INSTITUTE OF BIOLOGY
SRI LANKA

PROCEEDINGS OF THE 44TH ANNUAL SESSIONS 2024

ACHIEVING A CIRCULAR AND SUSTAINABLE BIOECONOMY

Sitting (from left): Dr. U. A. Jayawardena, Dr. C. D. Jayasinghe, Prof. H. D. D. Bandupriya, Dr. K. G. S. U. Ariyawansa, Dr D. Halwatura, Prof. K. B. S. Gunawickrama, Prof. H. S. Amarasekera.

Standing (from left): Dr. P. D. Dayananda, Dr. P. K. C. B. Wijerathna, Mr. K. M. S. Ruvinda, Dr. P. Dharmasena, Dr. I. U. Kariyawasam, Dr. A. M. Wickramasuriya, Dr. V. K. Fernando.

Absent: Prof. S. A. C. N. Perera, Dr. R. Wimalasekara, Prof. B. D. R. Prasantha, Dr. I. A. J. K. Dissanayake

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Theme

Achieving a Circular and Sustainable Bioeconomy

Institute of Biology, Sri Lanka

27th September 2024

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Proceedings of the 44th Annual Sessions

27th September 2024

Colombo, Sri Lanka

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Editor, IOBSL

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Cover design: Mr. Gihan Rajapaksha
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ISSN: 2012-8924

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About the Institute of Biology, Sri Lanka

The Institute of Biology is a leading professional body of biologists in Sri Lanka. The institute was formulated in a small way by a group of Sri Lankan biologists led by late Prof. B. A. Abeywickrama (Emeritus Professor of Botany University of Colombo) in 1981. It became an incorporated organization by the Act of Parliament No 22 in 1984.

The objectives of the institute are:

1. To promote and advance the science of biology and its applications in Sri Lanka.
2. To advise the government, and give counsel to public corporations, local bodies and other institutions on all matters connected with the application of biology in the progress and development of the country.
3. To promote acquisition, dissemination and interchange of biological knowledge by providing a forum for the presentation of original communications and discussions and maintaining libraries which publish matters of interest to the profession of biology.
4. To promote education in biology at all levels.
5. To promote, encourage and foster original research in biology.
6. To ensure the maintenance of high standards in the professional activities and the general conduct of its members.
7. To establish liaison with other scientific organizations.
8. To establish and enhance the status of the profession of biology in Sri Lanka.

Membership

The institute has around 612 members, working in industry, research, education and healthcare. The institute also awards Fellowships and Charter of Biology status for members. There are seven categories of membership and members are encouraged to transfer to other grades in due course. Eligibility for each category depends upon a combination of professional experience and academic qualifications. Fellows are entitled to use the abbreviated designation F.I. Biol (Sri Lanka) while the Chartered Members are eligible to use C. Biol (Sri Lanka), Members M.I. Biol (Sri Lanka). The designation 'Chartered Biologist' endorses the high standards expected of biologists and is for international recognition as a hallmark of professional competence and ethical conduct.

Activities

The Institute of Biology Sri Lanka (IOBSL) is a premier scientific body that plays a vital role in advancing education and professional development by organizing a wide array of courses, workshops, seminars and training programs for students at all levels and professionals in both academia and industry. The institute is also engaged in encouraging public interest in biology, by conducting fora on current topics in biology on a regular basis. The annual national Biology Olympiad competition is organized and administrated exclusively by the IOBSL is a hallmark event in the country. Sri Lankan Biology Olympiad competition offers the students interested in the field of biology an opportunity to explore and challenge skills in biology. The IOBSL is dedicated to providing necessary training to the students selected to participate in the International Biology Olympiad; the world's largest biology competition for secondary school students that takes place annually in a selected country. ‘Inter-University Biology Quiz Competition’ conducted by the IOBSL is an initiative taken to promote and popularize biology education among the undergraduates in the stream of biological sciences of the state and non-state universities and educational institutions in Sri Lanka. ‘Inter-University Biology Challenge’ is another competition organized by the IOBSL to promote awareness of undergraduates of universities in Sri Lanka in biology and interdisciplinary studies. The ‘Young Scientist Award’ is bestowed in the motive of recognizing outstanding contributions and achievements in research of the early career corporate members of the Institute. A national competition on biology photography initiated by the IOBSL offers an opportunity for the professional, amateur, and young photographers in Sri Lanka to communicate with the general public on wide arena of themes in biology.

‘BIO-NEWS’ is the official e-newsletter of the IOBSL that reports activities conducted by the IOBSL, updates on latest research, feature articles, art and creative writing and corner for young biologists. Sri Lankan Journal of Biology (SLJB), a biannual open access journal published by the IOBSL, creates the platform for researchers to disseminate the findings of biology related research under a Creative Commons Attribution 4.0 International License. IOBSL Facebook page publishes activities, competitions and research news with the intention of recognizing the valuable contribution made by the institute toward research and development and bridging the gap between researchers and the general public.

The annual sessions of IOBSL provide a forum for both senior and junior biologists to communicate their research findings for a multifaceted audience. The annual sessions continue for the 44th time this year.

Contents

PRESIDENTIAL ADDRESS

The role of fungi in a sustainable and circular bioeconomy: Current status and future prospects

K.G. Sameera U. Ariyawansa, PhD.
Department of Plant Sciences, University of Colombo

It is with great honor and privilege that I deliver the presidential address before this esteemed assembly of biologists as the President of the Institute of Biology, Sri Lanka, during its 44th Annual Sessions. With over 600 corporate members, the Institute of Biology stands as the leading professional organization for biologists in the country. The institute's primary objectives are to advance the field of biological sciences and to promote the application and education of biology throughout Sri Lanka. In light of the pressing environmental challenges and resource depletion we currently face, I believe that the IOBSL and its members have an even greater responsibility to advocate for and facilitate environmentally sustainable economic development. Specifically, Sri Lankan biologists bear a critical obligation to utilize their expertise to explore the nation's biological resources, thereby steering the economy towards a circular and sustainable bioeconomy. In this regard, I would like to discuss the potential of fungi—an often overlooked and inadequately studied biological resource both in Sri Lanka and globally—in contributing to the establishment of a circular bioeconomy.

The biosphere is home to a vast diversity of organisms, each characterized by distinct genetic traits, lifestyles, and ecological functions. Among these, microorganisms that are not visible to the human eye constitute a significant and largely undervalued aspect of biodiversity. These microorganisms, particularly fungi, are essential for the sustainability of the biosphere. Current estimates suggest that there are between 2 to 5 million fungal species on Earth, highlighting their remarkable prevalence across nearly all aquatic and terrestrial environments.

Fungi exhibit a wide range of life modes, functioning as pathogens of animals, plants, and other organisms, as well as forming mutualistic relationships and existing as free-living microbes. Their extraordinary nutritional adaptability allows them to grow on complex substrates, including lipids, proteins, and polysaccharides, which has facilitated their use as microbial cell factories for centuries.

Fungi are prolific producers of an array of enzymes, organic acids, and bioactive secondary metabolites, all of which are of considerable industrial significance. They can thrive on complex, cost-effective, and readily available substrates, including waste materials, making them suitable feedstock for numerous industries. Given these abilities, fungi are positioned to play a pivotal role in promoting a sustainable and circular bioeconomy.

The circular bioeconomy represents an integration of the circular economy and the bioeconomy, wherein the two concepts complement each other to establish a sustainable framework aimed at addressing long-term challenges. The circular economy has gained prominence as a viable alternative to the prevailing linear economic model, which involves the extraction of resources, production of goods, and their eventual disposal following consumption. By transforming waste generated at the end of the cycle into resources for the production of new products, the circular economy enhances resource efficiency and minimizes waste accumulation. Bioeconomy refers to the knowledge-based production and utilization of biological resources, innovative biological processes, and the sustainable provision of goods and services across all sectors of the economy. The rise of the circular economy has garnered increased attention recently, largely due to growing environmental awareness and the negative impacts of overexploiting natural resources and waste accumulation.

Fungi are playing an increasingly pivotal role in the ongoing biotechnological revolution. In 2019, the famous magazine, Scientific American stated, "the mycelium revolution is upon us," highlighting the resurgence of fungal biotechnology a century after its origins. Fungi have become key contributors to white biotechnology, which involves the use of living cells or enzymes to produce industrial products that often surpass those made through conventional chemical methods, offering advantages in biodegradability, energy efficiency, and waste reduction. Given the remarkable diversity of fungi, fungal biotechnology is poised to accelerate the transition from a petroleum-based economy to a bio-based circular economy.

The metabolic capabilities of fungi are exceptionally diverse and unmatched in nature. They can produce a wide range of compounds, including organic acids, antibiotics, alkaloids, secondary bioactive metabolites, as well as immunosuppressants, proteins, enzymes, meat alternatives, vitamins, polyunsaturated fatty acids, detergents, and biosurfactants. Fungal enzyme products play an important role across various critical industries, such as food and feed, detergent, pulp and paper, textile, fuel, pharmaceutical, agriculture, and chemical. Additionally, numerous filamentous fungi are edible and most have been classified as Generally Recognized as Safe (GRAS). Within this context, I would like to highlight several fungal applications that can meaningfully contribute to the advancement of a sustainable and circular bioeconomy.

Fungi have been shown to produce phytohormones, including indole-3-acetic acid (IAA) and gibberellins, as well as siderophores, phosphate solubilizers, secondary metabolites, and various bioactive compounds with antibacterial, anti-herbivory, and insect-repellent properties. These characteristics position fungi as valuable tools for enhancing agricultural productivity in an environmentally friendly and sustainable manner, reducing the reliance on agrochemicals. Additionally, plant-associated fungi have the ability to enhance tolerance against both biotic and abiotic stresses, and function as bio control agents.

The capabilities of fungi have been demonstrated in several ongoing studies within our laboratories, particularly in research on endophytic fungi. For example, the isolation of putative endophytic fungi from *Piper nigrum* yielded 86 fungal taxa, of which 17 tested positive for ACC deaminase (ACCd) production, 51 for hydroxamate and carboxylate siderophores, and 5 exhibited phosphate-solubilizing activities. Similarly, in another study, 38 endophytic fungal taxa isolated from leaf, stem, and root segments of the mangrove plant *Avicennia marina* from the Puttalam Lagoon, showed the ability to produce hydroxamate and catechol-type siderophores, indole-3-acetic acid (IAA), along with promising amylolytic, cellulolytic, and phosphate-solubilizing activities, as well as antibacterial properties against both Gram-positive and Gram-negative bacteria.

Siderophores are low-molecular-mass organic compounds synthesized by microorganisms and plants in environments characterized by low iron availability. The primary role of these compounds is to chelate ferric ions, thereby enhancing its bioavailability for microbial and plant cells. The biotechnological applications of siderophores include their use as biocontrol agents, biosensors, and in bioremediation processes. Additionally, the enzymatic activity of ACC deaminase, referred to as a "stress modulator," mitigates excessive ethylene synthesis under various stress conditions, thereby protecting plants against abiotic stress conditions. Ongoing investigations aim to elucidate their potential industrial applications in future.

Fungi significantly contributes to environmentally sustainable technologies through their capacity to break down and decompose organic materials. They secrete a diverse array of enzymes, including cellulases, xylanases, lignin peroxidases, manganese peroxidases, laccases, proteases, and α-amylases, which enable the degradation of cellulose, hemicellulose, lignin, starch, and proteins into their respective monomeric units. This enzymatic activity is vital for the natural recycling of nutrients within ecosystems and holds considerable promise for application in waste management and recycling systems.

Human activities generate substantial quantities of organic waste and residues. Biowastes include both difficult -to-digest materials, such as lignocellulosic biomasses from agricultural residues, and more readily digestible materials, including food waste, municipal organic waste, and wastewater. Agricultural residues are often disposed of on-site in farms, with many cases resulting in incineration, which poses significant environmental challenges and threatens public health. The role of agriculture in the transition towards a bioeconomy can be notably enhanced by converting agricultural wastes into value-added products, thereby fostering socioeconomic development and environmental sustainability. Given their abundance, biowaste presents a viable alternative to fossil fuel-derived resources without necessitating additional land. Consequently, utilizing fungi to convert biowaste into biomass and various value-added products offers promising opportunities for establishing a sustainable circular economy.

A prime example of biowaste utilization within a circular bioeconomy is the production of fungal mycelium-based biocomposites (MBCs). This process has been made possible through multidisciplinary collaboration involving biologists, chemists, bioengineers, process engineers, and material scientists, who have enabled the transformation of agricultural and forestry byproducts into mycelium-based biocomposites. Mycelium-derived materials show great potential as alternatives to leather, textiles, insulating materials, and certain plastics and polystyrene products. Mycelium-based biocomposites are characterized by low energy consumption during production, minimal by-product generation, high biodegradability, excellent mechanical strength, and broad applicability across various industries.

In this context, a research initiative has been undertaken to develop natural biodegradable biocomposites utilizing fungal mycelia. This study investigates the feasibility of employing locally sourced fungal species, including *Ganoderma* spp., *Pleurotus* spp., *Agaricus* spp., and *Trametes* spp., in combination with agricultural waste to produce fungal composite materials characterized by a range of chemical, mechanical, and physical properties. Presently, various agricultural residues—such as corn stalks, corn husks, rice husks, and fibers from banana leaves and stems—are being assessed for their potential to yield composites with different properties. Subsequently, these composites will be further analyzed to explore their potential applications in textiles, leather production, and as alternatives to conventional plastic and polystyrene products.

Continuous research into fungi, as well as their products and uses, is critical to the long-term viability of a circular bioeconomy. However, the global knowledge of fungal diversity and its applications is incomplete and fragmented. The global richness of fungi has been a popular topic among mycologists with diverse predictions made over the past three decades and the most recent estimate predicts 2 to 3 million species of which only approximately, 156,000 species have been scientifically documented, leaving more than 90% of these species unknown. In Sri Lanka, it is estimated that the island has over 25,000 fungal species, however only about

2,000 have been identified so far. Most have never been cultured and studied for their characteristics; therefore, their potential applications are virtually untapped. Before the decline in fungal biodiversity escalates into a significant global issue, it is essential to take proactive measures to discover more fungal species and to preserve the ecosystems they inhabit. Neglecting to do so could have serious consequences for the environment, human health, and overall well-being.

I wish to present the findings of an ongoing study that underscores the significance of exploring previously uncharted habitats for the discovery of novel fungal taxa and their potential industrial applications. This research focuses on the isolation and characterization of endophytic fungi associated with seagrass species in Sri Lanka, representing, to the best of my knowledge, the first comprehensive investigation of its kind within the region. To date, the study has identified 43 potential endophytic fungal taxa from leaf samples of *Enhalus* sp., a seagrass collected from the Kalpitiya lagoon. Preliminary morpho-molecular characterization suggests that approximately 20% of the isolated fungi are likely to represent novel taxa, with several identified as obligate halophiles. Furthermore, initial screening for industrial applications has revealed promising bioactivity, including anticancer and antimicrobial properties, thereby highlighting the potential biotechnological value of these isolates.

It is crucial to recognize that several challenges impede the full integration of fungal applications into a circular bioeconomy. A major challenge is the insufficient understanding of the mechanisms underlying fungal biodegradation and bioproduction, which impedes their effective integration into circular bioeconomy frameworks. Comprehensive research is essential to elucidate the molecular mechanisms underlying these processes in order to fully harness the potential of fungi. Another critical challenge is the scalability of fungal processes. While fungi are currently employed in various laboratory and pilot-scale applications, these systems require further development and optimization to enhance their feasibility for large-scale implementation.

Despite existing limitations, fungi are poised to play a critical role in the future development of a bioeconomy. With less than 0.4% of fungal species currently referenced in patents, there remains substantial scope for innovation and advancement within fungal research. This untapped potential suggests that interdisciplinary and trans disciplinary research on fungi will drive significant scientific breakthroughs. Furthermore, the exploration of fungal diversity and valuable properties holds promise for addressing several key challenges outlined in the United Nations Sustainable Development Goals (SDGs). Recent evaluations indicate that global progress toward achieving the Sustainable Development Goals has delayed for a second consecutive year, reflecting the complexities of reaching these objectives within current political and governance frameworks. Nevertheless, fungal biotechnology has the potential to contribute significantly to 10 of the 17 Sustainable Development Goals, positioning fungi as vital organisms in addressing pressing global challenges. To facilitate this progress, it is crucial that scientists urgently interpret the biochemical information encoded in fungi and convey actionable insights to policymakers. Thus identifying novel fungal species likely to yield beneficial compounds, properties, and characteristics will be instrumental in advancing efforts toward a more sustainable future for all.

