tannins, diterpenes, saponins and glycosides in both *Catharanthus roseus* crude extracts. The results of the disk diffusion test demonstrated that both *C. roseus* extracts exhibited significant antibacterial activity ($p < 0.05$) against *Vibrio parahaemolyticus* with the Minimal Inhibitory Concentration (MIC) determined to be 50 (mg/mL). Therefore, the leaf extract of *Catharanthus roseus* demonstrates promising antimicrobial potential and may serve as a valuable source of bioactive compounds for the development of novel antimicrobial agents.

Keywords: *Antimicrobial, Catharanthus roseus, Crude extracts, Minimal Inhibitory Concentration, Vibrio parahaemolyticus*

Abstract No: PP27

Novel approach in natural cosmetics: Formulating and assessing the potential of *Ulva lactuca* extract in a cosmetic cream

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The growing demand for natural and marine-derived cosmetic products has increased interest in seaweed-based cosmeceuticals due to their rich bioactive composition and potential skin benefits. This study aimed to develop, optimize, and evaluate a stable cosmetic cream formulated using ethanol extract of *Ulva lactuca*, a green marine alga abundant along the coastal regions of Sri Lanka. Fresh samples of *Ulva lactuca* were manually harvested from the coastal area of Talpe, Sri Lanka. The dried seaweeds were subjected to ethanol extraction via maceration, and the resulted extract was incorporated into water-in-oil emulsion-based cream formulations. Three formulations (315, 316, and 308) were initially developed. Formulation 308 exhibited the most desirable organoleptic properties, including a smooth texture and homogeneous appearance. Consequently, formulation 308 was selected as the optimized formulation for further physicochemical and biological evaluations. Physicochemical stability assessments of formulation 308 over six weeks revealed consistent spreadability with no observable phase separation or texture deterioration. The pH remained within an acceptable cosmetic range which was 6.3 ± 0.26 to 7.2 ± 0.26. The formulation also demonstrated acceptable acid value of 1.78 mg NaOH/g, indicating minimal lipid degradation; however, the peroxide value 11.6 meq/kg at week three was slightly exceeded the recommended limit, suggesting mild oxidative changes during storage. Phytochemical screening of the extract confirmed the presence of alkaloids, saponins, tannins, and glycosides, indicating bioactive properties for dermatological benefits. However, the antimicrobial assay against *Escherichia coli* and *Staphylococcus aureus* showed no measurable inhibition zones (0.00 ± 0.00 mm), indicating no direct antibacterial activity of cream under the tested conditions. Overall, the formulated *Ulva lactuca* cream demonstrated promising physicochemical stability and phytochemical richness, supporting its potential as a natural cosmetic base. Further studies, including antioxidant, anti-inflammatory, and in vivo evaluations, along with clinical trials, are recommended to validate its efficacy and safety for human use.

Keywords: *Marine algae, Ulva lactuca, Natural cosmetic, Phytochemicals, Cosmeceuticals*

Abstract No: PP28

Screening and Preliminary Identification of Oxytetracycline Residues in Commercial Milk Samples by TLC and HPLC

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Milk is a valuable dietary component that provides essential nutrients and bioactive compounds important for human health. The widespread use of antibiotics in food-producing animals for therapeutic and preventive purposes may result in the presence of antibiotic residues in milk. The occurrence of these residues can adversely affect milk quality and pose potential risks to public health. As milk is consumed regularly by people of all age groups, continuous monitoring of antibiotic residues is necessary to ensure food safety and consumer protection. Therefore, this study aims to determine oxytetracycline residues in milk and assess associated dietary health risks. Raw, pasteurized, and processed milk samples were collected from local markets and stored at −20 °C prior to analysis. Antibiotic residues were extracted using a mixture of 0.2 M sodium EDTA and methanol. Initial screening of the extracted samples was performed using Thin Layer Chromatography (TLC), followed by confirmatory analysis using High-Performance Liquid Chromatography (HPLC). TLC analysis revealed visible spots comparable to those of the oxytetracycline standard. HPLC analysis of the oxytetracycline standard produced a characteristic peak at 11.079 min with UV absorption maxima at 192, 220, 250, 276, and 356 nm. A selected pasteurized milk sample showed a peak at 12.726 min with UV absorption maxima at 194, 222, 266, and 366 nm, while several other samples exhibited peaks at 13.558 min with UV absorption maxima at 202, 238, 268, and 346 nm. These peaks displayed chromatographic profiles and UV spectral characteristics similar to those of the oxytetracycline standard. Our results suggest the possible presence of oxytetracycline or degraded oxytetracycline products in the milk samples analyzed. Further confirmatory analyses will be carried out to verify these findings and evaluate their implications for food safety and regulatory compliance in Sri Lanka.

Keywords: *Antibiotic, Oxytetracycline, Milk, HPLC, TLC*

Acknowledgements: ***This study was*** *financially supported by the Institute of Chemistry Ceylon. We thank Ms P.R. Kumari for the assistance provided during the study*

Abstract No: PP29

Evaluation of Antibacterial, Anti-inflammatory and Cytotoxic Activities of *Semecarpus subpeltata* (Kabara Badulla) Leaf Extract