FELICITATION OF

Emeritus Professor Nelum Deshappriya

Citation Presented by

Prof Priyanganie Senanayake
Department of Plant and Molecular Biology, Faculty of Science,
University of Kelaniya.

It is a great privilege and honour for me to stand before you today to present Prof Nelum Deshappriya, a long-standing colleague and friend, and a renowned academic and researcher who receives the lifetime achievement award presented by Institute of Biology, Sri Lanka for the year 2024.

She is a friend who brings sense of humor into our lives, interestingly we happen to share many things in common, our love for reading novels, knack of creating funny stories on worlds around pets, we have spent countless hours creating hilarious tales about their lives, personalities and adventures. I am so grateful to Prof Nelum, for the relation we share in this regard.

Paying tribute to Prof Nelum Deshappriya is of special significance and pride to IOBSL as she is a Fellow, Chartered Member and a past President of the Institute.

Over the years, her dedication in the realms of academia, research & development and administration has not only strengthened the field of Biology in the country but has also uplifted the lives of students, faculty members and researchers alike.

To begin with, allow me to take a moment to reflect upon her remarkable journey that has contributed immensely to the fields of Plant Pathology, Botany and Biology. The foundation for this journey was laid at Visakha Vidyalaya, Colombo, which was further strengthened by the knowledge, skills and ideals inculcated at the Faculty of Science, University of Kelaniya from where she graduated with a Bachelor of Science (Honours) in Botany. Her pathway towards an even deeper engagement in the scientific world began with an MPhil in Plant Pathology in 1987 awarded by the University of Kelaniya. In 1993, she received a Commonwealth Academic Scholarship tenable in the UK and earned her PhD in Plant Pathology and Tissue Culture from the University of Bath, United Kingdom. This accomplishment strengthened her proficiencies in research and teaching significantly and positioned her as a key figure in the field of Plant Pathology.

Her appointment as an Assistant Lecturer at the Department of Botany, University of Kelaniya, in 1986 marked the beginning of a distinguished academic journey. After graduation from the University of Bath, UK, she returned to the academia and served in the positions of Senior Lecturer Grade II, then as Senior Lecturer Grade I. These years were marked by her efforts to contribute not only to the teaching activities but also to the development of the department and her research in Plant Pathology. In 2009, she was promoted to the position of Professor in the Department of Botany, University of Kelaniya. She served as Head of the Department of Botany, University of Kelaniya, from 2006 to 2009, showcased her leadership abilities and her dedication to the advancement of teaching and research in the department.

Over the years, her contributions have shaped the direction of the academic programs of the Department of Botany, Faculty of Science, University of Kelaniya with great impact on the students, faculty, and the broader academic community.

Her long-standing and continued role in curriculum development helped to elevate the quality of academic programs in the Faculty of Science, ensuring that courses remain current and updated. In 2003, the department of Botany reached a significant milestone with the introduction of the new subject Molecular Biology and Plant Biotechnology to the curriculum. Prof Deshappriya's contribution in taking initiatives and coordination in the curriculum development and introduction of this new subject opened new avenues for research and teaching in the department. Furthermore, initiating and coordinating the curriculum development and introduction of the MSc Programme in Crop Protection and Plant Biotechnology in 2016 offered advanced learning opportunities to students.

Moreover, her contribution in the proposal writing team of the Biological Sciences Study Programme under world Bank funded, IRQUE QEF Project, in 2005, was instrumental in securing resources for the quality enhancement of Biological Science Study programme of the faculty. Additionally, she served as person in charge of the activity, improving English proficiency among Biological Science students as part of the same project which helped to equip the students with essential English language skills, broadening their academic and professional horizons.

During this period, her contribution has not been limited to the Faculty of Science at the University of Kelaniya but have extended to other universities and institutions across Sri Lanka. Serving as visiting lecturer, moderator and second examiner in a range of courses, in University of Colombo, Rajarata University, University of Sri Jayewardenepura and University of Ruhuna enriched the learning experience of students and has ensured the academic standards in other universities.

Prof Nelum is a perfectionist in the best way possible, whatever task is placed, she approaches it with commitment and gives it her absolute best. She ensures it is done right and well, one of the things we admire most, and it is inspiring to watch her perform with such passion and focus. Whether it is teaching a lesson or giving advice, she always aims for excellence and inspires people to be better versions of their lives.

She served as a Student Counsellor of the faculty and as Academic Advisor of the Department of Botany, provided continuous academic guidance, support and mentorship to the students to thrive in their academic performance.

Prof Deshappriya takes great pride in her participation as a member of editorial board of the Golden Jubilee Commemorative Volume of the Faculty of Science, she was the Chairperson of the Faculty Research Review Committee for the Ethics Review Committee, committed to uplift and maintaining the integrity and quality of research.

In 2017, she joined the Faculty of Applied Sciences, of the University of Sri Jayewardenepura where she was promoted to Senior Professor at the Department of Botany, in the same year. She retired in 2022 after serving a period of 36 years in academia and in appreciation of her long years of distinguished and dedicated service to the state university system, she was awarded the esteemed title of Professor Emeritus and continues to inspire future generations with her legacy of scholarship and mentorship.

During her tenure at the Department of Botany, University of Sri Jayewardenepura, her service as a member of the committee for the development of the Administrative Policy document, contributions to the AHEAD, ELTA-ELSE Faculty Development Project as a member of the proposal writing team were key to the development opportunities of the Faculty of Applied Sciences of University of Sri Jayewardenepura. Moreover, she served as Faculty Coordinator and one of the Activity Coordinators of the same project playing a leadership role in fostering faculty advancement. At University of Sri Jayewardenepura, she contributed to the uplifting of curriculum and related activities by working with the Quality Assurance Cell of the Faculty of Applied Sciences, during which time a significant input was provided, ensuring that the standards of academic activities are elevated so that the programmes offered by the Faculty are of the expected high standard.

Her commitment to higher education is evidenced by her supervision and evaluation of numerous MPhil and PhD students, MSc research, honours degree students, ensuring that the next generation of researchers in the country are well-equipped to contribute to the uplifting and expansion of the new areas in biological sciences. Prof Deshappriya has served as a resource person in many seminars and workshops providing guidance to graduate students and researchers embarking on their research journeys. Her involvement in workshops conducted to develop guidelines for study guides demonstrated an unwavering commitment to student success and faculty development by ensuring both students and staff were well-prepared to meet the evolving demands of academia.

She has been serving as Chief Examiner in Botany and Biology for the GCE Advanced Level examinations since 1997 and as Co-Controller in Biology since 2021 ensuring the standards in education at national level.

Additionally, the role as Reviewer of academic programmes in state universities, appointment by University Grants Commission, since 2016 has been a vital contribution toward maintaining and enhancing the quality of higher education across the country. The contribution as Co-Chair of the committee to develop the Subject Benchmark Statement in Botany in 2020 further highlights Prof Deshappriya's commitment to shaping the future of the subject Botany in the higher education system in Sri Lanka.

In addition, membership ~~i~~n external research committees, such as in the Plant Virus Indexing Center and Rubber Research Institute of Sri Lanka, have demonstrated her commitment to sharing knowledge and advancing research for the benefit of the scientific community. Prof Deshappriya also serves as a Technical Expert in Microbiology for Sri Lanka Accreditation Board.

Over the years, she has held a variety of offices in professional associations and has contributed to the growth and development of the scientific community in Sri Lanka. Her service to the Institute of Biology is impressive. She served as Editor, Assistant Treasurer, and Assistant Editor and became Vice President of the Institute of Biology, 2010- 2013 and the President in 2013/2014. These leadership roles reflect her dedication to fostering collaboration, research and learning within the scientific community.

Also, she is a member of the Sri Lanka Association for the Advancement of Science, a founding member of the Sri Lanka Association for Mycology and Plant Pathology and a member of the Alumni Association of the University of Kelaniya and an Honorary member of the Alumni

Association of the University of Sri Jayewardenepura. Furthermore, she served as a committee member of Section B, Popularization of Science~~,~~ Rapporteur of Section D~~,~~ Council Member and Assistant Editor and Editor of the Sri Lanka Association for the Advancement of Science

She has received a number of fellowships including the Commonwealth Fellowship, and carried out research at the University of Calgary, Canada~~,~~ on soil fungal diversity and at Warwick HRI, University of Warwick, UK, on biological control of onion white rot. She obtained training in tissue culture techniques for crop improvement from Bogor Agricultural University in Indonesia. She received a fellowship focused on research investigating H_2S as an inducer of resistance genes in bacteria at the University of West of England, UK. The knowledge, skills and expertise gained during post-doctoral research were instrumental for the advancement of teaching and research in the faculty. She has received numerous competitive research grants that led to post graduate student research and laboratory development.

Producing research of high quality requires both immense effort and a deep passion for discovery. Prof Deshappriya's work has been published in prestigious journals, a testament to its relevance, and the attention it has garnered in the scientific community is also indicated through many citations of her work. Her publications in indexed journals have earned her Senate awards from the University of Kelaniya and Research Awards from University of Sri Jayewardenepura. In addition to her academic achievements, she has been the strength in her family. Her husband, Mr. Wasantha Deshapppriya, a Senior SLAS officer, former Secretary to the Ministry of Telecommunications and Digital Infrastructure and she brought up a son, Ramindu and a daughter, Hansi, who are both graduates of local state universities. Ramindu is now serving as a senior consultant and Tech Lead in a private company while Hansi is pursuing higher studies in the USA, continuing the family tradition of academic excellence.

While appreciating Prof Deshapriya's contributions towards the progress of the state university system and the advancement of science education and research, her professionalism and commitment to her work should be an example to young academics and scientists in Sri Lanka.

As we celebrate achievements of Prof Nelum Deshappriya today, we are reminded that her legacy will continue to impact the fields of Plant Pathology, Botany and Biology for many years to come. Her students, colleagues, and the academic community are fortunate to have witnessed the excellent work ethics and high standards always maintained by her and the generosity of her spirit.

On behalf of the Institute of Biology Sri Lanka, scientific community and academia I wish her good health and success in future endeavours.

ABSTRACTS – ORAL PRESENTATIONS

Investigation of antileukemic enzyme production and antioxidant activities of fungal endophytic communities in *Hellenia speciosa* (J. Koenig) S.R. Dutta (Thebu) of family Costaceae

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Fungal endophytes can generally be referred to as fungi that inhabit the internal tissues of plants at some stage during their life cycle, without causing any visible defects to the host. At present research on endophytes has gained significant attention due to their potential to generate valuable bioactive compounds. *Hellenia speciosa*, locally known as 'Thebu,' is a well-known medicinal plant that belongs to the Costaceae family. Accordingly, the present study explored the antileukemic enzyme production and the antioxidant activity of the fungal endophytes in *H. speciosa*. Fungal endophytes were isolated from various parts of the *H. speciosa* plant, including leaves, bracts, rhizomes, flowers, and stems. To assess the bioactivities, ten fungal isolates were chosen based on their higher growth rates, and their extracts were obtained using ethyl acetate. For antileukemic enzyme production specifically L-asparaginase and L-glutaminase enzyme production were assessed. Qualitative enzyme production was detected using Modified Czapex Dox agar medium. Positive isolates were quantitatively assessed via the nesslerization method estimating the amount of Ammonia liberated. Furthermore, the antioxidant activity was evaluated via the 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging. Isolates were identified using morphological characteristics and most active ones were identified using molecular techniques. Isolates obtained from the bract of *H. speciosa; Fusarium* sp. 1, *Fusarium* sp. 2, *F. equiseti*, *F. luffae* were able to produce L-asparaginase enzyme and *Fusarium* sp. 1 and *F. equiseti* produced L-glutaminase. The L- asparaginase production was in the range between 0.158 – 0.526 Units/mL and L – glutaminase production was in the range of 0.361 - 0.379 Units/mL. All ten isolates exhibited antioxidant activity and the IC_{50} value ranged between 143.284 – 369.807 µg/ mL. *F. equiseti* displayed positive results for all three bioassays, thus it could serve as a promising candidate in the search for novel bioactive compounds.

Keywords: *Hellenia speciosa*, endophytes, L-asparaginase, L-glutaminase, antioxidant activity

Investigating the changes in the microbial composition of Sri Lankan milk microbiota influenced by varying farm sizes

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Microorganisms in Cattle milk have a critical impact on the shelf life of raw milk, the quality of milk products, and consumer and cattle health. Therefore, it is important to study changes in the milk microbiome (microbial composition) in response to varying farm sizes. The first study on the Sri Lankan cattle milk microbiome was conducted in 2022 using 16s rRNA gene sequencing on 82 samples from 18 dairy farms from the three different agroclimatic zones. Using a compositional analysis, this work utilized the above-generated data to study the effect of different farm sizes (large and medium to small: med small) on milk microbiome composition. A pathogen analysis was conducted to identify the distribution patterns of known pathogens in the milk microbiome. A co-occurrence network analysis was conducted to investigate changes in milk microbiome community interactions and identify keystone genera. All analyses were performed using R and Python programming languages. The results indicated no observable difference between the alpha diversities of large and med small farm-size microbiomes. This was further validated by Wilcoxon rank sum tests. The pathogen analysis revealed a lower abundance and diversity of four human pathogens (*Staphylococcus saprophyticus, Streptococcus agalactiae, Rothia nasimurium,* and *Enhydrobacter aerosaccus*) in large farm-size than in med_small farms. A consistent core microbiome dominated by the same top five phyla, including Firmicutes, Proteobacteria, Actinobacteria, Bacteroidetes, and Saccharibacteria (TM7), and top five genera, including *Streptococcus*, *Macrococcus, Elizabethkingia, Enhydrobacter,* and *Staphylococcus,* was identified in all farms. The identified keystones differed across farm size levels. In conclusion, the results indicate that large farms can produce dairy milk with lower pathogen abundance and diversity. This information can be used to develop guidelines for hygienic milk production for small and medium-scale dairy farmers and maintaining cleaner large farms is recommended to produce healthier dairy milk with lower pathogen abundance and diversity.

Keywords: milk microbiota, 16s rRNA gene sequencing, farm size level, compositional analysis, pathogen analysis

Acknowledgement: Financial assistance by National Science Foundation (RG/2016/AG/02) and Treasury Research Grant (TG15/117)

Curvularia tuberculata from a mangrove lichen as a potential antifungal agent against crop pathogens

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Mangroves are home to a diverse range of fungal communities known as manglicolous fungi, specifically adapted to live under the challenging conditions of the mangrove ecosystem. As a result, they have the potential to produce an array of bioactive compounds with various biotechnological applications. The primary objective of this study was to isolate and identify mangrove inhabiting fungi with promising antifungal activity. Eleven fungal isolates obtained from different sources in Kalpitiya Lagoon, Sri Lanka were coded initially and subjected to primary screening. The antifungal activity was investigated against 3 phytopathogenic fungi: *Rhizoctonia solani*, *Fusarium* sp., and *Aspergillus* sp. through a modified dual culture assay. The mean colony diameters of test pathogenic fungi were analyzed by one-way ANOVA and Tukey's HSD tests with the R Studio version 4.2.2. According to the results, CN04 fungal isolate obtained from an unknown crustose lichen on *Avicennia marina* plant exhibited significantly higher antifungal activity against all three pathogens making the growth kinetics of those fungal strains co-cultured, reaching a stationary phase by day 6 from inoculation. Then the secondary metabolites of CN04 were extracted into ethyl acetate via sonication-aided extraction. The antifungal activity was evaluated against *Rhizoctonia solani* and *Fusarium* sp. using poisoned food assay and the percentage growth inhibition was calculated. CN04 crude extract showed 34.14% and 53.10% of mean antifungal activity against *R. solani* and 51.24% and 62.19% of mean antifungal activity against *Fusarium* sp. with 2 mg ml^{-1} and 4 mg ml^{-1} concentrations, respectively. The isolate CN04 was identified via morphology and molecular techniques. According to the BLAST results of the consensus sequence, CN04 isolate showed a 99.83% similarity (42% query coverage) compared to *Curvularia turberculata* CBS 146.63 isolate (NR_138222.1). Overall, this study showed the importance of mangrove-derived fungi as a valuable source for agricultural products such as fungicides.