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The widespread resistance of microbes to conventional antibiotics as well as the adverse effects of synthetic antibiotics necessitate the discovery of the natural anti-bacterial agents. *Semecarpus subpeltata* (Kabara Badulla), a plant belonging to the Anacardiaceae family, is reported to be a source of bioactive compounds with the ability of providing therapeutic effect against microorganisms based diseases. Therefore, this research work was done with the aim of determining the anti-bacterial potential of the methanol extract of the leaf of *Semecarpus subpeltata* on the strain *Staphylococcus aureus* (ATCC 25923). Leaves were collected fresh from the Kanneliya forest reserve and dried in shade. Extracts were prepared by using 80% methanol. The anti-bacterial property was determined through agar well diffusion method and the MIC and MBC values of the extract were obtained by using the standard methods over the concentration range of 50, 800 mg/mL. Ciprofloxacin IV was the positive control. For anti-inflammatory activity (egg albumin denaturation assay), 0.3125, 0.625, 1.25, 2.5, 5, 10 mg/ml concentration of diclofenac was used as positive control while for cytotoxicity, brine shrimp lethality assay (10, 1000 µg/ml) was the method used. All the tests were performed in duplicate. Concentration dependent anti-bacterial efficacy of the extract was demonstrated as the mean diameters of the zones of inhibition were 27.8 mm, 21.8 mm, and 17.0 mm at concentrations of 800, 400, and 200 mg/ml, respectively. The above mentioned values were lower than that of ciprofloxacin (43.2 mm).MIC and MBC were the same at 200 mg/ml. In the egg albumin denaturation model, the elicited anti-inflammatory effect was quite prominent (74.64, 94.51%) while the maximum inhibitory effect was seen at 0.3125 mg/ml which was also the level of diclofenac (87.27, 97.63%) in the model. Brine shrimp lethality assay test showed cytotoxicity in a dose dependent manner where mortality increased from 20% (10 µg/ml) to 100% (500, 1000 µg/ml), and LC_{50} was estimated to be near 100 µg/ml. In short, Semecarpus subpeltata possesses antimicrobial, anti-inflammatory, and cytotoxic effects, which not only support the rationale of its use in the folk medicine but also highlight it as a potential lead for on-going drug discovery.

Keywords: *Semecarpus subpeltata, Staphylococcus aureus, Antibacterial activity, Anti-inflammatory activity, Cytotoxicity*

Abstract No: PP30

Phytochemical and Bioactivity Assessment of an Endemic Medicinal Plant of Sri Lanka

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Semecarpus coriaceus Thwaites (Family: Anacardiaceae), an endemic Sri Lankan plant, has shown potential therapeutic effects, including tumour regression. Therefore, this study investigated the total phenolic content (TPC), antioxidant, anti-inflammatory, and cytotoxic activities of the methanolic leaf extract of *Semecarpus coriaceus* Thwaites. TPC was determined using the Folin–Ciocalteu method, antioxidant activity using the DPPH assay, and anti-inflammatory activity using the human red blood cell (HRBC) membrane stabilisation assay. Cytotoxicity was evaluated by the MTT assay against the Vero cell line and the DLD-1 human colorectal cancer cell line. All assays were conducted independently in triplicate. Probability values were calculated by Student's t-test using GraphPad Prism software. The total phenolic content (TPC) of the extract was 78.85 ± 3.07 mg GAE/g extract. The extract exhibited moderate antioxidant activity, with a DPPH IC_{50} value of 0.214 mg/mL compared to 0.178 mg/mL for the standard, butylated hydroxytoluene. A statistically significant difference ($p < 0.05$) was observed between the extract (76.81±0.39%) and standard (82.31±0.96%) inhibition values at 1 mg/mL, with the extract showing slightly lower inhibition than the standard. Furthermore, the extract demonstrated strong HRBC membrane stabilisation activity, with an IC_{50} value of 0.055 mg/mL, comparable to that of aspirin (IC_{50} = 0.052 mg/mL). The difference between the inhibition values of the extract (80.09±0.35%) and the standard (90.27±0.23 %) observed in HRBC membrane stabilisation activity at 1mg/mL was statistically significant ($p < 0.05$), with the extract showing slightly lower inhibition than the standard. MTT assay results demonstrated that the extract was non-toxic to Vero cells, with 100% cell viability observed at 1 mg/mL. At the same concentration, the extract exhibited moderate cytotoxic activity against DLD-1 colorectal cancer cells, resulting in 46.86 ± 3.52% cell inhibition. Overall, the results demonstrate that *Semecarpus coriaceus* Thwaites possesses moderate antioxidant, anti-inflammatory, and cytotoxic properties, supporting its potential as a source of bioactive compounds for further pharmacological investigation.

Keywords: *Natural Products, Endemic plants of Sri Lanka, Bioactivity*

Abstract No: PP31

Assessment of total phenolic content and total flavonoid content of three selected medicinal plants; *Artocarpus nobilis, Vernonia zeylanica* and *Bacopa monnieri*

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Sri Lankan medicinal plants are rich in polyphenols and flavonoids, collectively known as phytochemicals, associated with a wide range of biological activities. This study investigated the total polyphenolic content (TPC) and total flavonoid content (TFC) of three selected plants; *Artocarpus nobilis*, *Vernonia zeylanica* and *Bacopa monnieri*. Root extracts of *A. nobilis;* methanol/ dichloromethane (MDE) and ethyl acetate (EtOAc) leaf extracts of *V. zeylanica;* MDE, hexane (Hex), chloroform (Chlo), EtOAc, methanol (Met) and aqueous extract of *B. monnieri* were evaluated. The TPC was determined using Folin-Ciocalteu assay and expressed as mg gallic acid equivalents (GAE)/g of plant extract. TFC was determined using aluminium chloride colorimetric method and expressed as mg quercetin equivalents (QE)/g of plant extract. The TPC of *A. nobilis* with the EtOAc extract showed the highest value of 1395.22±3.85 mg GAE/g of plant extract and the lowest for the MDE extract of 152.07±23.40 mg GAE/g of plant extract. For *V. zeylanica* TPC ranged from 21.89±1.05 to 87.63±17.64 mg GAE/g of plant extract with MDE showing the highest value 87.63±17.64 mg GAE/g and hexane showing the lowest 21.89±1.05 mg GAE/g of plant extract. The aqueous plant extract of *B. monnieri* contained 71.89±24.51 mg GAE/g of plant extract. The TFC of *A. nobilis* with the MDE showed the lowest value of 117.44±4.99 mg QE/g of plant extract and highest for the EtOAc extract of 298.10±21.39 mg QE/g of plant extract while *V. zeylanica* exhibited values ranging from 14.03±0.32 to 49.44±1.12 mg QE/g of plant extract. The aqueous extract of *B. monnieri* showed a comparatively low flavonoid content of 16.44±0.94 mg QE/g of plant extract. In conclusion, *A. nobilis* exhibited considerably higher TPC and TFC values compared to *V. zeylanica* and *B. monnieri,* indicating its potential as a rich source of phenolic and flavonoid compounds.