Keywords: Antifungal, Mangrove Fungi, *Curvularia*, Bioassays

Formulation and evaluation of new Ayurvedic polyherbal gargle therapy for promoting oral health

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Ayurvedic medicines derived from natural resources can be identified as a cost-effective and alternative solution for conventional treatments with less side effects. The aim of the present work is to formulate an effective gargle therapy consisting of six herbal ingredients including dried rhizome of *Zingiber officinale* (ginger), dried immature fruit-spikes of *Piper longum* (long pepper), dried fruit of *Piper nigrum* (black pepper), dried pericarps of *Phylllanthus embilica* (Nelli), *Terminalia bellerica* (Aralu), and *Terminalia chebula* (Bulu). Rock salt and mint essence were added as the additional ingredients as the preservative and flavoring agent respectively. The anti-microbial susceptibility of the prepared polyherbal preparation was investigated against selected bacterial pathogens *Staphylococcus aureus, Escherichia coli* and *Klebsiella pneumoniae* by agar well diffusion method. The Minimum inhibitory (MIC) was determined by microbroth dilution method and expressed in mg mL^{-1}. According to the results of the *in-vitro* antimicrobial susceptibility, the best formulation was selected, and it was evaluated for some selected organoleptic and physicochemical properties including color, odour, foaming ability and pH. The developed gargle resulted in a significant antimicrobial activity against Gram-positive bacteria *Staphylococcus aureus* with the mean Zone of Inhibition (ZOI) of 19.000± 1mm. The formulation was shown 0.125mg mL^{-1} of MIC against *Staphylococcus aureus.* Moreover, as physicochemical parameters gargle has shown a pH of 4.1 and a foaming ability of 5 mL. Considering all the results, the polyherbal formulation is effective in mitigating the growth of oral pathogen *Staphylococcus aureus* and hence has a potential for promoting oral health. Furthermore, this research proves the effectiveness of integrating natural resources into healthcare and medicines by providing scientific evidence.

Keywords: Anti-microbial susceptibility, Ayurveda, Oral heath, MIC, *Staphylococcus aureus*

In silico discovery of antimicrobial peptides of fungal origin

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Antimicrobial peptides (AMPs) represent a class of small-molecule peptides abundantly distributed in nature, constituting a fundamental element within the innate immunity of nearly all living organisms. They play a crucial role in the resistance against invading microbes. This study lays the groundwork for the *in silico* analysis of fungal AMPs, with the primary goal of devising an approach to uncover and functionally characterize putative AMPs of *Trichoderma harzianum* CBS 226.95 utilizing genomic, proteomic, and cDNA data. The pipeline developed in this study included an initial screening of the databases using several strategies: local alignments (NCBI-BLAST+ search), pattern-matching approaches (HMMER, FIMO, and ScanProsite), and domain analysis (InterProScan). The resulting candidate AMPs were subjected to secretome analysis to identify secretory peptides. Consequently, a total of 305 peptides from the proteome and 283 peptides from the translated ESTs were retrieved as 'secreted' peptides. The secreted proteome was further subjected to proteolytic cleavage (using the ProP tool) to identify mature sequences. All the AMP candidates were analyzed using AMP prediction tools (AMP Discover, CAMPR$_4$, AMP Scanner vr.1, and vr.2) and AMP physicochemical properties (peptide length, molecular weight, pI, hydrophobic residue percentage, and net charge). Putative AMPs were functionally characterized using ClassAMP, NCBI-BLAST, and InterProScan domain analysis. The pipeline used for AMP prediction yielded 33 AMP candidates out of which, 10 satisfied all the physicochemical AMP property thresholds. Secondary structure modeling and visualization using trRosetta and PyMOL servers of the 10 candidate AMPs resulted in 3 highly probable AMPs with helical wheel projections, which interact with microbial membranes and cause membrane disruption via the hydrophobic faces. Further characterization of the 3 highly probable AMP candidates is in progress and experimental investigations are necessary to confirm the antimicrobial activity of the *T. harzianum* AMPs, identified.

Keywords: In silico, AMPs, Fungi, Trichoderma harzianum, ESTs

Optimization of reaction components for a low-cost probe-based quantitative polymerase chain reaction (qPCR) assay to detect the 22q11.2 A-D microdeletion

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Microdeletion of chromosome 22q11.2 affects around 1 in 4,000 live births and causes variable manifestations including autism spectrum disorder (ASD). Availability of low-cost testing enables early interventions for better therapeutic outcomes. This study aimed to optimize a TaqMan-based duplex qPCR assay by identifying the optimal template DNA, Mg^{2+}, and primer concentrations. The assay targets *PI4KA* (located in 22q11.2) and *SHANK3* (located in 22q13.3) as the target and control genes respectively, due to their strong and stable expression across brain regions. To determine the optimum template DNA concentration and primer concentrations, monoplex reactions were carried out using QuantiNova SYBR Green PCR Kit. Accordingly, 10ng to 60ng DNA concentrations were tested in 10ng increments for template DNA. For each primer, 0.2-0.8μM concentrations were tested in 0.2μM increments. For Mg^{2+}, 1.5mM to 5mM concentrations were tested in 0.5mM increments for the duplex reaction using in-house designed TaqMan probes labelled with FAM and HEX. All reactions were conducted in duplicates using the Bio-Rad CFX96 Touch™ system with 2min of initial denaturation at 95ºC followed by 40 cycles of 5sec at 95ºC, and 10 sec at 60ºC. Results were visualized using the Bio-Rad CFX Maestro application. The lowest Ct values observed for 60ng of DNA for both reactions (Ct_{PI4KA}=19.47 and Ct_{SHANK3}=22.26). However, acceptable Ct values were obtained from 40ng of DNA (Ct_{PI4KA}=20.0 and Ct_{SHANK3}=25.03). Lowest Ct values for primer concentrations were *SHANK3* F/R 0.4μM/0.8μM (Ct=23.43) and *PI4KA*F/R 0.8μM/0.4μM (Ct=20.01). The $MgCl_2$ concentration of 4.5mM gave both the highest Relative Fluorescence Unit (~640 RFU) and lowest Ct value for both reactions (Ct_{PI4KA}=24.29 and Ct_{SHANK3}=26.20). The optimum parameters were 40ng of template DNA, 4.5mM Mg^{2+} concentration and *SHANK3* F/R 0.4 μM/0.8 μM and *PI4KA* F/R 0.8 μM/0.4 μM primer concentrations. The assay needs further validation against a standard method of detecting microdeletion, before adopting it for routine clinical use.

Keywords: qPCR Optimization, 22q11.2 microdeletion, primer concentration, Mg^{2+} concentration, template DNA

Acknowledgement: The project is partially funded by the University of Colombo

Designing low-cost probe-based quantitative polymerase chain reaction (qPCR) assay to detect the chromosome 22q11.2 A-D microdeletion among children with neuropsychiatric phenotypes

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22q11.2 microdeletion is associated with multiple manifestations including neuropsychiatric phenotypes. Early detection improves patient management. The study aimed to design a low cost, probe-based qPCR assay for identification of 22q11.2 haploinsufficiency within the low copy number repeat region A-D (LCR22A-D). Assay is designed to amplify a DNA region within the target (22q11.2) and control (22q13) regions simultaneously. The target region was identified by analysing single copy genes within LCR22C-LCR22D for associations with neuropsychiatric features and absence of multiple intragenic repeats. The control locus was the 22q11.3 region, commonly used in diagnostic testing. Custom primers and TaqMan probes designed for conserved exon sequences of the target and control genes were evaluated for optimal parameters and potential primer dimer formation using the OligoArchitectTM. BLAST tool was used to identify off-target primer binding. *PI4KA* and *SHANK3* were selected as target and control genes for the qPCR assay. The optimal primer pairs *PI4KA*-F (CGTCTCATCACATGGTAC), *PI4KA*-R (GCTAGGTAGGGAGAGATG), *SHANK*3-F (GAGGAGAAAGATCGTGAC), *SHANK3*-R (CTACCTGATCTTGCTTTG), and probes (TTGTCCTCCACTGCTTCTCACT for *PI4KA* and CGACCAGGAGAGCAACATCAGT for *SHANK3*) were specific and showed Tm between 58.8°-61.4°C. The ΔG values obtained were -0.6 kcal/mol and 0 kcal/mol for the forward and reverse primer of *PI4KA*, and 0 kcal/mol for both primers of *SHANK3*. The ΔG values for self-dimer formation were -2.4 kcal/mol and -1.7 kcal/mol for the forward and reverse primers of *PI4KA*, and -2.1 kcal/mol for both the primers of *SHANK3*. Typically, a 3' end self-dimer or 3' end cross-dimer with a $\Delta G<-5$ kcal/mol and an internal self-dimer or internal cross dimer with a $\Delta G<-6$ kcal/mol indicate a low risk of primer-dimer formation. This together with their specificity suggests the suitability of the designed primer/probe combination. This study proposes a probe-based qPCR design using *PI4KA* as target and *SHANK3* as control for detecting the 22q11.2 microdeletion.

Keywords: 22q11.2 microdeletion, qPCR, primer designing, probe designing, PI4KA

Acknowledgement: The project is partially funded by the University of Colombo.

Genome-wide analysis and characterization of Lysin Motif – Receptor Like Kinase (LysM-RLK) gene family in *Vigna radiata* (Mung bean)

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Lysin-Motif receptor-like kinases (LysM-RLK), which play essential roles in plant defense against pathogens and establishing symbiotic relationships, are widely distributed in plants. Genome-wide identification and analysis of LysM-RLK family members in the *Vigna radiata* (Mung bean) genome had not been done previously. To identify, analyze, and perform the first-ever genome-wide analysis of LySM-RLK gene family of *Vigna radiata* in silico, we used bioinformatics tools including BLAST, HMM-search, NCBI CD-Search, ProtParam, TBtools-II, MapGene2Chrom, MEGA11, iTOL, MEME, GSDS, PlantCARE and WoLF PSORT. We identified 11 LysM-RLK genes. All genes contained the conserved LysM and kinase domains but the number of LysM domains differed indicating functional divergence. Physicochemical properties varied in coding sequence length (1761-4288 bp), protein length (437-1185 amino acids), molecular weight (48664.56-132467.48 kDa), and isoelectric points (4.91-7.19). Chromosomal locations revealed dispersion throughout six chromosomes and two scaffolds. Phylogenetic analysis separated the *Vigna radiata* LysM-RLKs into five major clades. Homology relationships were found between *Vigna radiata, Glycine max*, and *Arabidopsis* LysM-RLK in synteny analysis. Seventeen conserved motifs were identified, with five (3, 4, 5, 8, and 9) present in all genes, indicating regulatory importance. Gene structures showed varying exon-intron structures across subclades, with similarities within subclades. Cis-acting regulatory elements analysis identified 26 regulatory elements related to phytohormones, growth, development, and stress responses. Gene ontology analysis highlighted roles in protein phosphorylation, kinase activity, ATP binding, immune response, and membrane-related functions similar to known LysM-RLK proteins in other species. Most LysM-RLK proteins were localized to the plasma membrane, with some in the nucleus, chloroplast, and endoplasmic reticulum, indicating varied cellular functions. Overall, this analysis provides valuable insights into the LysM-RLK gene family in *Vigna radiata*, focusing on its role in plant immunity and symbiosis. Understanding these genes can enhance mung crop improvement strategies and resilience to abiotic stresses by improving plant microbiome interactions.

Keywords LysM-RLK, *Vigna radiata*, genome-wide analysis, plant immunity, bioinformatics

Comparative analysis of protein-protein interaction network modules responsible for C3 and C4 photosynthesis: A systems biology approach

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Photosynthesis, the main source of nourishment on earth, is constantly being targeted to be improved to meet the rising food demand by improving efficiency. A key strategy is introducing the more efficient C_4 pathway into C_3 plants. The C_4 pathway is particularly effective in hot, dry environments, minimizing photorespiration and enhancing water-use efficiency. This makes C_4 plants more productive, while C_3 plants, common in cooler climates, are less efficient under stress. Systems biology studies play an important role in understanding complex biological processes, though proteomic-level studies have not yet explored the C_3-to-C_4 transition. Protein-protein interaction (PPI) networks provide valuable insights to identify key proteins and their interactions, which motivated this study to focus on the comparative analysis of PPI networks associated with C_3 and C_4 photosynthesis using local network alignment. The C_3 and C_4 PPI networks were constructed using *Oryza sativa japonica* and *Zea mays* PPIs retrieved from the STRING database, respectively. Global network analysis of individual C_3 and C_4 PPI networks revealed the conservation of fundamental machinery in both photosynthesis types, as both networks showed a similar clustering pattern of the light reaction being distributed among different submodules, while the dark reaction remained confined to a single submodule. The study revealed a conservation of 77% for C_3 proteins and 67% for C_4 proteins after network alignment. Highly conserved hub proteins were identified in the Calvin cycle submodule, crucial for the RuBP regeneration step. Key enzymes involved in the C_4 pathway, including PEPC, malate dehydrogenase, malic enzyme, and aspartate aminotransferase, were identified as hub proteins specific to the C_4 PPI network. These diverse hub proteins hold promise as potential targets for genetic engineering to install the C_4 pathway in C_3 plants to enhance photosynthetic efficiency, potentially ensuring global food security through increased crop productivity.

Keywords: Protein-protein interaction network, C_3 and C_4 photosynthesis, Network alignment, Submodules, Hub proteins.

Artificial intelligence in crop development: application of deep learning for predicting seed development genes

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Recently, deep learning algorithms have become popular, yet their full potential remains underexplored in the field of automated function prediction (AFP) methods in plant sciences. Protein Function Predictor (PFP), a deep learning model aimed at predicting plant protein functions with higher accuracy than existing models, was introduced in this study. PFP was compared to the state-of-the-art AFP model, Deep Functional Residue Identification (DeepFRI), to assess its performance in predicting plant protein functions. The study aimed to identify candidate proteins associated with rice (Oryza sativa) seed development as the biological use case.

PFP was trained on a dataset of experimentally determined protein structures and sequences. This dataset consisted of 20,075 protein chains belonging to the NCBI taxonomy lineage of Viridiplantae. PFP showed better performance than DeepFRI based on its higher micro- and macro-averaged area under the precision-recall (AUPR) and protein-centric maximum F-score (F-max) scores on a test dataset of plant proteins. The model predicted Biological Process-Gene Ontology (BP-GO) terms for rice proteins. Subsequently, these predictions were used to identify candidate proteins associated with the GO term "seed development" in rice, which were then computationally validated. Out of 43,649 AlphaFold-predicted structures of the rice proteome used as inputs, 216 candidates were predicted for seed development by applying a final prediction score threshold of 0.95. This analysis revealed a strong relevance of the candidate genes for seed development, as evidenced by their significant enrichment in key BP-GO terms such as mRNA splicing, regulation of growth, protein polyubiquitination, brassinosteroid-mediated signalling pathway, mRNA processing, regulation of seed growth, and regulation of leaf development. Among the candidate records, six proteins (Q7X742, Q8LNC7, Q10R47, Q0DDF6, Q6YUX0, Q0DUR2) emerged as final predictions based on bioinformatics analysis and literature data. These validated proteins can be targeted for genetic research aimed at enhancing rice grain quality and advancing agricultural productivity.

Keywords: Automated function prediction, Deep learning, Seed development, Graph convoluted network, Gene Ontology

Performance evaluation of tools for predicting transcription factor binding sites

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The precise prediction of transcription factor binding sites (TFBSs) is crucial for unravelling gene regulatory networks. Despite the emergence of *in silico* TFBS prediction tools, comprehensive evaluation of their performance remains limited. In this study, we assessed twelve widely used TFBS prediction tools and four *de novo* motif discovery tools using a benchmark dataset containing TFBSs from *Arabidopsis thaliana* and *Homo sapiens* genomes. The tool performance was evaluated across sensitivity, positive predictive value, performance coefficient, geometric accuracy, and average site performance, considering several overlap percentages between known and predicted binding site lengths. Both TFBS prediction tools and four *de novo* motif discovery tools were ranked based on these parameters to determine the best performer(s). Among TFBS prediction tools, the Multiple Cluster Alignment and Search Tool (MCAST) emerged as the best performer, followed by Find Individual Motif Occurrences (FIMO) and MOtif Occurrence Detection Suite (MOODS). Moreover, MotEvo and Dinucleotide Weight Tensor Toolbox (DWT-toolbox) demonstrated the highest sensitivity (1.0) in TFBS prediction at both 80% and 90% overlaps. Notably, MCAST and DWT-toolbox consistently demonstrate the highest sensitivity (1.0) across the benchmark dataset. Among *de novo* motif discovery tools, MEME (Multiple Em for Motif Elicitation) emerged as the best performer across all parameters. To validate the performance of the top three TFBS prediction tools, we analyzed the promoter sequences of genes involved in the anthocyanin biosynthesis pathway in *A. thaliana* because it is a well-studied pathway. MCAST identified the highest number of binding sites for myeloblastosis transcription factors, which are known to hold a dominant position in the regulatory network of anthocyanin biosynthesis. This study provides groundwork for selecting optimal TFBS prediction tools. Given the variability in tool performance, using multiple tools for TFBS prediction is recommended. Further efforts should focus on integrating different TFBS prediction tools into a toolbox to enhance precision and accuracy.