Keywords: *Polyphenols, flavonoids, phytochemicals, medicinal plants, solvent extracts*

Acknowledgements: *This work was supported by the Cellular and Molecular Immunology MSc program, IBMBB*

Abstract No: PP32

In silico molecular docking and ADMET profiling of *Borreria verticillata* bioactive compounds against endometrial inflammatory receptors; identifying lead candidates for endometriosis therapy

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Endometriosis is a chronic inflammatory gynecological disorder affecting approximately 5–10% of women worldwide. It is characterized by the ectopic implantation of endometrial-like tissue and is driven by abnormal cytokine signaling, including TNFR1- and IL-1R-mediated pathways that promote inflammation and lesion persistence. Because current treatments are associated with high recurrence, there is a need for novel multi-target therapeutic agents. This study integrated molecular docking and ADMET profiling to evaluate 17 bioactive phytochemicals from *Borreria verticillata* as inhibitors of Tumor Necrosis Factor Receptor 1 (TNFR1) and Interleukin 1 Receptor (IL 1R). Molecular docking revealed that ursolic acid exhibited the strongest binding affinity toward TNFR1 (−8.07 kcal/mol), while borreverine bound favorably to both TNFR1 (−7.52 kcal/mol) and IL-1R (−7.89 kcal/mol). Hydrogen bonding dominated TNFR1 binding, whereas hydrophobic interactions were more prominent within the IL-1R pocket. Borreverine established stable hydrogen-bond and hydrophobic interaction networks with both targets, indicating its potential as a multi-target anti-inflammatory compound. SwissADME indicated that borreverine, isoborreverine, and emetine possess physicochemical properties favorable for gastrointestinal absorption while ursolic acid and stigmasterol showed lower predicted oral bioavailability. Toxicity assessment using ProTox 3.0 predicted relatively moderate acute toxicity for borreverine (LD50 ≈ 1000 mg/kg, toxicity class 4). Ursolic acid, despite strong binding, raised hepatotoxicity and carcinogenicity concerns. Ramachandran analysis placed key residues in favored regions, supporting docking plausibility. These findings suggest *B. verticillata* as a promising source of anti-inflammatory compounds for endometriosis, with structural optimization and formulation improvements warranted for future development.

Key words: *Endometriosis, Molecular Docking, Toxicity Assessment, Borreverine, Anti-inflammatory Compounds*

Abstract No: PP33

In vivo liver protective effects and toxicity studies of a commercially available nutraceutical *(LiverU)* capsule

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Osbeckia octandra, Atalantia ceylanica, Oryza sativa subsp. Indica, Camellia sinensis, Curcuma longa, Zingiber officinale, Glycyrrhiza glabra, Piper nigrum, and desiccated coconut are included in *LiverU*, a unique polyherbal formulation. In accordance with OECD guidelines 425 and 407, this study assessed its preclinical safety using acute and 28 days repeated dose oral toxicity assessments in Wistar rats. For the acute toxicity study, female rats were administered a single oral dose of 2000 mg/kg. Male and female rats were given 102.8, 205.6, or 411.2 mg/kg for 28 days in order to test for repeated-dose toxicity. Mortality, clinical symptoms, body weight, food and water intake, hematological, biochemistry, organ weights, and histology were among the parameters monitored. No mortality or adverse clinical signs were observed in either study. The acute toxicity test revealed no significant changes in any parameters. Similarly, the 28 days toxicity test demonstrated no toxicologically relevant effects, as most parameters showed no statistically significant variations. Isolated variations specifically in male lung weights (205.6 mg/kg), female heart weights (102.8 and 411.2 mg/kg), and low dose male hematological and biochemical parameters (MCV, creatinine, and ALT at 102.8 mg/kg) lacked dose dependency and histopathological correlation. In conclusion, the preclinical safety of *LiverU* was confirmed, with an oral LD_{50} greater than 2000 mg/kg and a lack of systemic toxicity up to four times the therapeutic equivalent dose.

Keywords: *Hepatoprotective agent, Polyherbal formulation, LD_{50}, Acute and 28-day repeated oral toxicity*

Abstract No: PP34

Evaluation of antioxidant and antimicrobial properties of plant-derived silver nanoparticles from Peanut Butter Fruit (*Bunchosia* sp.)

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The prevalence of antibiotic resistance and oxidative stress related diseases, such as cancer, have been increasing rapidly, urging the need for novel bioactive remedies. Plant-derived silver nanoparticles (AgNPs) have garnered major significance due to their antimicrobial and antioxidant properties, and green synthesis process. Peanut Butter Fruit (*Malpighiaceae*), native to tropical areas of Central and South America, is enriched with bioactive compounds that facilitate green synthesis. However, research regarding *Bunchosia* sp. in green nanotechnology, remains limited, providing the rationale for this study. Water extracts (WE) were tested for the presence of phytochemicals using standard phytochemical screening procedures. WEs and synthesized AgNPs were analyzed for Total Flavonoid Content (TFC), Total Phenolic Content (TPC) and Total Antioxidant Content (TAC) through spectrophotometric assays, and their antimicrobial activity by agar well diffusion method against *Staphylococcus aureus* and *Escherichia coli*, using Gentamicin as a positive control. Phytochemical profile showed the presence of reducing sugars, proteins, saponins, tannins, coumarins, and alkaloids in leaf, root and flower_WEs. AgNPs were synthesized under optimal condition of 90 ^{o}C for 60 minutes. Formation was confirmed by a color change and a strong surface plasma resonance peak around 400-500 nm, detected by UV-Vis spectrophotometry. The AgNPs exhibited a significantly higher phytochemical content and antioxidant properties compared to WEs; TFC ($p<0.001$), TPC ($p<0.001$) and TAC ($p=0.007$). Pearson's correlation between TPC, TFC and TAC, concluded that phenols contributed significantly to antioxidant activity ($r=0.974$, $p<0.001$). The Bark and Fruit_AgNPs exhibited antibacterial activity against *S.aureus* and *E.coli*, with Bark_AgNPs displaying the largest zones of inhibition (ZOI), 0.9 and 1.1cm respectively, with the corresponding ZOIs of the positive control to be 2.0 and 2.3 cm. Among the WEs, only Bark_WE displayed antibacterial activity against *S.aureus.* These results show that *Bunchosia* sp. AgNPs possess promising antioxidant and antibacterial activity, with potential healthcare applications in combating various diseases.