Keywords: Transcription factor binding sites, bioinformatics tools, performance evaluation

Genome-wide analysis of the lipoxygenase gene family in oil palm: insights and implications

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Lipoxygenases are non-heme iron-containing dioxygenases ubiquitously distributed across plants, animals, and fungi. They catalyze the hydroperoxydation of polyunsaturated fatty acids into oxylipins that are involved in various plant physiological processes including stress responses and development. Given the economic significance of oil palm, the present study employs computational approaches in identifying and characterizing the LOX family genes (*EgLOX*) in this palm. Through BLAST search and HMM analysis, a total of 12 *EgLOX* genes were identified. The putative genes were checked for the presence of LOX C-terminal and PLAT/LH2 domains through InterProscan and NCBI batch CD-search. Subsequent phylogenetic analysis classified the EgLOX proteins into 9-LOX and 13-LOX subfamilies comprising four and eight members, respectively. Based on the presence of chloroplast transit peptides, the LOX proteins were further classified into type-I and type-II subfamilies. Furthermore, the physiochemical properties and subcellular localization were analyzed to gain insight into potential functions and evolutionary relationships. Almost all the EgLOXs exhibited nine exons and were randomly distributed across eight chromosomes. The average length and molecular weight of EgLOX protein were determined to be 894 amino acids and 101.04 kDa, respectively. Interestingly all the 9-LOX subfamily proteins were cytoplasmic, whereas 13-LOX proteins were chloroplast localized. The conserved motif analysis revealed a similar motif distribution within subfamilies, while the histidine-rich characteristic motif was present in all EgLOX proteins. The cis-acting regulatory elements (CRE) in 1500 bp upstream of the transcription start sites were analyzed and found to include CREs associated with various functional categories. Segmental gene duplication events were identified through gene duplication analysis. The major findings including the evolutionary relationships and potential functions provide the basis for further characterization of LOX genes. Moreover, the knowledge gained from the present study can be exploited for genetic improvements to increase the productivity and stress resistance of the oil palm species.

Keywords: *Elaeis guineensis*, Lipoxygenase gene family, Phylogenetic analysis, HMM search, motif analysis

Effects of Low-Density Polyethylene (LDPE) mulching generated microplastics on the shoot growth of *Phaseolus vulgaris* L.

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Plastic mulching, particularly with low-density polyethylene (LDPE) is widely used in agriculture due to its numerous benefits. However, its widespread use raises environmental concerns including the generation of microplastics (MPs). These MPs can affect plant development in various ways, including effects on germination, root and shoot growth, as well as soil properties and microorganisms. The aim of the study was to investigate the effects of LDPE mulching generated MP (≤1000 µm; arbitrarily shaped) on the shoot growth of common bean (*Phaseolus vulgaris* L.). Plants were grown inside an outside shed under natural conditions, in cement pots containing 0% (control), 1%, 3%, and 5% (w/w dry weight of soil) concentrations of LDPE-MPs mixed into the soil. Prior to the experiment, soil was assessed for the presence of MP using Fourier-transform infrared spectroscopy. Vine length (daily), number of leaves, and stem diameter (weekly) were recorded for 6 weeks. Data were analysed using a regression model/two-way ANOVA followed by a Tukey Pairwise Comparison test. Total chlorophyll and proline contents of mature leaves were also assessed after 6 weeks. A concentration-dependent reduction of the growth parameters was observed when grown under 1%, 3%, and 5% w/w LDPE-MP. Compared to the control, mean vine length decreased significantly ($p<0.001$) by 13.58%, 23.31%, and 26.78% and the mean number of leaves reduced significantly ($p<0.001$) by 18.03%, 27.90%, and 37.30% respectively at 1%, 3% and 5% w/w LDPE-MP, during the 6-week period. Mean stem diameter decreased significantly ($p<0.001$) by 5.04%, 16.19%, and 23.38% respectively at 1%, 3%, and 5% w/w LDPE-MP, over the 6 weeks compared to the control. In comparison to the control, a declined total chlorophyll content (7% at 5% LDPE-MP) and a higher proline accumulation was seen with all LDPE-MP treatments. The results indicated that soil LDPE-MP alters the morphology and physiology of the shoot growth of the common bean.

Keywords: Common bean, Microplastics, Proline, Shoot growth, Total chlorophyll

The potential of waste flowers as a sustainable source for cosmetic production

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The use of plant waste for sustainable value-added products has grabbed the attention of research and development lately. Countries like Sri Lanka and India have been seen with a huge amount of temple waste flowers which is vastly less addressed in terms of their potential to be transformed into innovative wellness products ranging from beverages to cosmetics. These include beauty teas, hydrosols, essential oils beneficial for skin health and natural pigments that can colour cosmetic formulations. Utilizing waste flowers not only provides an environmentally friendly sustainable waste management solution but also contributes to the development of nature-based cosmetics. Thus, this research aims to investigate the antioxidant and *in-vitro* sun protection potential of 8 waste flowers commonly found in temple areas of Sri Lanka (*Nymphaea x erangae*, *Nymphaea rubra*, *Nymphaea pubescence*, *Nelumbo nucifera*- red and white, *Clitoria ternatea*, *Tagetes erecta*, *Ixora coccinea*) in three forms of extractions potential for cosmetic formulations: infusions, hydrosols and crude pigment extracts. All extracts were tested for their antioxidant potential: Total Phenol Content (TPC), Total Flavonoid Content (TFC), and DPPH free-radical scavenging percentage (DPPHfrs%) and *in-vitro* Sun Protection Factor (SPF). The studied extracts were in the pH range of 4.8-6.4. TPC, TFC, DPPHfrs% and SPF detection and quantification limits ranged from 0.003 to 0.927 g/L (Gallic Acid Equivalent), 0.002 to 0.167 g/L (Rutin Equivalent), 22.316% to 88.974%, and 1 to 46 respectively in infusions, hydrosols and crude pigment extracts. The highest antioxidant and sun protection activities were observed in *N. nucifera* (white), *N. rubra*, *I. coccinea*, and *Nymphaea x erangae*. These bioactivities suggest the potential to heal, brighten, and hydrate skin. Crude pigments were water, ethanol and glycerine soluble. They showed the ability to colour basic cosmetic base formulations. Thus, waste flowers possess a potential for value-added, sustainable and innovative cosmetic production.

Keywords: Nature-based cosmetics, Waste flower extractions, Natural pigments, Antioxidant capacity, Sun protection factor

Antioxidant and sun protection capacity of selected medicinal plants in Sri Lanka

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Medicinal plants comprise potent primary sources of bioactive compounds with beneficial bioactivities that can be incorporated into innovative products in food/beverage to cosmetics. Sri Lanka, a country with rich medicinal plant diversity and intensive traditional knowledge, has massive potential for the herbal cosmetic industry, which is relatively less discovered. The current study investigates the cosmetic potential of 11 selected medicinal plants (*Flueggea leucopyrus*; *Osbeckia octandra*; *Hellenia speciosa*; *Bacopa monnieri*; *Atalantia ceylanica*; *Peperomia pellucida*; *Olax zeylanica*, *Vetiveria zizanioides*; *Cassia auriculata*; *Mesua ferrea* and *Cyperus rotundus*) in terms of their antioxidant and *in-vitro* sun protection capacity. The selected medicinal plants were extracted as herbal decoctions, herbal glycerites, and crude ethanolic extracts. All extracts were tested for their antioxidant potential: Total Phenol Content (TPC) as Gallic Acid Equivalent (GAE), Total Flavonoid Content (TFC) as Rutin Equivalent (RE), and DPPH free-radical scavenging percentage (DPPHfrs%), followed by *in-vitro* Sun Protection Factor (SPF). The studied extracts were in the pH range of 4.8-6.4. TPC, TFC, DPPHfrs%, SPF of decoctions and glycerites ranged from 0.008 g/L to 0.852 g/L (GAE), 0.001 g/L to 0.846 g/L (RE), 37.140 % to 92.353 % and 6 to 40 respectively. Crude ethanolic extracts in 1 mg/ml showed the following TPC, TFC, DPPHfrs%, and SPF range: 0.038 g/L to 0.154 g/L (GAE), 0.001 g/L to 0.009 g/L (RE), 2.355 % to 70.145 %, 1 to 35 respectively. The highest antioxidant capacity and SPF were observed in *H. speciosa*, *F. leucopyrus*, *M. ferrea* and *O. octandra* extracts. Herbal glycerites with antioxidant properties and SPF, suggest the possibility of functioning as green extractants that can be directly incorporated into cosmetics. Thus, selected medicinal plants have a high potential for new or modified cosmetic formulations that can heal, brighten, and hydrate skin.

Keywords: Medicinal plants, Herbal cosmetics, Herbal extractions, Antioxidant capacity, Sun protection factor

Patterns of phylogenetic diversity of sub and upper montane forest communities in Hatton-Nallathanniya area of the Adam's Peak Wilderness in Sri Lanka

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Adam's Peak Wilderness is within the Central Highlands UNESCO World Heritage Site in Sri Lanka. It features montane forests rising to 2000 m above sea level, with extremely high biodiversity. The study aimed to identify and compare the phylogenetic diversity in sub and upper montane tree communities in the Hatton-Nallathanniya area of the Adam's Peak Wilderness. The sub montane forest formation in Adam's Peak Wilderness begins at around 1070 m altitude, while the upper montane starts at approximately 1680 m elevation due to the mass-elevation effect. Data were taken from 12 plots in each sub and upper montane tree community from a study conducted in 2019. Phylogenetic trees, Faith's phylogenetic diversity (Faith's PD), Mean Pairwise Distance (MPD), and Mean Nearest Taxon Distance (MNTD) were determined using V.PhyloMaker (version: 0.1.0). Phylogenetic structure was assessed using Nearest Taxon Index (NTI) and Net Relatedness Index (NRI) by using the "picante" R package. Patterns between phylogenetic diversity and elevation were studied using Generalized Additive Modelling (GAM). The relationship between Faith's PD and species richness was determined using Pearson correlation test. Clustering or overdispersion was used to assess the phylogenetic structure. Patterns of phylogenetic diversity and structure differ between sub and upper montane forest communities. Phylogenetic diversity metrices showed no elevation-related trends in sub montane, contrasting with significant elevation-associated increases in MPD and Faith's PD in the upper montane indicating higher phylogenetic diversity at higher elevations. A positive correlation was obtained with species richness and Faith's PD. In the sub montane forest, NTI and NRI remained stable but shifted towards overdispersion in the upper montane. Increase of elevation suggesting the role of facilitation and convergence in shaping the forest community composition of Adam's Peak Wilderness. The findings of this phylogenetic diversity study further highlighted the importance of protecting the upper montane forest formations in Adam's Peak Wilderness.

Keywords: Adam's Peak Wilderness, Biodiversity, Elevation, Montane Forest communities, Phylogenetic diversity

Acknowledgement: Authors acknowledged Ms. H. T. Gamhewa for the support in fieldwork.

Anther culture potential of aromatic rice varieties and their F1 hybrids with local germplasm

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Aromatic rice has high consumer preference due to its distinct fragrance. Anther culture is a vital *in vitro* technique utilized to fix homozygosity in crop improvement rapidly. This technique has been successfully used in *japonica* rice. However, integrating anther culture in *indica* rice breeding is difficult due to its innate recalcitrance to the process. When *indica* varieties are hybridized with aromatic rice, the resulting hybrid genotypes have a mixed genetic background and may be more responsive to anther culture. In this study, F1 hybrids were produced through reciprocal crosses in which at least one parent was an aromatic variety. Pusa Sugandh, Pusa Basmati, Basmati 370, At 306, At 309, At 405, At 311, At 313, Ld 253, Ld 376 and Bw 18-1541 were used as the parent varieties. Anthers of hybrids from successful crosses and their parents were subjected to anther culture. Out of 8 reciprocal crosses, only 6 were compatible and produced seeds to generate F1 hybrids. For callus induction, 3 previously reported modified N6 media formulations were investigated (Modified N6 – 2 mgL^{-1} 2,4-D, N3 - 2 mgL^{-1} 2,4-D, 0.5 mgL^{-1} BAP, and N6NDK - 1 mgL^{-1} 2,4-D, 2.5 mgL^{-1} NAA, 0.5 mgL^{-1} kinetin, 0.5 gL^{-1} L-proline and 0.5 gL^{-1} L-glutamine). After 6 weeks, induced calluses (approx. 5 mm diameter) were transferred to the MS regeneration medium (1 mgL^{-1} BAP, 1 mgL^{-1} kinetin, 1 mgL^{-1} NAA). The increase in callus growth was measured after 10, 20 and 30 days and observations on regeneration were recorded. Data were analyzed by one-way ANOVA, using RStudio version 3.2.2022. Among the 3 media formulations tested, callus occurred in only the N6NDK medium. Six genotypes (three hybrids and three parents) showed callus induction; Bw 18-1541 x At 405, At 405 x Bw 18-1541, Pusa Sugandh x At 306, Bw 18-1541, At 405, and At 306. The local rice line, Bw 18-1541 had a significantly higher ($p \leq 0.05$) average callus induction percentage (22.21 ± 4.16%) compared to other genotypes. A significant difference ($p \leq 0.05$) in callus growth was only observed at 10 days. Bw 18-1541 had significantly higher ($p \leq 0.05$) callus growth at 10 days (6.42 ± 0.72 mm) compared to others. After 30 days, most calluses developed necrotic regions, with one from At 405 x Bw 18-1541 producing an albino shoot. Analysis of callus induction and growth data highlights At 405 and Bw 18-1541 as promising candidates for anther culture. Further investigation on morphogenesis is required to enhance the success of the promising genotypes.

Keywords: anther culture, aromatic rice varieties, *indica* rice, hybridization, reciprocal crosses

Assessment of carbon sequestration by trees and lianas in Kodigahakanda: a regenerating small forest patch

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Disturbed small forest patches promote prolific growth of lianas during natural regeneration affecting the forest structure and function. The study assessed the woody biomass distribution and carbon sequestration capacity of the Kodigahakanda forest (6°46'59"N - 6°46'42"N and 80°0'50"E - 80°0'56"E, 135-380 msl) infested by 13 species of lianas. Eleven random 10m x 10m sampling plots enumerated the density, height and diameter of canopy trees. Liana stem counts per diameter classes were recorded in 44 subplots. Using available allometric equations for tropical trees, the above-ground and below-ground biomass of trees and lianas were estimated and converted to carbon stocks. Biomass and carbon stock partitioning between trees and lianas were evaluated. Normalized Difference Vegetation Index (NDVI) values derived from Sentinel-2 multispectral imagery using ArcGIS Pro software were employed for interpolating maximum possible total woody carbon stock the forest can hold in absence of lianas. Lianas contributed 18% of the total woody biomass. The mean carbon density of the forest was 134.818 ± 80.514 Mg/ha, a respectable amount for secondary forests. Lianas contributed 25.40 ± 22.85 Mg/ha to the carbon stock, though their distribution was uneven across the forest. It has been found that foliage of lianas has higher carbon assimilation rates compared to tropical trees, however, their carbon stock remains lower. In this forest, trees with the highest diameter class (30-40 cm) holds the highest tree carbon stock despite their fewer numbers. *Dipterocarpus zeylanicus* exhibited the highest tree carbon stock, followed by *Artocarpus nobilis, Melicope lunu-ankenda, Antidesma bunius, Alstonia macrophylla, Mimusops elengi,* and *Pagiantha dichotoma.* Current and predicted values using NDVI suggest a potential 71.9% increase in carbon stock for a dense canopy cover with possible habitat improvements. We suggest that the impact of lianas on forest functions and services is vital to be taken into consideration for assessing forest health and/or degradation. Restoration efforts, alongside tree planting for canopy re-establishment, should pay attention to pilot scale liana removal activities in monitoring of habitat recovery of degraded forests.