Keywords: *Silver nanoparticles (AgNPs), Phytochemicals, Green synthesis, Antioxidant activity, Antibacterial activity*

Abstract No: PP35

Antibacterial screening of local medicinal plants *Mimosa pudica, Ocium tenuiflorum and Vernonia cinera*

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Antibiotic resistance has become a major issue in the world. Therefore, the identification of novel plant-based antibacterial drugs is a promising strategy to overcome this problem. Sri Lanka has a large variety of medicinal plant species yet the antibacterial potential of many of these have not been explored. This research aimed to screen some selected medicinal plants for their antibacterial activity and to use in novel therapeutic development. Plants from the families Fabaceae (*Mimosa pudica*), Lamiaceae (*Ocium tenuiflorum*) and the Asteraceae (*Vernonia cinera*) were selected for the study. The present study aimed to screen the phytochemical profiles and test the individual and synergistic antibacterial activities of the leaf extracts against the Gram-positive bacterium *Staphylococcus aureus* and the Gram-negative bacterium *Escherichia coli*. Initially, a phytochemical screening to test alkaloids, flavonoids, terpenoids, resins and phenolic compounds was done for each leaf extracts. Positive results were obtained for *Mimosa pudica* and *Ocimum tenuiflorum* for all the tested phytochemicals, whereas *Vernonia cinerea* lacked flavonoids. Agar well diffusion method was used to test antibacterial activity. Methanol extracts of *M. pudica* and *V. cinerea* inhibited *S. aureus* giving an inhibitory zone of 11.67 ± 0.88 mm. For synergistic studies, combinations of *M. pudica + V. cinerea, O. tenuiflorum + M. pudica, V. cinerea + O. tenuiflorum,* inhibited *S. aureus* giving zones of (11.67 ± 0.34, 12.0 ± 0.6, 9.34 ± 0.34, 10.0 ± 0) mm. No inhibition was observed on *E. coli* with individual methanol extracts and combinations. This might be due to the presence of the rigid cell wall structure in *E. coli* compared to *S. aureus*. To test this assumption research has been further extended to nanoparticle development. This study would serve as a foundation to evaluate the synergistic combinations of plant extracts of above families and their efficiency against bacterial infections.

Keywords: *Antimicrobial, phytochemical, therapeutics, well diffusion*

Acknowledgement: *This work was supported by Wayamba University Research Grant 2024*

Abstract No: PP36

Antibacterial effects of fungal endophytes isolated from seaweeds likely belonging to *Gracilaria* spp. and *Sargassum* sp. collected from Pamunugama, Sri Lanka

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Seaweeds and endophytic fungi are known to produce a broad spectrum of biologically active compounds with pharmaceutical properties. However, the ability of marine algal endophytes to produce novel bioactive secondary metabolites remains underexplored. This study aimed to isolate and evaluate the antibacterial properties of endophytic fungi obtained from two morphologically identified seaweeds likely belonging to *Gracilaria* spp. and *Sargassum* spp. collected from Pamunugama, Sri Lanka (7.1422222°N, 79.8319167°E). The seaweeds were surface sterilized, fragmented, and implanted on potato dextrose agar. Through successive subculturing, five pure fungal isolates were obtained. Morphological and biochemical analyses suggested that isolates recovered from *Gracilaria* spp. likely belonged to *Aspergillus* spp. (N2-b, N2-d), *Nigrospora* spp. (N2-a), and *Acremonium* spp. (N2-x), while the isolate recovered from *Sargassum* spp. likely belonged to *Penicillium* spp. (N3-c). Using the agar disc diffusion method, antibacterial activity of mycelial methanol extracts and ethyl acetate extracts of secondary metabolites was evaluated against *Staphylococcus aureus*, *Bacillus cereus*, *Escherichia coli*, and *Pseudomonas aeruginosa*, with ciprofloxacin (1 mg/mL) and dimethyl sulfoxide as positive and negative controls, respectively. The ethyl acetate extract of N2-a (20 mg/mL) exhibited significant antibacterial activity against *S. aureus*, producing an inhibition zone of 1.14 ± 0.28 mm. Similarly, the methanol extract of N2-a (7 mg/mL) showed significant activity against *B. cereus* (0.98 ± 0.34 mm; $p < 0.05$). Although methanol extracts of N2-d, N3-c, N2-b, and N2-x exhibited inhibition zones of 1.38 ± 0.63, 1.50 ± 0.75, 2.44 ± 1.19, and 0.67 ± 0.58 mm against *B. cereus*, respectively, these inhibitions were not statistically significant compared to the negative control. These findings suggest that *Nigrospora* spp. associated with *Gracilaria* spp. represents a promising source of antimicrobial metabolites. Further studies on fungal identification, solvent optimization, and compound characterization are needed.