Keywords: Liana, forest, regeneration, biomass, carbon stocks

A molecular characterization of some selected *Madhuca* spp. (Sapotaceae) in Sri Lanka

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The Genus *Madhuca* J.F.Gmel., distributed in the tropics including Sri Lanka, India, Vietnam, Pakistan, Nepal, Myanmar, etc., belongs to the family Sapotacaeae. Species of *Madhuca* have reported a wide array of economic uses such as a source of food and nutrition, pharmaceutical ingredient, bio-fertilizer and bio-fuel. Seven *Madhuca* species are reported in Sri Lanka, out of four being endemic to the island. This study aimed to address the research gap present in genetic studies of the genus *Madhuca* in Sri Lanka. Samples were collected from Kanneliya Forest Reserve and Kitulgala Forest Reserve. Molecular authentication of each sample was done using the database of Basic Local Alignment Search Tool of The National Center for Biotechnology Information. The Nuclear Internal transcribed spacer 1 (ITS1) region, a highly polymorphic non-coding region was amplified, using specific primers in the following five *Madhuca* species, *Madhuca fulva* (Thwaites) J.F.Macbr.(endemic), *Madhuca microphylla* (Hook.) Alston (endemic), *Madhuca clavata* Jayas.(endemic), and *Madhuca longifolia* (J.Koenig ex L.) J.F.Macbr. and *Madhuca neriifolia* (Moon) H.J.Lam. According to the ITS1 marker, two distinct clades were observed within the ingroup of the genus *Madhuca* in Sri Lanka. All studied endemic *Madhuca* species have clustered as a single monophyletic group. The second clade only includes *Madhuca longifolia*, which has a wide geographical distribution. An unexpected sequence similarity, 99.57% in the ITS1 region was observed between *Madhuca clavata*, a point endemic species to Sri Lanka and *Madhuca bourdillonii*, a critically endangered species native to India. The results of this preliminary molecular phylogenetic study support the currently accepted morphological species concepts of the genus *Madhuca* in Sri Lanka. More sampling and multi-locus phylogeny will merit resolving the species delimitation issue between *Madhuca clavata* and *Madhuca bourdillonii*.

Keywords: Madhuca, Sapotaceae, Sri Lanka, Taxonomy, ITS1 marker

Comparative morphological and phytochemical evaluation of *Plectranthus amboinicus* (Lour.) Spreng. (Kapparawalliya) and *Plectranthus barbatus* Andr. (Wal-Kapparawalliya) in Sri Lanka

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Plectranthus amboinicus (Kapparawalliya) and *Plectranthus barbatus* (Wal-Kapparawalliya) are medicinal plants belonging to the Lamiaceae family that are used to treat many diseases in traditional therapeutic systems in Sri Lanka. However, *P. barbatus* tends to get misidentified as *P. amboinicus* due to confusion in vernacular names and similarities in both morphology and aroma. This study was conducted with the objective of establishing reference standards on morphological characters and phytochemical constituents that will enable *P. amboinicus* to be distinguished from *P. barbatus*. Organoleptic, macro-morphological, and anatomical characters of leaves and stems, powder microscopy, and quantitative microscopy conducted on leaves (30 samples from 10 plants) were evaluated under morphological study. Phytochemical evaluation was conducted for methanolic extracts of leaves using preliminary phytochemical screening tests and quantitative estimations of total phenol contents (TPC). Thin Layer Chromatographic (TLC) fingerprints were developed in toluene: ethyl acetate: acetonitrile (7:2:1), chloroform: acetone: formic acid: ethyl acetate (18:4:2:1), and ethyl acetate: hexane (3:2) solvent systems. Laminar and petiole size, vain areolation, trichome distribution, stomatal index, palisade ratio, vein islet, and veinlet termination numbers were identified as prominent morphological indicators for the differentiation of *P. amboinicus* from *P. barbatus*. Both species revealed the presence of alkaloids, flavonoids, glycosides, saponins, diterpenes, and triterpenoids. Compared to *P. amboinicus*, a relatively higher TPC was recorded from *P. barbatus*. Despite the similarities of TLC fingerprints, characteristic additional blue (Rf-0.75), green (Rf-0.05, 0.11), and yellow (Rf-0.92) fluorescent bands were observed only from *P. barbatus* under UV-365 nm in the above solvent systems. The present study reported the significant differences between two species for proper identification and establishment of standards for *P. amboinicus* and *P. barbatus*, eliminating unintentional adulteration of raw materials in herbal formulations. However, further studies with plants from more localities and both species grown under same conditions are needed to confirm the findings.

Keywords: *Plectranthus amboinicus*, *Plectranthus barbatus*, Kapparawalliya, Sri Lanka

Floristic analysis of a restoration site and adjacent forest patch in the lowland wet zone of Sri Lanka

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Diyakothakanda forest site situated in Baduraliya, Kalutara district (6° 45' N - 80° 31' E), was heavily degraded in the past due to human activities. The restoration site, initiated in 2016 was demarcated into three zones A, B, and C from lower to higher elevation based on the relay floristic method. The site covers an area of 2 hectares and includes a reforestation block. The main objective of the present study was to compare the floristic composition of the restoration site with an adjacent reference forest. Vegetation sampling was conducted using a stratified random sampling approach, with 15 (5x5m) and 9 (10x5m) random plots respectively in the restoration site and natural forest. Rank abundance curves were generated using the vegan package (R version 4.2.2) and diversity indices were calculated considering only the naturally succeeded plants. Hierarchical cluster analysis was performed with occurrence data of naturally succeeded plants to identify the major floristic groups among plots. There were 136 species recorded at the study site, 99 in the restoration site and 55 in the natural forest where 12 species were common for both sites. The predominant plant family was family Fabaceae in both sites (Genera: *Adenanthera, Humboldtia, Gliricidia*). The rank abundance curve gave the pattern of a disturbed habitat with a long tail with a higher number of rare species and a lesser number of high-abundance species. An ascending gradient of species diversity was identified from zone C to A. *Humboldtia laurifolia* was found more abundantly in natural forest while *Alstonia macrophylla, Symplocos cochinchinensis, Carallia brachiata* and *Nepenthes distillatoria* were observed frequently under natural succession in restoration site. While most natural forest plots clustered separately from restoration site plots in hierarchical clustering, the mature zone A plots of the restoration site clustered closer to forest plots. This floristic similarity shown even at this early stage validates the management practices that have been used in the restoration site and shows that tree plantation in the restoration site has improved the diversity of the naturally occurring species.

Keywords: Restoration, species diversity, hierarchical clustering, Diyakothakanda, floristic comparison

Micropropagation of *Passiflora edulis* var. Horana Gold through shoot tip-derived nodal culture

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Passiflora edulis (passion fruit) is a high-value crop consumed fresh and confectionery. A new cultivar, *P. edulis* var. “Horana Gold” was recently developed in Sri Lanka and *in-vitro* propagation techniques are useful for continuous mass production due to the inefficiency in conventional propagation methods. Previous studies on *P. edulis* demonstrated that high 6-Benzylaminopurine (BAP) concentrations (3.0 – 5.0 mg/L) yielded up to four shoots per explant but reduced shoot height, complicating shoot separation for subculture. This study aimed to develop a modified shoot tip culture protocol, introducing a nodal subculture step, for recovering multiple shoots per explant without negatively impacting shoot growth. Shoot tips were cultured on MS medium supplemented with varying BAP concentrations (0.0, 1.5, 2.5, and 4.0 mg/L). Ten replicate culture bottles, each with four explants, were maintained for each treatment. After six weeks, elongated shoots were separated into nodal segments and subcultured on MS medium supplemented with 2.0 mg/L BAP and 1.0 mg/L Gibberellic acid (GA3). Developed axillary shoots were rooted on half-strength MS medium with 0.5 mg/L indole butyric acid (IBA) and then transferred to pots containing cocopeat for acclimatization. The growth regulator concentrations used in experiments were based on previous literature. A significant difference ($p \leq 0.05$) in height was observed among shoots under different BAP treatments. The highest mean height (17.57 mm) and number of nodes per explant (3.1) were obtained from shoot tips cultured on BAP-free MS medium. In contrast, shoot height and number of nodes per explant decreased to 6.38 mm and 1.5 nodes on MS medium with BAP (4.0 mg/L). A total of 354 nodal segments were sub-cultured: 125, 88, 80, and 61 from BAP treatments 0.0, 1.5, 2.5, and 4.0 mg/L respectively. From 354 nodal segments cultured, 229 axillary shoots were developed. Of these, 100 shoots were transferred to the rooting medium and 61 shoots produced roots, while 42 plants could be acclimatized in cocopeat. Initial shoot tip culture followed by nodal subculture improves micropropagation efficiency compared to shoot tip culture on MS medium with BAP.

Keywords: Passiflora edulis, Horana Gold, Shoot tip, Nodal subculture, Multiplication

Leaf anatomical variation of selected mangrove species on the east coast of Sri Lanka

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Mangroves are coastal woody plants which show distinct anatomical adaptations. Anatomical studies on mangroves are limited in the east coast of Sri Lanka. A study was conducted to determine the variation of leaf anatomical characteristics; thickness of laminar (LT), palisade layer (PL), spongy layer (SL), water storage tissues (WST), and epidermal layers (EL) of three mangrove species (*Avicennia marina, Excoecaria agallocha,* and *Lumnitzera racemosa*) growing under varied salinity environments in the Eastern Coast of Sri Lanka (Sathurukondan: 0.6±0.55 ppm, Thampalagamuwa: 2.9±0.15 ppm, and Panama: 9.6±0.55 ppm). Mature leaves from each species at each site were collected during the wet season. The sections were observed under light microscopy. One-way ANOVA was performed using MINITAB 18.1. The species *L. racemosa* showed higher values in most of the laminar characteristics. The thickness of WST varied significantly ($p<0.05$) among species at all study sites, with the highest value in *L. racemosa* and the lowest value in *E. agallocha*. *A. marina* showed significantly higher values of LT in study sites except in Sathurukondan. *A. marina* and *L. racemosa* showed 3-4 PLs, whereas *E. agallocha* showed lower values (2). SL is absent in *L. racemosa*. A higher number of SLs was recorded in *E. agallocha* (8-9 nos.) than in *A. marina* (4-5 nos.). The ratio between PL and SL was significantly higher in *A. marina* than in *E. agallocha*. The above finding could be the reason for shedding leaves in *E. agallocha,* during the onset of rain. The studies so far have revealed that the variations in laminar characters among species across the study sites with different salinity levels are not statistically significant, except for WST. A long-term cohort study is essential to validate the effect of salinity variation on leaf anatomical structure. Understanding the leaf anatomy would be useful for selecting species for successful restoration.

Keywords: Eastern Coast, Leaf anatomy, Mangroves, Salinity, Water storage tissue

Study on the influence of organic mucilage on seed germination, and seedling growth of *Phaseolus vulgaris*. L – A legume crop with high economic potential.

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Phaseolus vulgaris. L, a significant legume, frequently receives chemical pretreatments to enhance germination, although these treatments can harm the environment. Therefore, this study explores natural alternatives including mucilage extracts from *Aloe vera* (M1), *Hibiscus rosa-sinensis* (M2), *Neolitsea cassia* (M3), and *Abelmoschus esculentus* (M4) to enhance seed germination and vigor. The leaves of *A. vera*, *H. rosa-sinensis*, *N. cassia*, and the young pods of *A. esculentus* were separately blended, squeezed through muslin cloths, and their mucilage was individually collected. Healthy *P. vulgaris* seeds were sterilized with 2% NaOCl and three serial washings. Seeds were soaked in each mucilage for ten minutes, then ten seeds were placed on petri dishes lined with filter paper moistened with 2.5 mL of distilled water. Untreated seeds served as the control (M0) with water, and each treatment had six replicates. Petri dishes were incubated at 27°C and 83% humidity under normal light for six days, with daily germination observations. Root and hypocotyl lengths were measured at the end. Less-effective bio-gel was tested at a 1:1 dilution (M5) under the same conditions. Germination metrics including Mean Germination Rate (MGR), Mean Germination Time (MGT), Mean Germination Index (MGI), Mean Germination Energy (MGE), and Mean Coefficient of Velocity of Germination (MCVG) were calculated. Data were analyzed using One-way ANOVA and Tukey pairwise comparisons. Although M1 had the highest MGR (100.00 ± 0) and MGE (100.00a ± 0) it showed a high MGT (2.52c ± 0.354). M2 showed the second-highest MCGV (43.1b ± 5.71%). M3 and its dilution (M5) resulted in significantly lower MGR and MCGV, and M3 had the highest MGT (3.32 ± 0.337 days) suggesting inhibitory compounds. M4 showed moderate MGR and MGE but had the highest MGI (7.14 ± 0.56), MGCV (63.4a ± 3.87), and lowest MGT (1.58 ± 0.09 days), significantly differing from the control and other treatments. Considering all the parameters, this study identifies *A. esculentus* (M4) as an effective alternative to chemical treatments for enhancing seed germination and can be recommended to farmers for use in agricultural fields.

Keywords: *Phaseolus vulgaris,* Seed germination enhancement, Coefficient of velocity of germination, germination index, germination rate

Habitat dissimilarity in a regenerating wet lowland small forest reflects the importance of habitat specific improvements for assisted natural restoration

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Topographic and geomorphologic variability, nutrient availability and the other local influences of plant species bring about a broad spectrum of habitat heterogeneity in small forest patches. This study assessed the heterogeneity in abiotic factors and plant communities in a regenerating wet lowland suburban forest to optimize restoration efforts. The study area was rich in plant species but disturbed from nature-walking and rock-climbing activities. Plant composition, cover and density of the canopy, understory and undergrowth strata and liana abundance were enumerated in eleven random 10 m x 10 m plots. A dendrogram was constructed by the average clustering method with Bray-Curtis dissimilarity index to identify vegetation communities and named with species of high synoptic value. Composite samples of topsoil from plots were chemically analysed for carbon, nitrogen, phosphorus, potassium, pH, conductivity, moisture, carbon: nitrogen ratio. A hierarchical cluster analysis using soil and floristic parameters reflected the habitat heterogeneity among plots. R software was used for the analysis. Three plant communities in the forest dominated by *Dipterocarpus* sp., *Mimusops elengi,* and mixed species were identified. Clusters of plots separated in the dendrogram reflected four main habitat heterogenous zones. The zone with naturally regenerated *Dipterocarpus* sp. was a unique habitat. This could be further improved by facilitating the growth of naturally regenerated *Dipterocarpus* seedlings. Plots nearby rocks clustered together demonstrating a mixed species habitat dominated with lianas and invasive species *Ochlandra stridula,* and low content of soil Phosphorous. This habitat zone required regular maintenance of the vegetation to control the growth of herbaceous species. Possible enrichment of soil is also required if native tree species are established in this zone. Areas with high abundance of *M. elengi* was also noted as a cluster while the remaining cluster also reflected a mixed tree species zone with rich soil. Many restoration programs merely target on improving plant species diversity and consideration of the habitat heterogeneity in species selection has been often overlooked. Our study demonstrated the importance of assessing vegetation, soil and other geomorphic features in determining habitat specific improvements in assisted natural regeneration of a regenerating small forest patch in sub urban area to boost the ecosystem functions and services and its sustenance.

Keywords: Regeneration, forests, heterogeneity, habitat improvement, restoration

Risk factors associated with chronic kidney disease of unknown etiology (CKDu) in Jaffna district, Sri Lanka

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Chronic Kidney Disease of Unknown etiology (CKDu) is scarcely studied in Nothern Province. The present study thus aimed to analyze the risk factors of CKDu in Jaffna district. Recently recorded 610 CKD/CKDu cases in the Jaffna hospital were screened down to 85 suspected CKDu cases using a questionnaire survey while the water quality parameters were analyzed. Sociodemographic data (Age, sex, etc), disease indicators (serum creatinine, hypertension, diabetes, etc) were recorded while water quality index (WQI) was calculated, and the serum creatinine levels were used to calculate the estimated glomerular filtration rate (e-GFR). According to the results, male preponderance (60%) was observed in the age class of 41-50 (25%) showing no association with agriculture-related occupation or consumption-related habits such as smoking, alcohol or betel chewing. Electrical conductivity, total dissolved solids (TDS), total hardness, calcium and sodium ions exceeded the relevant standards for potable water, showing a higher correlation towards increasing the WQI, which is used to categorize water into good, poor and unsuitable. Thus, more than 60% of the sources were identified as poor to unsuitable for consumption. The eGFR ranges between 6 -114 (ml/min/1.73m^2) showing a significant negative correlation with calcium and marginal significance with total hardness, TDS, sodium, sulphate, and salinity, suggesting their role in CKDu progression in the study area. Hofmeister series of ion follow the order of $Na^+ > Cl^- > Ca^{2+} > NO_3^{2-} > SO_4^{2-} > Mg^{2+} > K^+ > F^- > PO_4^3$ confirming the salting-out effect of kidneys with elevated levels of sodium, chloride, and calcium. The presence of higher As and Cd levels in nearly 30% of the suspected sources may have further contributed towards disease progression. Collectively, the data supported the hypothesis that drinking water quality may have led to CKDu disease progression in the study area of the Jaffna peninsula, highlighting the importance of introducing safe drinking water sources and practices for the inhabitants.