Keywords: *Antibacterial activity; Endophytic fungi; Seaweeds; Secondary metabolites*

Synergism of *Andrographis paniculata* and *Datura metel* Extracts on the Metastatic Ability of the Human Glioblastoma Cells

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Glioblastoma multiforme (GBM) is a highly aggressive and therapeutically resistant brain tumour that requires novel treatment strategies capable of simultaneously suppressing tumour growth and metastatic progression. This study investigated the synergistic anti-glioblastoma and anti-metastatic potential of combining bioactive fractions from *Andrographis paniculata* (AP-C9) and *Datura metel* (DM-F3) against invasive LN-229 glioblastoma cells. Ethyl acetate and methanolic crude extracts of *A. paniculata* and *D. metel*, respectively, were subjected to bioactivity-guided fractionation, and AP-C9 and DM-F3 were identified as the most potent antiproliferative fractions. Combination effects were evaluated using the Chou-Talalay method (CompuSyn) based on MTT assay data. Functional efficacy was assessed through scratch wound-healing, colony formation, cell scattering, transwell migration, and Matrigel invasion assays. Antiproliferative interactions were strongly ratio-dependent, with the 1:8 ratio (C9:F3) producing potent growth inhibition (IC_{50} = 23.58 μg/mL) and maximizing dose reduction of AP-C9 (DRI = 4.97). Functional assays demonstrated broad suppression of glioblastoma metastatic traits. The combination markedly inhibited LN-229 migration in the scratch assay, achieving up to 92.2% wound-closure inhibition and exhibiting synergistic anti-migratory interactions across all tested concentrations (CI = 0.058-0.655). Colony formation assays revealed pronounced low-dose synergy, with approximately 92% suppression of clonogenic survival at 0.0225-0.0450 μg/mL and substantial dose-reduction benefits (DRI >17 for both fractions). However, higher concentrations displayed antagonistic interactions, indicating a biphasic response. Cell-scattering analysis further predicted synergistic inhibition at high effect levels (CI = 0.588-0.145 at fa = 0.90-0.95), suggesting enhanced suppression of glioblastoma cell dispersal with considerable dose-reduction advantages. Transwell migration and Matrigel invasion assays further demonstrated marked suppression of migratory and invasive behaviour, confirming the combination's ability to inhibit both two-dimensional motility and three-dimensional penetration of the extracellular matrix. Collectively, these findings demonstrate that the AP-C9 and DM-F3 combination cooperatively suppresses GBM migration and invasion, highlighting this phytochemical combination as a promising strategy for limiting GBM metastatic progression

Keywords: *Glioblastoma, Chou-Talalay, Compusyn, Andrographis paniculata, Datura metel, Metastasis, Combination therapy*

Acknowledgements: *This research was supported by the Institute of Biochemistry, Molecular Biology and Biotechnology (IBMBB)*

Abstract No: PP38

Probiotic Pre-feeding Enhances the Protective Efficacy of a *Streptococcus agalactiae* Biofilm Vaccine in Nile Tilapia (*Oreochromis niloticus*)

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Nile tilapia (*Oreochromis niloticus*), a major aquaculture species, faces recurring streptococcosis outbreaks that threaten production and profitability. The increasing global burden of antimicrobial resistance (AMR) necessitates the development of sustainable alternatives to conventional antimicrobial use. This study aims to investigate the effects of probiotic pre feeding following biofilm vaccination in Nile tilapia against *Streptococcus agalactiae.* The *S. agalactiae* biofilm vaccine was prepared using chitin flakes as substrate and inactivated with 1% formalin. Healthy Nile tilapia fingerlings (10±2g) were assigned to four experimental groups in triplicate: Negative control (NC), Probiotic-only (Pro), IP vaccine-only (IPVac), and probiotic-trained vaccine group (IPVacPro). Fish in the Pro and IPVacPro groups were fed with 1×10^9 CFU/g *Bacillus licheniformis*-coated feed for 28 days, after which the IPVac and IPVacPro groups were intraperitoneally injected with complete inactivated *S. agalactiae* biofilm vaccine at 3×10^7 CFU-equivalent/fish. The blood samples were collected on 7, 14, 21, 28, 35, 42 and 49 days post-trial to assess non-specific immune parameters, as superoxide dismutase, catalase, myeloperoxidase, and lysozyme activity. On day 42, serum IgM was quantified by ELISA, and IgM and IL-1β gene expression was evaluated by qRT-PCR in head kidney tissue. Fish were challenged intraperitoneally with virulent *S. agalactiae* (1.7×10^4 CFU-equivalent/ fish) to determine the survival rate. The IPVacPRO group demonstrated significantly elevated non-specific immune responses in serum. Higher serum IgM levels and upregulated IgM and IL-1β gene expression were observed in the IPVacPro group compared to all other groups ($p < 0.05$). The IPVacPro group showed 83% survival rate with reduced clinical signs of infection compared to other groups and negative control. These results indicate that probiotic pre-feeding can enhance the biofilm-based vaccine efficacy to strengthen immune responses in Nile tilapia, offering a sustainable strategy to manage streptococcosis towards one health approach.

Keywords: *Streptococcus agalactiae; Nile tilapia; biofilm vaccine; probiotics; trained immunity*

Isolation, Characterization and assessing Degradation kinetics of Fluorene degrading bacteria from marine water – A bioremediation approach

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Polycyclic Aromatic Hydrocarbons (PAHs) are persistent organic pollutants widely distributed in marine water, sediment and marine organisms, posing significant threats to marine organisms. Among 16 PAHs designated by the United States Environmental Protection Agency, Fluorene is considered as a priority pollutant due to its mutagenic & carcinogenic effects and environmental persistence by transforming to fluorene derivatives, Oxy-PAHs, Nitro-PAHs. This study aimed to identify potential bacteria for fluorene degradation from marine water samples collected at the Dockyard, Colombo Harbor, Sri Lanka. As the central port of Sri Lanka, Colombo Port Dockyard sustains intensive port operations which is exposed to hydrocarbon pollutants. In the European and African context several studies have been conducted to identify PAHs occurrence and bioremediation potential however; PAH degrading bacterial communities indigenous to tropical waters were poorly characterized. Especially in Sri Lanka no studies have been conducted specifically to identify Fluorene degrading bacteria identification. Bacterial isolation using the pour plate method and streak plate (quadrant) method yielded thirteen different bacterial colonies based on morphological characteristics. Using an ELISA plate reader, three bacterial colonies exhibiting the highest absorbance at 590nm when grown with fluorene as the sole carbon source were selected for further study. Selected standard three bacterial species were introduced into a mixture of autoclaved seawater and fluorene 50ppm, 25ppm and 1ppm concentrations. The control sample was used without adding bacteria for the degradation study. Subsamples were collected from each concentration from all three bacterial species at 48hrs. over a 6-day incubation period. and HPLC analysis was conducted to quantify fluorene concentration. Based on the HPLC results the highest degradation percentages of all three bacteria were observed on sixth day of the subsampling. Results revealed that 2nd has the highest capacity to degrade fluorene at 99.54% following 1st bacteria 98.80% and 3rd bacteria 73.20%. There was no significant reduction in fluorene concentration in control sample. 1st bacteria showed the lowest half lifetime of 2.2 days of incubation whereas 2nd and 3rd species showed a half lifetime of 2.5 and 3.8 days respectively. These findings demonstrate that isolated bacteria from Colombo Harbor possess capacity of fluorene degrading. This study provides foundational data for bioremediation strategies as solution for PAHs contamination in tropical marine water including Sri Lanka.

Keywords: *Polycyclic Aromatic Hydrocarbons (PAHs), Fluorene, Degradation, Colombo harbor, Bioremediation*

Abstract No: PP40

Isolation and characterization of indigenous potassium-solubilizing bacteria for biofertilizer development

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Plant growth-promoting rhizobacteria (PGPR) promote plant growth and increase crop yield by enhancing nutrient mobilization, increasing nutrient uptake and facilitating potassium solubilization in soil. Potassium solubilization is one the important mechanism plays a crucial role in increasing the availability of solubilized potassium in soil for plants. However, the identification and application of indigenous potassium-solubilizing bacteria are still at an emerging stage. Therefore, this study aimed to isolate, identify, and characterize efficient potassium-solubilizing bacteria from different regions in Sri Lanka and to evaluate their potential for the formulation of a biofertilizer. In this study, potassium solubilizing bacteria were isolated from soil samples collected from eleven geologically different locations, including paddy fields, coconut estates and agricultural lands. A total of 32 morphologically different bacteria were isolated after serial dilution of soil samples and screening on Aleksandrov agar medium. Potassium solubilization indices (KSI) were different among all isolates, isolate I-31 produced the highest KSI (2.14 ± 0.02) and I-25 produced KSI (1.97 ± 0.04). According to quantitative assays, Isolate I-31 released significantly higher concentrations of solubilized potassium (102.00 ± 2.51 mg L^{-1}), while Isolate I-25 produced solubilized potassium of 91.10 ± 2.60 mg L^{-1}. Using 16S rRNA gene sequencing, Isolate I-31 was identified as *Bacillus aryabhattai* and Isolate I-25 as *Priestia megaterium*. *Bacillus aryabhattai* and *Priestia megaterium* demonstrate significant potential as potassium-solubilizing bacteria. As non-pathogenic isolates, these species are suitable candidates for biofertilizer formulation to enhance soil fertility and support sustainable agricultural practices in Sri Lanka.

Keywords: *Potassium-solubilizing bacteria; Bacillus aryabhattai; Priestia megaterium; biofertilizer; plant growth-promoting rhizobacteria*

Abstract No: PP41

In silico screening and *in vitro* validation of anticancer properties of synthetic compound libraries

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Cancer is a complex and heterogeneous disease involving multiple genes and proteins. Although significant progress has been achieved in cancer treatment, therapeutic success remains limited by challenges such as tumour heterogeneity, drug resistance, and adverse effects on healthy tissues. Therefore, the discovery of novel anticancer agents with unique mechanisms of action remains an important research priority. In the present study, two synthetic compound libraries (01 and 02) were evaluated using an integrated approach combining network pharmacology, molecular docking, molecular dynamics (MD) simulation, and *in vitro* screening to identify promising anticancer candidates. Network pharmacology analysis identified key cancer-related targets and hub proteins, including EGFR, ESR1, SRC, and STAT3 in library 01 and AKT1, MAPK1, PIK3R1, and SRC in library 02. Gene Ontology (GO) and KEGG pathway enrichment analyses identified the biological functions and signaling pathways associated with these targets. For each library, twenty protein targets were selected and subjected to molecular docking to validate the docking protocol; co-crystallized ligands were re-docked into their target protein structures to obtain the same binding conformation. Among the 54 synthetic compounds evaluated, 19 compounds exhibited stronger binding affinities than their reference drugs and were subsequently subjected to MD simulation. The Sulforhodamine B assay was used to assess the compound's anti-proliferative potential against estrogen receptor-positive breast cancer (MCF-7) cells. With an IC_{50} of 0.9893 µg/mL for the library 01 Isatin derivative, DC-27 had the highest cytotoxic activity, followed by Isatin derivatives DC-18, DC-13, and DC-16. The most active molecule in Library 02 that contains coumarin derivatives was A-10. Overall, the isatin compound DC-27 demonstrated the most promise due to its strong anti-proliferative effects and excellent drug-like properties.