Keywords: CKDu, Jaffna District, Water Quality Parameters, Hofmeister ions, eGFR

Acknowledgement: Financial Assistance from the Open University of Sri Lanka is gratefully acknowledged.

Assessment of Tributyltin induced changes in the blood profile of Giant Danio *(Devario malabaricus*)

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Tributyltin (TBT) is an organotin endocrine disruptor that can be toxic to aquatic organisms when released to surface waters. A recent study reports a presence of 303 ng/L in the coastal surface waters of Sri Lanka. This is much higher than the ambient TBT levels recommended for protecting aquatic life from chronic toxic effects. This study investigated the toxicity induced by chronic exposure of TBT in fingerlings of *Devario malabaricus*. The endpoint for assessing toxicity was the alteration of the blood profile of the fingerlings exposed to 100 and 300 ng/L levels for six weeks using static renewal system. Three replicates (each with n=10 fingerlings) were exposed per treatment and control (without TBT). Blood was collected at the end of exposure to assess total RBC, WBC, platelet counts, and differential WBC counts. One-way ANOVA was followed by the Tukey's test with an accepted significance level of $p<0.05$ to analyze the data. It was evident that TBT induced changes in the blood profile of fingerlings at both exposure levels compared to those in the control. This included a 37% decrease in RBC counts and a 31% decrease in WBC counts at 300ng/L, a 32% increase in WBC count at 100 ng/L ($p<0.05$), a 29% reduction of neutrophils at 100 ng/L, a 28% decrease at 100 ng/L and a 42% decrease at 300 ng/L of platelets. The present study provides evidence for the toxicity of TBT on the blood parameters of *D. malabaricus* which is native to Sri Lanka and is closely related to the well-known model organism Zebrafish. More importantly, these changes in hematological parameters were recorded at environmentally relevant levels.

Keywords: Tributyltin, Organotin, *Devario malabaricus,* endocrine disruptor, blood profile

Acknowledgment: Assistance by the Department of Zoology and Environment Sciences, University of Colombo.

A preliminary study on mites associated with solitary bees in Sri Lanka

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Bees (Order Hymenoptera) are vital pollinators, with 15% of crops pollinated by honey bees and 80% by solitary bees. However, anthropogenic threats such as habitat loss, fragmentation, excessive pesticide usage, and natural enemies like parasites severely impact bee populations. This study investigated the current diversity and distribution of mites in solitary bees in Sri Lanka. A total of 248 bees, representing 25 species and 16 genera, were collected from four locations across both wet and dry zones using a non-destructive sweep net. Morphological identification using published keys revealed new records of 11 mite species from two Sarcoptiformes families (Chaetodactylidae, Acaridae) and two Trombidiformes families (Scutacaridae, Neopygmephoridae) on seven bee species: *Amegilla comberi, Hoplonomia westwoodi, Ceratina binghami, Lasioglossum* sp., *Austronomia* sp., *Xylocopa amethystina*, and *Xylocopa fenestrata* in Sri Lanka. Mite attachment sites varied among these bees, primarily found between bee sternites (66.7%), tergites (11.1%), and within axillar acarinarium (11.1%) and metasomal acarinarium (11.1%). The intensity of mite infestations varied among different bee species, while some bee species were heavily infested with numerous mites, others hosted relatively few mites: *Ceratina binghami* was infested with 15 conspecific mites, whereas only one mite was found on *Lasioglossum* sp. ANOVA and subsequent Tukey's honestly significant difference (HSD) tests indicated a significant difference in mite prevalence between wet and dry zones, with the dry zone exhibiting higher prevalence and species richness (63.64%). The Simpson's index reflected greater species diversity in the dry zone (0.62). Mites of the order Astigmata showed the highest relative abundance (63.64%), while those of the order Prostigmata exhibited the lowest abundance (36.36%). These findings underscore the need for further research and conservation efforts for these understudied arthropod groups in Sri Lanka.

Keywords: Solitary bees, bee mites, attachment sites, abundance, prevalence

Acknowledgement: Department of Zoology and Environment Sciences of University of Colombo is acknowledged for funding and the facilities provided.

Environmental risk assessment of microplastic pollution on Negombo Beach, Sri Lanka, using index models

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The small particles of plastics, less than 5 mm, are known as microplastics. The present study aimed to assess the abundance, diversity, and environmental risk of microplastics in the Negombo Beach, Sri Lanka. Two sites (10mX10m) were selected from the beach: Site A: at the fishery harbour; Site B: with proximity to the tourist hotels. The surface sediment samples (0-50cm depth) were collected from each site to assess the number, colour, and shape of microplastics (MPs) using standard analytical methods. The polymer types of MPs were identified through FTIR spectrophotometry. MP-based Shannon-Wiener Diversity Index, Potential Ecological Risk Factor (PRF), Pollution Load Index (PLI), and Polymer Hazard Index (PHI), were calculated for two sites. The variation of different types of microplastics between the two sites was assessed by Student's t-test (Minitab 19 software). Site B showed a significantly higher abundance of MPs (56±1.53 MPs/m^2) in sand. MPs of different shapes (fragment, film, fibre, and filament), colours (blue, green, white, red, and translucent), and polymer types (Polypropylene, Epoxy resin, Polyvinyl chloride, and Polystyrene) were recorded from both sites. Significantly ($p<0.05$) high mean percentage of fragment (53.0%±0.6), fibre (25.0%±0.5), and filament (14.0%±0.2) shaped MPs, higher mean percentage of Polypropylene (65.0%±0.3), and Epoxy resin (10.0%±0.7) polymer types, higher mean percentage of blue (38.0%±0.1) and red (22.0%±0.1) coloured MPs were recorded from site B. Site B recorded high PRF (1.24), PLI (1.11), and PHI (928.80). Site A recorded a higher Shannon-Wiener Index, indicating greater microplastic diversity in colour (1.5294), shape (1.2206), and polymer type (1.0969). The PHI indicated the Negombo Beach as a high-risk area (Category IV) for microplastic pollution, The PLI categorized it as a low-risk area (Category I). Continuous monitoring and controlling the input of plastic waste to the Negombo beach will help to mitigate environmental problems associated with microplastic pollution.

Keywords- Microplastics, Abundance, Polymer type, Microplastics shapes, Microplastics colour

Environmental transformations along an urban-rural land use gradient from Colombo to Sinharaja Man and Biosphere Reserve

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Urban expansion leads to significant loss of vegetation and alterations in land use, thereby contributing to global temperature rise. However, research in Sri Lanka regarding temperature changes caused by land use change is currently limited. Therefore, the present study investigates the alterations in Land Surface Temperature (LST), Normalized Difference Vegetation Index (NDVI), and Normalized Difference Built-up Index (NDBI) across an urban-rural gradient using GIS and RS. The research encompasses a study area that stretches 100 km in length and 6 km in width from Colombo to Sinharaja MAB Reserve, divided into 20 zones of 5 km each, covering the period from 2015 to 2024. Each zone consisted of an excess of 30,000 data points which were used to extract data from the LANDSAT 8 and 9 (OLI) imagery obtained in the dry season for the analysis of environmental attributes using ArcGIS 10.8.2. The research found declining LST and NDBI trends and increasing NDVI trends from urban to rural areas. The Spearman correlation tests revealed a positive correlation ($r = +0.655$, $p = 0.000$) between LST and NDBI and a negative correlation ($r = -0.533$, $p = 0.000$) between LST and NDVI across the study period. The mean LST of the highest urbanized region (Zone 1; Colombo) was 28.6ºC in 2015, 29.7ºC in 2019 and 31.8ºC in 2024. The mean LST of the least urbanized region (Zone 20; Sinharaja) was 22.2ºC in 2015, 22.3ºC in 2019 and 24.1ºC in 2024. The difference of LST between these two zones showed an increasing trend over the years which can be attributed to the rapid urbanization in Colombo and suburbs. An area with unusually high LST outside Colombo suburbs which deviated from the trend was identified with the highest LST recorded (38.6ºC in 2024) in Horana. Ground truthing and community surveys revealed that a new industrial facility has resulted in a significant loss of vegetation cover (0.5 km2) which they link to this "heat-island" away from the urban areas. This study emphasizes the necessity for urban planners to prioritize the expansion of green spaces within urban and industrial areas to effectively mitigate the increase in temperatures and improve the overall environmental quality.

Keywords: LST; NDVI; NDBI; Urban-rural gradient; Heat Island

Acknowledgement: University of Colombo for funding this research

Effects of environmentally relevant concentrations of Amoxicillin Trihydrate on *Hypophthalmichthys molitrix* (Silver carp)

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Amoxicillin (AMX) is a widely used antibiotic in human and veterinary medicine, as well as in aquaculture, and it is frequently found in wastewater. In Sri Lanka, AMX has been detected in aquatic environments, posing a threat to aquatic organisms. However, there is a lack of studies on the environmentally relevant toxicity of AMX in Sri Lanka. Therefore, this study was conducted to investigate the toxicological impacts of AMX at environmentally relevant concentrations on the freshwater fish *H. molitrix* (Silver Carp) concerning their mortality, growth, and hematological parameters. Silver carp fingerlings were exposed to four AMX concentrations (0.001, 0.01, 0.1, and 1 mg/ L) and a control for 35 days. The change of standard length and weight of fingerlings were assessed on days 4, 14, and 35; total RBCs and WBCs were counted on days 14 and 35, and Hb, platelet counts, and RBC morphometry were determined on day 35. Blood was obtained via caudal vein puncture. No mortality was recorded throughout the study period. The length and weight significantly increased in treated groups compared to the control with time ($p < 0.05$) (Length: 3.70–11.81%, Weight: 4.40–15.72%). There was a significant increase in total RBC count in both 0.01 and 0.1 mg/ L on day 35 than on day 14 compared to the control and other treated groups ($p<0.05$) (3.9–10.4×10/ mm^3). Total WBC count was significantly higher in 0.001 mg/L concentration on day 14 ($p<0.001$) (3.66–4.93$\times 10^3$/ mm^3). It showed a significant decrease by day 35 compared to day 14 ($p<0.05$). Hb concentrations of 0.1 and 0.01 mg/L were significantly higher on day 35 ($p<0.05$). There was no significant difference in platelet count between the control and treated groups ($p > 0.05$). All treated groups showed a significant difference in at least one RBC morphological index compared to the control ($p<0.05$). The present study suggests that environmental levels of AMX may not be lethally toxic to Silver carp. However, prolonged exposure to very low concentrations may significantly affect the growth of Silver carp fingerlings and stimulate hematology. Thus, it is important to further assess AMX toxicity on fish, especially in aquaculture settings where antibiotics are frequently used and regulate its release into natural waters.

Keywords: Amoxicillin, Antibiotic toxicity, Silver carp, Growth, Hematology

Acknowledgement: Department of Zoology and Environment Sciences, University of Colombo.

Drivers of human-leopard encounters in Ambagamuwa, central highlands of Sri Lanka

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Panthera pardus kotiya is a subspecies of leopard endemic to Sri Lanka. The leopard is categorized as a locally and globally endangered species. Its population decline across the island is mainly attributed to habitat loss, but increased fatalities from human-leopard encounters are also a serious concern. The Nuwara Eliya district in the Central Highlands has been a hotspot for leopard fatalities. Twenty-one leopard fatalities have been reported in Ambagamuwa (AB) from 2015 to 2023. Here we examine the possible drivers of the leopard counters in the hill country using data from three tea estates in AB falling within the hotspot and comparing it with that in the Morningside (MS) tea estate, where leopards are encountered. Still, no fatalities have been reported during the period. Based on the premise that encounters are driven by the lack of habitat (forest) and/or prey, AB and MS would differ in (i) the extent of forest cover and (ii) consumed prey types. Analysis using Fragstat showed that in an area of 10 km^2 in each site, AB supported much smaller and more fragmented forests than MS (mean size of a patch: AB = 4.97 ha, MS = 5.76 ha) in 2023. Scat analysis of the leopards at both sites showed that they preferably consumed forest prey with only a minor fraction in AB feeding on domestic prey. But differences were evident in preferred prey types: greater prey diversity in AB (10 prey species), with Indian porcupines (21.4%), barking deer (17.9%), and mongoose (17.9%) being preferred. In contrast, in MS only seven prey species were recorded, with sambar (28.6%) and purple-faced langur (28.6%) being preferred. These findings demonstrate that managing human-leopard encounters in the hill country requires collaborative efforts involving state authorities and estate administration to protect all remnant forest patches in the hill country that could serve as refuges for leopards. Leopards feeding on forest prey is beneficial since the risk to domestic species from leopards is low. These initiatives would facilitate human-leopard coexistence, ensuring the survival of leopards.

Keywords: Prey, Eastern Sinharaja, forest fragmentation, wildlife conflict, coexistence

Acknowledgement: Department of Zoology and Environment Sciences of University of Colombo is acknowledged for funding and the facilities provided.

Ecological study of mosquito breeding sites in Dunumdalawa forest, Kandy, Sri Lanka: Implications for mosquito control

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Mosquitoes are a widely distributed, epidemiologically important group of insects of the order Diptera and family Culicidae. Many mosquitoes in tropical countries, including Sri Lanka, are important vectors of pathogens. *Anopheles, Culex, Aedes* and *Mansonia* are major vectors of devastating human diseases such as Malaria, Japanese Encephalitis and Dengue. Understanding the distribution of vector mosquitoes in a densely populated area is important for public health authorities to assess the potential risk of human infections and implement appropriate control measures. Therefore, the objective of the present study was to investigate mosquito breeding habitats in Dunumadalawa Forest, Kandy, Sri Lanka. Water samples were randomly collected from the positive and potential breeding sites in seven sampling sites, i.e., Pine tree forest patch, natural forest patch near pine trees, Invasive plant area: *Myroxylon balsamum,* left side from the Rosnith Lake, Invasive plant area: *Myroxylon balsamum,* right side from the Rosnith Lake, *Myroxylon balsamum* removed area, Natural Forest area, Natural Forest area near entrance. Some of the weather-related parameters and physical parameters of breeding sites were recorded in the field. Collected water samples were used to measure water quality parameters. Collected larvae were identified using standard mosquito larvae identification keys based on the external morphological features. Fifty-nine *Culex* species were found in positive breeding sites across seven distinct locations. There were strong correlations between larvae counts and water quality parameters, especially Total Dissolved Solids (TDS) and conductivity (correlation coefficient = 0.7). Water temperature also significantly influenced larvae counts, with a 1°C increase correlated to a 0.896 rise in larvae count. The study highlighted the importance of managing water quality and the physical characteristics of breeding sites for effective mosquito control, highlighting implications for public health in the region.

Keywords: Dunumadalawa, *Anopheles, Culex, Aedes, Mansonia*

Acknowledgment: Officer-in-Charge and the staff at the Dunumadalawa Forest Reserve and the staff at the Department of Zoology, the Open University of Sri Lanka, Kandy Regional Centre are greatly acknowledged.

Assessing the embryonic toxicity of Tributyltin, at environmentally relevant concentrations in Sri Lanka, using the Fish Embryo Acute Toxicity (FET) Test

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Tributyltin (TBT) is a highly toxic organotin compound used in antifouling paints for boats, resulting in its widespread presence in water and sediment. A recent study in Sri Lanka has detected TBT levels as high as 303 ng/L in coastal waters. This study aimed to assess the embryonic toxicity of these particular TBT levels, employing the FET test in line with The Organization for Economic Cooperation and Development (OECD) Guidelines (No. 236) for Testing of Chemicals. Zebrafish embryos (n=20) were exposed to a series of concentrations of Tributyltin, starting from 3.1- 300 ng/L along with distilled water and ethanol as the negative and vehicle control respectively for four days in 24-well microtiter plates. Each setup was duplicated, and each solution was renewed daily. At the 24-hour mark, the embryos were observed to detect coagulation, non-detachment of the tail, and lack of somite formation, whereas at 48, 72, and 96-hour marks, coagulation, lack of heartbeat, and hatchability were observed. Except for hatchability, the rest of the observations were used as toxicological endpoints to determine embryo mortality. LC_{50} values were calculated using the probit method in the SPSS 20.0 package. One-way analysis of variance (ANOVA) followed by Tukey's multiple comparison post hoc was used to identify the significant differences between the groups. The LC_{50} value at 24 hours, 411.99 ng/L, was significantly reduced ($p<0.05$) to 338.51 ng/L at 96 hours. 200 ng/L and 300 ng/L TBT caused significantly higher ($p<0.05$) cumulative mortalities at all time intervals. They also significantly increased the hatchability of zebrafish embryos at 48 and 72-hour marks ($p<0.05$). Therefore, exposure of zebrafish embryos to environmentally relevant concentrations of TBT resulted in a time and concentration-dependent toxicity. Hence, this study warrants further research into investigating its toxicity, as well as measures to monitor its levels.