Keywords: *Cancer, Network pharmacology, Molecular docking, Molecular dynamics simulation, Antiproliferative activity*

Abstract No: PP42

Large-scale structure-based virtual screening of natural products for the discovery of CDK2 and CDK4 inhibitors

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Cyclin-dependent kinases 2 and 4 (CDK2 and CDK4) are key regulators of cell-cycle progression; their dysregulation drives the uncontrolled proliferation characteristic of many cancers, establishing them as validated anticancer targets. Although FDA-approved CDK4/6 inhibitors are clinically used, the discovery of novel selective scaffolds with favorable drug-like properties remains challenging. Natural products offer a privileged source of bioactive architectures, but their vast chemical space demands efficient computational triage. Here, we report a scalable, structure-based virtual-screening workflow to prioritize natural-product-derived inhibitors. The COCONUT database (approx. 695,000 compounds) was selected for its broad, curated coverage. High-throughput molecular docking against CDK2 and CDK4 was performed with smina, using docking scores for target-specific prioritization. Favorably scoring compounds were filtered by molecular weight, logP, TPSA, hydrogen-bond donors/acceptors, rotatable bonds, Lipinski violations, and QED drug-likeness. Sugar-rich compounds were excluded, and duplicates were removed via InChIKey. RDKit-valid molecules were encoded as Morgan fingerprints and grouped by Butina clustering (Tanimoto similarity) to reduce redundancy while preserving diversity, retaining the top-scoring representative per cluster. This produced two target-focused libraries of ~1,000 diverse candidates, compressing the COCONUT-scale space into compact, docking-enriched hit sets. These libraries enable comparative evaluation through higher-exhaustiveness redocking, interaction fingerprinting, hinge-region analysis, ADMET prediction, molecular dynamics simulations, and binding free-energy rescoring. This workflow establishes a scalable framework for natural-product-based CDK inhibitor discovery and a rational route toward novel scaffolds with potential CDK2 and CDK4 activity and selectivity.

Keywords: *CDK2, CDK4, Natural products, virtual screening, molecular docking*

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Abstract No: PP43

Electronic origin of the divergent bioactivities of eugenol and cinnamaldehyde in *Cinnamomum zeylanicum* leaf and bark: an integrated DFT, DPPH and GC-MS study

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Cinnamomum zeylanicum displays an organ-specific chemotype: eugenol in leaves and cinnamaldehyde in bark. The electronic origin of their divergent bioactivities remains unresolved. This study used density functional theory (DFT) to predict this divergence, validated by DPPH scavenging and GC-MS profiling of methanol crude extracts and steam-distilled oils. A five-step B3LYP protocol (geometry optimization, vibrational, frontier-orbital/electrostatic-potential, TD-DFT, and GIAO NMR) revealed that eugenol has a wide HOMO–LUMO gap (5.585 eV) and low electrophilicity (omega = 1.557 eV), consistent with a phenolic –OH hydrogen-atom-transfer antioxidant. Conversely, cinnamaldehyde shows a gap narrowed by 1.247 eV (4.338 eV) and 3.06-fold higher electrophilicity (omega = 4.773$ eV), identifying it as an electrophilic Michael acceptor rather than a radical scavenger. The DPPH assay (10,000 ppm) confirmed this: the eugenol-dominant leaf oil provided the highest scavenging (94.79% FRSA), while the cinnamaldehyde-dominant bark oil was lowest (76.76%), an 18.03-point gap matching the computed hierarchy. The anomalously high activity of the bark crude extract (91.41%), exceeding its oil by 14.65 points, was resolved by GC-MS, which revealed ~16.5% of co-extracted hydrogen-donating minor constituents (eugenol, cinnamyl alcohol, β-caryophyllene, and trans-cinnamic acid) acting synergistically, whereas cinnamaldehyde remained a poor scavenger. The convergence of computed descriptors, IR/NMR markers, and the experimental DPPH hierarchy establishes a robust electronic rationale for the bioactivity divergence of these phenylpropanoids and confirms DFT as a reliable predictor of natural-product antioxidant behavior.

Keywords: *Cinnamomum zeylanicum; density functional theory; eugenol; cinnamaldehyde; DPPH radical scavenging*

Abstract No: PP44

Synergistic antibacterial and anti-biofilm effect of Phyllanthus niruri extract with gentamicin against biofilm-forming Pseudomonas aeruginosa

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Pseudomonas aeruginosa, an opportunistic pathogen that can form biofilms that contribute to antimicrobial resistance and treatment failure. In the aspect of combating resistance, plant-derived components combined with conventional antibiotics have shown a promising strategy to enhance antimicrobial efficacy to overcome biofilm-associated resistance. This study focused on the synergistic antibacterial and antibiofilm potential of a methanolic Phyllanthus niruri extract in combination with gentamicin against biofilm-forming Pseudomonas aeruginosa ATCC 27853. Crude extract of Phyllanthus niruri was obtained using methanol via the cold maceration technique. Evaluation of antimicrobial properties was done by the broth macro-dilution method to determine minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC). Synergistic potential between the extract and gentamicin was assessed by the checkerboard assay and analyzed by calculating the fractional inhibitory concentration index (FICI). Qualitative biofilm activity was evaluated using the crystal violet tube assay. With regards to the antibacterial effect, the MIC of P. niruri and gentamicin against P. aeruginosa ATCC 27853 were 20 mg/mL and 4 µg/mL respectively. The corresponding MBC values were 20 mg/mL and 16 µg/mL. In synergy assay, prominent growth inhibition was observed at 2.5 mg/mL extract combined with 1 µg/mL gentamicin, which represents an 8-fold and 4-fold reduction in the MICs of the extract and gentamicin, respectively. Accordingly, the calculated FICI value was 0.375, which indicates a synergistic interaction. Crystal violet qualitative results revealed a marked reduction in the biofilm formation in combination, which showed a mild ring compared to extract and gentamicin MIC alone, which showed moderate and strong rings. The combination of Phyllanthus niruri extract with gentamicin exhibited a rewarding synergistic antibacterial and anti-biofilm effect against Pseudomonas aeruginosa ATCC 27853. These outcomes suggest that plant-antibiotic combinations possess a promising strategy for treating biofilm-associated infections and support further investigations using qualitative and in vivo biofilm analysis.