Keywords: Tributyltin, Zebrafish, OECD, hatchability, embryotoxicity

Patterns and variations of diurnal and nocturnal incubation behaviour of a ground-nesting waterbird, the Red-Wattled Lapwings (*Vanellus indicus*)

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Most ground-nesting birds do not build a well-insulated nest. Therefore, they exhibit specific incubation behaviour to maintain optimal egg temperatures (~37 ^{0}C) despite fluctuating environmental conditions (temperature could vary between 20 ^{0}C – 50 ^{0}C). To study these patterns of incubation behaviour, we studied the variation of the ground, air and egg temperature against the incubation behavior of Red-wattled Lapwing (*Vanellus indicus*). The study was carried out from July 2023 to March 2024 at six different locations across the wet, dry, and arid zones of Sri Lanka with 14 lapwing nests. Data collection involved a custom-built automated thermal-sensing data logger recording egg and surrounding temperatures (+/- 0.5 ^{0}C) in every 10 minutes, complemented by a camera system documenting parental behaviour. The predominant incubation behaviours observed were "Light Sitting," "Tight Sitting," and "Shading" as described in other literature. Light Sitting was the most frequently observed behaviour, occurring both day and night across a broad range of ground temperatures. Tight Sitting significantly increased at night. Shading behaviour began in the afternoon, coinciding with high air and ground temperatures. Daytime behaviour differs with mean frequency of 33.85 ± 3.34 for Light Sitting, 0.2 ± 0.41 for Tight Sitting, and 15.75 ± 2.15 for Egg Covering (One-way ANOVA: $P < 0.05$). The nighttime behaviours also showed significant differences, with mean frequency of 35.20 ± 3.02 for Light Sitting and 20.80 ± 2.93 for Tight Sitting (One-way ANOVA: $P < 0.05$). Significant differences in behaviours were also seen between the day and night times (Post-hoc Tukey tests: $P = 0.05$). The study highlights the adaptive incubation behaviours shown in these lapwings in maintaining egg temperature homeostasis that leads to successful incubation and reproductive success.

Keywords: Ground-nesting birds, Incubation behaviour, Temperature homeostasis, Thermal ecology

Acknowledgement: This study was supported by the Department of Zoology and Environment Sciences, Faculty of Science, University of Colombo. We are thankful to all the field assistants for their help in the field.

Assessment of landscape and railway features associated with elephant-train collisions

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Railway ecology addresses the adverse impacts of railways on biodiversity. Train-related elephant mortality is a threat to elephant conservation and is of socio-economic significance. We investigated correlates of elephant-train collisions in Sri Lanka, assessing specific landscape and railway-related features along four selected railway lines: Maho-Gal Oya, Gal Oya-Batticaloa, Gal Oya-Trincomalee, and Maho-Anuradhapura. Details of elephant-train collisions from 2010-2023 were obtained from the Department of Wildlife Conservation and Sri Lanka Railways. Data on landscape features at 86 collision locations, railway-related features at 56 collision locations and both at 30 random locations along the railway line within elephant range, were recorded, using Google Earth Pro images, ArcGIS 10.8 software, and ground-truthing. Data collected included distances to the nearest water source, protected area, railway station before and post-collision, and curved sections of the railway line. Mann-Whitney U tests were conducted to assess the significance of differences between collision and random locations. The analysis indicated significant differences ($p<0.05$) for protected areas and railway stations located before incident points. Collision locations were closer to protected areas than non-collision points (median: 0.03 km versus 0.82 km) and farther from railway stations before collisions (median: 8.43 km versus 5.86 km). Contrary to popular belief, the findings suggest that elephants accessing water sources and lack of early detection of elephants due to curvature of the railway line, were not associated with collisions. Proximity to protected areas increased collision risk, possibly indicating greater use of such areas by elephants. Collisions were higher at a greater distance from the railway station, which was its previous stop, perhaps indicating that the speeds of trains are a contributory factor to collisions. The study emphasizes the necessity of targeted interventions in high-risk areas to mitigate collisions between elephants and trains.

Keywords: Elephants, Train collisions, Water sources, Protected areas

Acknowledgment: The Department of Zoology and Environment Sciences, Faculty of Science, University of Colombo is acknowledged for funding.

Preliminary molecular phylogeographical analysis of the endemic freshwater fish *Belontia signata* (Anabantoiformes: Belontiinae) in three river basins of Sri Lanka

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Ceylonese Combtail (*Belontia signata*) is primarily a Wet zone endemic species in Sri Lanka, although there is an isolated population in the Mahaweli River, which drains across the Dry zone. It is the only genus of subfamily Belontiinae occurring in Sri Lanka. So far, only one molecular study has been reported involving this species. Freshwater fishes are prone to develop intraspecific variations, based on various attributes of the river they inhabit. However, the status of this species inhabiting country's multiple river basins has not been assessed yet. Therefore, this study conducted a molecular phylogeographical and phenotypic analysis of *Belontia signata* by investigating the populations in three rivers; Gin, Kelani, and Mahaweli. Their phylogeny was reconstructed based on the mitochondrial cytb gene region of the captured samples using Maximum Likelihood (ML) and Maximum Parsimony (MP) inferences. The molecular analysis revealed, indeed that the three *Belontia signata* populations were genetically different, with the Gin River population being the most genetically divergent. It was also shown that the Kelani and Mahaweli river *Belontia* populations were from the same genetic cluster, while the Mahaweli population had undergone a recent split. The phenotypic analysis was conducted for the samples (n=11) through Principal component analysis (PCA) and the Permutational multivariate analysis of variance (PERMANOVA) statistical technique using the R platform. The PCA of the morphometric data coincided with the phylogenetic findings, whereas the meristic data failed to exhibit any significant variation among populations ($P>0.05$). The PERMANOVA test results also showed that the Mahaweli population was the most divergent out of all, in terms of the morphometric data ($P<0.05$). Although the present study will be beneficial for the understanding of the differentiation of extant Ceylon Combtail populations, further larger sample size is required for extensive validation of the obtained results.

Keywords: Ceylonese Combtails, mtDNA, Freshwater fish, Phylogeny, Phenotypical analysis

Acknowledgement: Department of Zoology and Environment Sciences, Faculty of Science, University of Colombo

Variation of non-volant mammalian communities along a sub-montane elevational gradient in Sri Lanka

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A group of mammals consisting of populations of individuals with direct and indirect interactions is called a mammalian community. Elevational gradients profoundly affect such mammalian communities, shaping diverse patterns across altitudinal ranges. To investigate these elevation-associated effects on non-volant mammalian communities and to understand the factors driving these variations, we studied the elevational gradient from the Samanalawewa basin (480 meters Above Mean Sea Level) to Hawagala Peak (1420 AMSL) within the Issengard Biosphere Reserve, Belihuloya, in the Sabaragamuwa Province. Data collection, including camera trapping, scat and pellet sampling, small mammal sampling, and opportunistic observations, were conducted from November 2021 to April 2024 along 10, 50m transects along the contour lines in every 100m intervals spanned along the one-kilometer elevational gradient. A total of 20 mammal species were recorded during the study period. The mammalian community parameters considered were total abundance, average abundance, species richness, and Shannon and Simpson diversity indices. Scatter plot analysis indicated that all five community parameters exhibit a curved relationship with elevation. Spearman correlation revealed low negative correlations for total abundance and average abundance with the elevational gradient, and low positive correlations for other parameters. None of the community parameters showed a significant correlation with elevation ($p>0.05$). All five community parameters exhibited hump-shaped variation patterns along the elevational gradient, indicating the mid-domain effect. However, there was a significant and unexpected decline in all parameters between 1000 m and 1200 m elevations probably due to the high steepness and predominantly grassland habitat in this region. All parameters showed low values at lower elevations, highlighting the negative anthropogenic effect towards mammalian communities, as the low elevation range is dominated by human activities, including hunting.

Keywords: Community parameters, Elevational gradient, Issengard Biosphere Reserve, Mid-domain effect, Belihuloya

Acknowledgment: This study was supported by the Department of Zoology and Environment Sciences, Faculty of Science, University of Colombo. We extend our gratitude to all the field assistants for their invaluable help during the fieldwork.

Spatiotemporal distribution of seabirds in the Western EEZ of Sri Lanka determined using eBird: A Global Citizen Science Platform

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Citizen science is a growing branch of public participation in scientific research, where individuals contribute to data collection and monitoring, thereby enhancing scientific knowledge at local and global scales. With nearly a million contributors and 1.6 billion bird observations, eBird (www.ebird.org) is the largest global citizen science platform available for ornithology. Seabirds are among the most studied groups of birds globally, yet they remain the least studied in Sri Lanka. To fill this gap, eBird Data was used from 2010 to 2024 to study the spatiotemporal variation of seabirds in Sri Lanka's maritime zone called the Exclusive Economic Zone (EEZ). Analyses were implemented using VBA applications in Excel and RStudio. From January 2010 to January 2024, eBird recorded 17,293 valid seabird observations in the Western Zone of our EEZ, spanning from Mannar to Beruwala. Mannar had the highest percentage of observations at 47.6%, while Kalutara had the lowest at 1.1%. Both pelagic and coastal species of terns and gulls dominated the observations, accounting for 98.4% of the records. Northern Hemisphere migrants were most frequently recorded from September to April, and Southern Hemisphere migrants from May to September. Colombo and Mannar have the highest seabird diversity, followed by Gampaha. Kalutara had the lowest diversity, probably due to the lower number of sea-watchers in the area. Through the Avian Diversity Indices analysis, Puttalam ranked highest in Shannon and Pielou indices, indicating a high number of species and a uniform distribution of individuals. Mannar exhibited strong diversity metrics, particularly in the Margalef index, suggesting high species richness. These findings highlight the crucial role of citizen science initiatives such as eBird in filling research gaps in poorly studied and poorly understood groups of taxa like marine birds. Even though expensive and logistically challenging, these data underscore the need for more comprehensive seabird studies in Sri Lanka's EEZ.

Keywords: Citizen Science Platforms, eBird, Exclusive Economic Zone (EEZ), Pelagic Seabirds, Spatiotemporal Variation

Assessment of pollution impacts in selected tributaries reaching lower reaches of Kelani River using physicochemical monitoring and biomarker response of caged Slender Rasbora (*Rasbora daniconius* (Hamilton,1822))

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The pollution of freshwater lotic ecosystems is a significant environmental issue. This study examines pollution impacts on freshwater communities in selected tributaries of the lower Kelani River, employing a methodology that integrates physicochemical monitoring and cellular level biomarker responses in the caged indigenous fish species Slender Rasbora (*Rasbora daniconius* (Hamilton, 1822)). Two cages were dipped in the water column at each site, and fish (08) were randomly selected for introduction to each cage. Surface water samples were collected for physicochemical monitoring from two tributaries of Kelani River at Ruwanwella and Biyagama on the 01st and 07th days of the caged exposure. One sample t-test and one-way ANOVA were used for statistical analysis for spatiotemporal comparisons of physicochemical parameters and biomarker responses, and the accepted significance level is 0.05. Physicochemical monitoring revealed that measured surface water quality parameters in Biyagama and Ruwanwella respectively, viz., Temperature (26.8 ±0.6 & 29.3 ± °C), TDS (10.8 ± 1.8 & 204.1 ± 83.4 ‰), conductivity (23.4 ± 4.6 & 422.1 ± 168.3 μS/cm), BOD_5 (0.5 ± 0.1 & 2.3 ± 0.7 mg/L), COD (2.0 ± 0.9 & 4.7 ± 2.8 mg/L), total phosphate (0.2 ± 0.1 & 0.3 ± 0.1 mg/L), nitrate-N (0.3 ± 0.1 & 1.2 ± 0.1 mg/L) were significantly different in day 01 and 07 ($P < 0.05$). Statistical analysis showed a significant increase in erythrocyte nuclear abnormalities on day 07 at Ruwanwella (7.2±1.03) and Biyagama (11.36±1.68) compared to day 01 at Ruwanwella (2.58±0.3) and Biyagama (2.61±0.3) indicating that prolonged exposure at the same site increased pollution-indicative biomarker responses. For the first time in Sri Lanka, this study demonstrates the utility of caged culture in ecotoxicological studies. The findings emphasize the suitability of *R. daniconius* as a surrogate species for biological monitoring and the applicability of cage culture methodologies to pollution impact assessment in inland lotic freshwater bodies in Sri Lanka. In conclusion, the present study highlights the importance of comprehensively integrating physicochemical and biomarker analyses to evaluate pollution impacts on freshwater ecosystems. It establishes a robust framework for environmental monitoring and contributes to the conservation and management of freshwater resources.

Keywords: Kelani River tributaries, Indigenous fish, physicochemical monitoring, nuclear abnormalities, freshwater conservation.

Cytogenotoxic effects of tartrazine, a food colouring agent, on *Allium cepa* root meristematic cells

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Synthetic food colouring agents, such as tartrazine (E102), are frequently used in the food industry, raising concerns about their potential toxicity. This study investigates the cytotoxic and genotoxic impacts of tartrazine on *Allium cepa* root meristem cells. Healthy *A. cepa* bulbs were exposed to various concentrations of tartrazine (0.8, 4, 20, 100, and 500 ppm/mgkg^{-1}) for 24 hours, with dechlorinated water as a negative control and 5% dimethyl sulfoxide (DMSO) as a positive control. The doses were selected based on concentrations commonly used in commercial products and prepared according to standard laboratory protocols. Root growth was measured, and chromosomal aberrations were observed under the light microscope and analysed after staining with acetocarmine. Tartrazine significantly inhibited root growth and increased chromosomal aberrations in a dose-dependent manner ($p < 0.001$). ANOVA revealed a significant effect of concentration on root length ($F_{1, 58} = 109.4$, $p < 0.001$), with post-hoc Tukey's HSD tests indicating significant differences between each concentration and the control ($p < 0.001$). Pearson's correlation showed a significant negative correlation between concentration and mitotic index ($r = -0.351$, $p = 0.0059$). The half-maximal effective concentration (EC_{50}) was estimated at 257.37 ppm/ mgkg^{-1}. The Kruskal-Walli's test indicated significant differences in mitotic index among concentrations ($\chi^2 = 48.985$, df = 5, $p < 0.001$). Spearman's rank correlation demonstrated a perfect positive monotonic association between concentration and phase indices ($\rho = 1$, $p = 0.01667$). Chromosomal aberrations such as sticky metaphase, C-mitosis, apoptosis, necrosis, numerical aberrations, and anaphase bridges were prominent at higher concentrations. Tartrazine exhibits significant cytotoxic and genotoxic effects on *A. cepa* root meristem cells, highlighting potential health risks associated with its consumption. Since many food items, such as soft drinks and sports drinks, flavoured potatoes, sauces, ice cream, jellies, chewing gum, fruit cordials, and instant puddings use tartrazine as a dye, it is recommended to find natural alternatives for safe consumption. These findings underscore the need for stringent regulatory measures to limit tartrazine use in food products.