Keywords: *Antibiofilm, Antibiotic resistance, Combination treatments, Synergy, Plant extracts*

Genome-wide *in silico* analysis of iron-tolerant bacteria in paddy soils: unveiling genetic mechanisms for bioremediation

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Iron toxicity is a major abiotic stress in paddy soils that adversely affects microbial survival and agricultural productivity in Sri Lanka. Bacteria possess specialized adaptive mechanisms including iron transport, storage and oxidative stress defense systems to withstand high iron concentrations. However, detection of these mechanisms traditionally requires time-consuming and costly laboratory testing. Although bioinformatic approaches provide efficient alternatives for gene discovery, genome-wide studies focusing specifically on bacterial iron tolerance remain limited. Therefore, this study aimed to identify and characterize iron-tolerant genes through genome-wide and *in silico* analyses of selected iron-tolerant bacterial isolates obtained from iron-rich paddy soils. This *in silico* study focused on four bacterial species, *Bacillus altitudinis*, *Bacillus rhizoplanae*, *Rummeliibacillus pycnus* and *Lysinibacillus pakistanensis* chosen based on their reported iron-tolerant characteristics from previous studies. A manually curated reference database of iron-tolerant genes was established and genomic analysis identified numerous homologous genes across all four bacterial genomes. Orthology analysis identified 26 iron-tolerance related orthogroups across the four bacterial genomes, of which 18 were conserved among all strains, suggesting common adaptive mechanisms for survival under elevated iron conditions. The remaining orthogroups were distributed among subsets of strains, indicating evolutionary diversification among different bacterial taxa. Conserved protein domains, physicochemical properties as well as gene ontology and pathway enrichment analyses supported the functional significance of these genetic elements. Phylogenetic analysis indicated that proteins belonging to the same orthologous groups were clustered into closely related clades, indicating common evolutionary origins and functional conservation among the studied bacterial species. However, these findings require future laboratory validation to confirm precise regulatory mechanisms. This study successfully enhances the understanding of microbial adaptation and provides a significant basis for bioaugmentation and bioremediation approaches to alleviate iron toxicity in paddy soils, contributing to sustainable agriculture, environmental management and environmental biotechnology.

Keywords: *Bacterial iron tolerance, in silico analysis, Genome-wide identification, Orthology analysis, Phylogenetic analysis*

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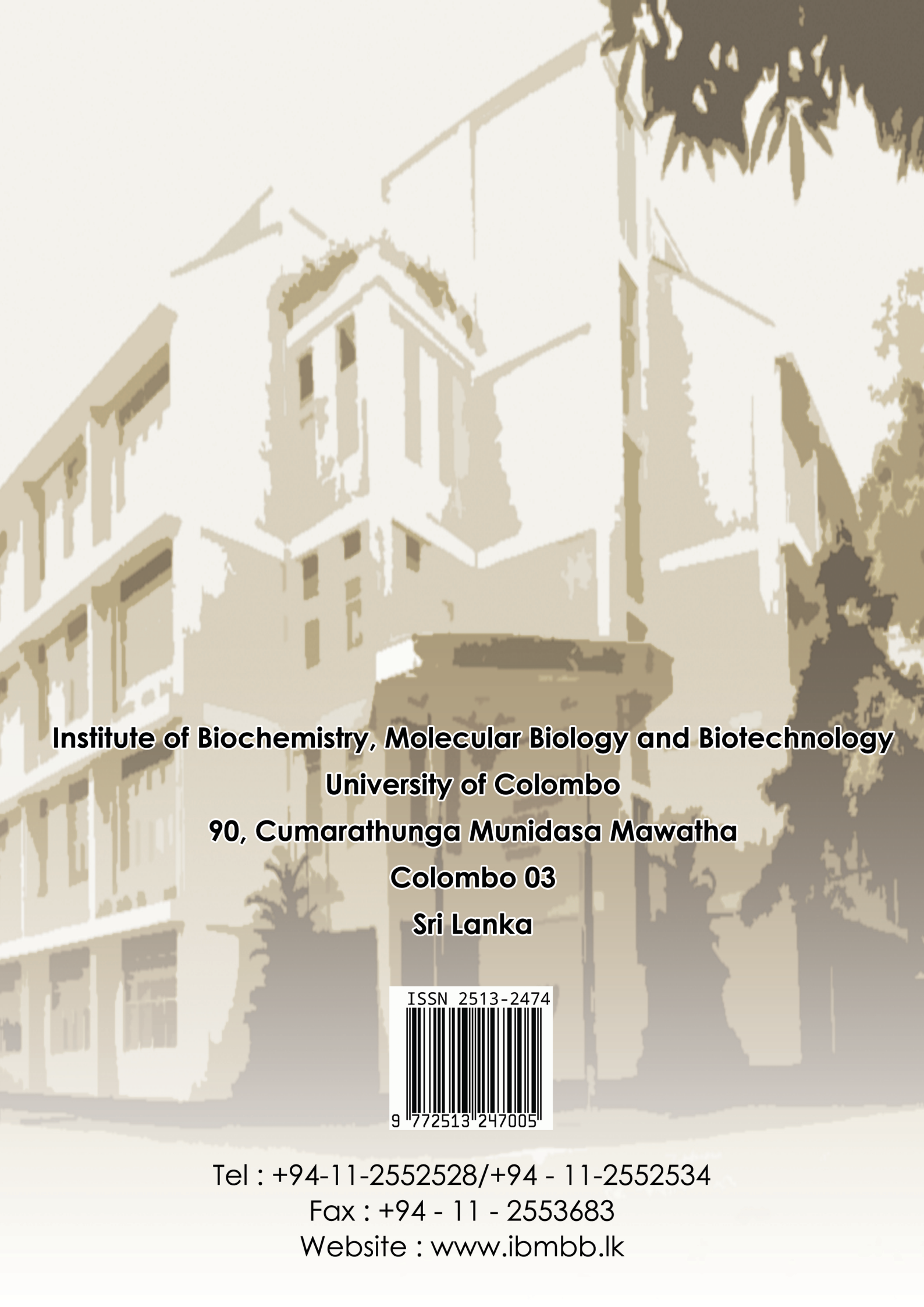
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