Keywords: Tartrazine, *Allium cepa*, cytotoxicity, chromosomal aberrations, food colorant

Evaluating the cytogenotoxicity of Stevia, a food sweetener, using *Allium cepa* assay

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Stevia is a widely utilised natural sweetener due to its intense sweetness and low-caloric profile and, is derived from the plant *Stevia rebaudiana*. Despite its widespread use and recognition as being safe by food safety authorities, stevia is often questioned for its potential cytotoxicity and genotoxicity. This study utilised the *Allium cepa* assay, a reliable and cost-effective method free of spontaneous chromosomal damages to assess stevia's cytotoxic and genotoxic effects. Fresh, healthy *A. cepa* bulbs were tested for commercially available stevia concentrations of 0.1, 1.0, 10, 100, and 1000 ppm/ $mgkg^{-1}$, with distilled water as the negative control and 5% DMSO as the positive control. Chromosomes were visualised with acetocarmine to analyse chromosomal aberrations and to calculate mitotic index (MI). Results indicated a significant reduction in root lengths with increasing stevia concentrations ($p<0.001$, Kruskal-Wallis), with the highest concentration (1000 ppm/$mgkg^{-1}$) showing higher inhibition compared to the control. The MI decreased significantly ($p<0.001$, Kruskal-Wallis) in a dose-dependent manner, dropping to 2.01 ± 0.25 at 1000 ppm/ $mgkg^{-1}$ from a control value of 27.6 ± 0.67. Higher stevia concentrations also led to substantial increases in chromosomal aberrations and cell death indicators, particularly at 1000 ppm/ $mgkg^{-1}$, suggesting strong cytotoxic and genotoxic effects. These findings align with previous studies, highlighting the need for cautious use of stevia in food products. The *A. cepa* assay proved effective in highlighting stevia's cytogenotoxic impacts, suggesting that while lower concentrations may be relatively safe, higher concentrations pose significant risks. Regulatory agencies should consider re-evaluating acceptable daily intake levels to ensure consumer safety. Further research is necessary to fully understand long-term implications of stevia consumption.

Key words: Steviol glycosides, Natural sweetener, Cytotoxicity, Genotoxicity, *Allium cepa* assay

ABSTRACTS – POSTER PRESENTATIONS

Exploring laccase producing fungi isolated from freshwater ecosystems in the Anuradhapura and Ratnapura Districts, Sri Lanka

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Laccases, classified as blue multicopper oxidases, catalyze the one-electron oxidation of a wide range of substrates and play a crucial role in lignin degradation. Fungal laccases can degrade lignin in plant materials and are used in the decolorization and detoxification of effluents from industrial discharges, such as those from the food, textile, paper, and plastic industries, that pollute water. This is because fungal laccases have a higher redox potential compared to bacterial laccases. The aim of this study was to isolate fungi from lentic and lotic freshwater habitats in the Anuradhapura and Ratnapura districts of Sri Lanka and to identify laccase-producing fungi. Single spore isolation (for saprobes) and surface sterilization method (for endophytes) were used to isolate the fungi. All isolates underwent morphological (macro and micromorphological characteristics), colony characteristics, and molecular characterization based on ITS gene region. The identification of laccase-producing fungi among 20 isolates involved qualitative analysis with 1-naphthol solution. Positive results were indicated by blue-purple coloration around the colony growth. Out of the 20 isolates, 14 fungal species showed laccase production, including *Aureobasidium melanogenum, Colletotrichum truncatum, C. siamense, Coniochaeta velutina, Lasiodiplodia pseudotheobromae, Microdiplodia* sp., *Montagnula donacina, Nemania primolutea, Neopestalotiopsis saprophytica, Neottiosporina mihintaleensis*, *Paraconiothyrium archidendri, Phyllosticta capitalensis, Rhytidhysteron neorufulum,* and *Talaromyces verruculosus*. Among these, *Neottiosporina mihintaleensis* showed the highest laccase production, represented by a 3.5 cm diameter blue-purple circle around the colony. The other isolates (*Chaetomella raphigera, L. crassispora, Lentinus tigrinus, Talaromyces stipitatus, Trichoderma harzianum,* and *T. koningii*) did not show laccase production. These identifications provide valuable insights into future biotechnological approaches for fungal applications.

Keywords: 1-naphthol, biotechnological applications, extracellular enzymes, lignin degradation, *Neottiosporina mihintaleensis*

Acknowledgements: This work was supported by the Science and Technology Human Resource Development Project, Ministry of Higher Education, Sri Lanka, funded by the Asian Development Bank and Tropical Microbiology Research Foundation. Darbhe J. Bhat and Turki M. Dawoud gratefully acknowledge the financial support under the Distinguished Scientist Fellowship Programme (DSFP) at King Saud University, Riyadh, Saudi Arabia.

Physicochemical characterization and evaluation of the antimicrobial activity of silver nanoparticles biosynthesized by marine brown algae *Padina commersonii.*

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Nanotechnology explores materials at the nanoscale (1-100 nm), which exhibit unique properties due to increased surface area. Silver nanoparticles (AgNPs) are recognized for their conductivity, stability, and therapeutic potential. Green synthesis of AgNPs provides an ecofriendly alternative using bioactive compounds from marine algae like *Padina commersonii*, an edible brown alga along Hikkaduwa coast of Sri Lanka. This study aims to synthesize silver nanoparticles using *Padina commersonii*, characterize them, and assess their antimicrobial efficacy. Silver nanoparticles were synthesized by mixing the crude methanol extract of *Padina commersonii* with silver nitrate. Characterization was performed using UV-Vis spectroscopy, Dynamic Light Scattering (DLS), Zeta potential analysis, Scanning Electron Microscopy (SEM), Energy Dispersive X-ray (EDX) analysis, X-ray Diffraction (XRD), FTIR spectroscopy, and Raman spectroscopy. A color change from pale yellow to reddish-brown within 48 hours indicated nanoparticle formation. UV-Vis spectrophotometry showed a surface plasmon resonance band peak at 424 nm, confirming the presence of AgNPs. DLS analysis revealed an average size of 73.19 nm, with zeta potential indicating stability at -21.5 mV. SEM images depicted spherical nanoparticles with smooth surfaces and no aggregation. EDX analysis confirmed 19.5% silver content by weight, and XRD analysis indicated a face-centered cubic structure and crystallinity. FTIR and Raman spectroscopy identified proteins, phenolic compounds, and amines as capping and stabilizing agents, while polyphenolic compounds and flavonoids acted as reducing agents. The antimicrobial potential of silver nanoparticles synthesized using *Padina commersonii* against bacterial strains *Staphylococcus aureus* (12.77 ± 0.58 mm), *Escherichia coli* (15.27 ± 0.58 mm), and fungal strains *Aspergillus niger* (18.10 ± 0.15 mm) and *Candida albicans* (17.43 ± 0.57 mm) was greater than that of the crude extract of *Padina sp.* (*S. aureus* = 11.17 ± 0.29 mm, *E. coli* = 10.50 ± 0.50mm, *A. niger* = 12.66 ± 0.10mm, *C. albicans* = 15.66 ± 0.10mm). These silver nanoparticles produced through an ecofriendly green synthesis method offer a therapeutic approach to treat bacterial and fungal infections and diseases.

Keywords-Silver nanoparticles; Characterization; *Padina;* Antimicrobial

Foliose lichens as essential hosts for Lichenicolous Fungi: Insights from Horton Plains, Sri Lanka

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Lichenicolous fungi, which exclusively inhabit lichen thalli, can be parasitic adversely affecting lichen growth or benign, simply finding a niche. Typically found on the upper surfaces of their host lichens, these fungi often manifest as discolored patches or oddly colored spots, indicating the development of fruiting structures. In this study, we investigated the diversity of lichenicolous fungi within Horton Plains National Park (HPNP), a region in Sri Lanka's Central Province, located at an elevation of 2100-2300m, which provides an ideal environment for lichen growth. Corticolous lichens showing signs of lichenicolous growth were collected across 22 localities along the trail to World's End from the park entrance. Lichen samples were identified using morphological characteristics and standard chemical methods. Each lichen thallus was meticulously examined under a stereoscopic microscope to identify lichenicolous fungi, focusing on discolorations, oddly coloured patches, and unique fruiting structures distinct from the host lichens. Based on those morphological differences, our observations revealed 15 different species of lichenicolous fungi and most of them are lichenicolous Basidiomycota. The majority (80%) of host lichens supporting lichenicolous growth were foliose, with the remainder being fruticose, squamulose, or crustose. Among the foliose lichens, species from the genera *Parmotrema, Heterodermia, Cococarpia,* and *Lobaria* were the most common hosts for lichenicolous fungi. These findings highlight that the HPNP area is rich in lichenicolous fungi, with foliose lichens serving as the primary hosts. This study underscores the ecological significance of foliose lichens in supporting lichenicolous fungi biodiversity in Horton Plains National Park. Furthermore, this study helps to observe the bioactivities of the secondary metabolites of the lichenicolous fungi, offering insights into their potential applications in various fields. Also, Future DNA-based identification methods will greatly improve the discovery and classification of lichenicolous fungi at the species level. The results contribute valuable knowledge to the understanding of lichen-fungi interactions and the role of lichens in supporting diverse fungal communities.

Keywords: Lichen-Fungi Interactions, Biodiversity, Fungal Communities, Morphological Identification, Tropical Ecosystems

Acknowledgement: We would like to acknowledge the Tropical Microbiology Research Foundation (TMRF) for their funding of this project.

Bioactivity profiling of termite-associated fungus *Trichoderma virens* for antibacterial, antioxidant, and anticancer activities

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Termite mounds represent unique and complex ecosystems that host a diverse array of microorganisms, including fungi. These fungi play critical roles in the ecological dynamics of termite colonies, particularly for the termite family Macrotermitinae. Termites of the family Macrotermitinae rely on their associated fungi for the decomposition of organic matter, nutrient cycling, and essential nutrition. *Trichoderma virens* is one of these fungi associated with termites of the family Macrotermitinae. This study investigates the antibacterial, antioxidant, and anticancer activities of *Trichoderma virens* (MH857383.1) isolated from a termite mound in the Gampaha district, Sri Lanka. The fungal isolate was cultured on malt extract agar media, and the resulting extract was used for subsequent bioassays. Bioactivity assays revealed significant antibacterial activity against *Staphylococcus aureus* ATCC 25923 (MIC = 0.250 mg/mL), *Bacillus cereus* ATCC 11778 (MIC = 0.500 mg/mL), *Pseudomonas aeruginosa* ATCC 25853 (MIC = 0.625 mg/mL), and *Escherichia coli* ATCC 25922 (MIC = 0.250 mg/mL). The DPPH radical scavenging assay was used to assess the antioxidant activity of the fungal isolate and resulted in an IC50 value of 344 µg/mL, demonstrating strong free radical scavenging properties. The anticancer activity of the *Trichoderma virens* isolate was assessed by L-asparaginase enzyme activity, indicating its potential application in treating cancers such as acute lymphoblastic leukemia. Thin-layer chromatography was used to assess the fungal extract and revealed the presence of multiple secondary metabolites. Subsequently, the extract was fractionated using solvent-solvent extraction into four fractions: hexane, chloroform, ethyl acetate, and aqueous. These fractions were then evaluated for their antibacterial properties, and the chloroform and ethyl acetate fractions exhibited broad-spectrum antibacterial activity, corroborating the initial bioactivity findings. These results highlight the comprehensive bioactive potential of *Trichoderma virens*, emphasizing its promise as a source of antibacterial, antioxidant, and anticancer agents, with potential applications in pharmaceutical and industrial fields.

Keywords: Secondary metabolites, Termites, Bioactivity, *Trichoderma virens,* Chemical analysis

Investigation of potential bioactive properties of macrofungi isolated from Anawilundawa wetland sanctuary, Sri Lanka

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Macrofungi are distinguished by their highly diverse fruiting bodies, allowing them to adapt to various ecological niches and perform essential roles in ecosystems, while serving as a repository of bioactive compounds in pharmaceutical and food industries. Anawilundawa, one of the Ramsar wetlands in Sri Lanka, provides favorable habitats for macrofungi with the combination of freshwater, saltwater, and terrestrial ecosystems. In this study, 42 macrofungi were collected from the Anawilundawa wetland sanctuary between October 2023 and January 2024 using random opportunistic sampling method. The collection comprised species from 5 orders of Phylum Basidiomycota including Agaricales, Auriculariales, Boletales, Cantharellales, Polyporales, and 3 species of Ascomycota. The macrofungi were cultured on PDA media, yielding 14 isolates. Bioassays were conducted using ethyl acetate crude extracts of isolates and methanol crude extracts of fungi. Antibiotic activity was investigated via the disk diffusion method, and isolate obtained from *Daldinia* sp. (As1L9) exhibited inhibition zones against both gram-positive *Staphylococcus aureus* and gram-negative *Pseudomonas aeruginosa*, showing the inhibition zones of 35.333 ± 0.577 mm and 31.333 ± 0.577 mm respectively. The methanolic extract of *Fulvifomes* sp. (P2L2) demonstrated the highest antioxidant activity through the DPPH scavenging assay, with the lowest IC50 value (9.277 ± 0.305 µg/mL) and the highest total phenolic content (2346.778 ± 1.06 µg/mL) for the same sample determined by the Folin Ciocalteu method. Total flavonoid content was examined by aluminum chloride colorimetric method, with the highest content (100.435 ± 0.495 µg/mL) found in the ethyl acetate crude extract of the isolate derived from *Daldinia* sp. To quantify antileukemic properties, L-glutaminase enzyme assay was conducted using the nesslerization method, whereas the isolate from *Peniophora* sp. exhibited the highest enzymatic activity (19.533 ± 0.825 Unit/mL enzyme). These findings demonstrate the promising potential of macrofungi as sources of bioactive compounds, encouraging further research to explore the lead compounds of crude extracts.

Keywords: Macrofungi, Bioactivities, Antibacterial, Antioxidant, L-glutaminase

Morphology, phylogeny, and pathogenicity of pestalotioid-like taxa associated with scab disease of guava in the Ratnapura District of Sri Lanka

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Scab disease, caused by pestalotioid species, significantly impacts guava cultivation by reducing fruit quality and yield. These fungi exhibit complex and overlapping morphological traits, complicating their classification. This research aims to bridge this gap by identifying various morphotypes and establishing their pathogenic relationships through comprehensive morphological and molecular analyses. A total of 35 trees were sampled from 25 distinct locations within the Ratnapura district, including fruit and leaf specimens from eight guava varieties. The collected samples presented symptoms characterized by blackish-gray, necrotic, and brittle spots at leaf apices, alongside round to oval, brown, corky lesions on the fruit epidermis. From the 35 guava fruit samples inoculated onto Potato Dextrose Agar, 45 isolates were recovered based mainly on conidial morphology. A custom-built 'MycodataLab' data management system was developed to store and visualize data. Conidial length and width were measured for 30 conidia per isolate using custom-built software 'Sporify,' and mean values were calculated with their standard deviations. Pathogenicity tests on guava leaves and fruits showed that isolates from Morphotypes 1, 3, and 5 induced brown lesions on wounded leaves, with Morphotype 1 being the most virulent. On fruits, isolates from all three morphotypes developed symptoms, with Morphotype 1 again showing the highest virulence. From these results, three morphotypes were selected, and molecular identification was conducted using ITS, β-tubulin, and tef1- α markers. Maximum Likelihood phylogenetic analysis showed that Morphotype 3 clusters with *Pseudopestalotiopsis* species (*P. cocos* and *P. indica*), Morphotype 1 with *Neopestalotiopsis* species (*N. brasiliensis*), linked to guava scab in Colombia, and Morphotype 2 with *Neopestalotiopsis formicarum* and *N. cubana*, associated with rubber leaf fall disease in Thailand. This research emphasizes the necessity of integrating advanced molecular techniques to accurately classify and understand the pathogenic mechanisms of these fungi for effective disease management in guava and potentially other crops.

Keywords: Guava pathology, Multigene phylogenetic analysis, Conidial morphology

Unveiling and managing pathogens of Leaf Fall Disease in Sri Lankan rubber trees (*Hevea brasiliensis*)

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New Leaf Fall Disease (LFD) is a serious disease that affects rubber plantations, leading to a 30% reduction in rubber production in Sri Lanka after 2019. This disease is characterized by out-of-season leaf fall but the exact pathogen in LFD in rubber cultivations in Sri Lanka is still unknown. This study aimed to determine the pathogens responsible for LFD and to develop effective biocontrol methods for managing this disease in Sri Lanka. Diseased leaf samples were collected from rubber plantations in Kalutara and Colombo. Pathogens were isolated on Potato Dextrose Agar (PDA) through single spore isolation. After ten days of incubation, the morphology of each isolate was recorded. Pathogenicity tests involved by establishing koch's postulate, both attached and detached, and calculating Disease Index (DI) values for each leaf. DNA was extracted using a modified CTAB (Cetryltrimethylammonium bromide) method, and variations in the gene regions ITS, β-TUB, and TEF-1α were analyzed to reconstruct phylogenetic trees of the pathogens. Selected pathogens were tested for biocontrol with *Trichoderma* sp. and *Daldinia eschscholtzii* using the dual culture plate method. Percentage Inhibition of Radial Growth (PIRG%) were measured. Data were analyzed using one-way ANOVA. According to the molecular results, *Colletotrichum siamense*, *Pseudopestalotiopsis simitheae,* and *Neopestalotiopsis saprophytica* were identified as the pathogens of LFD in Sri Lanka. All isolates, except the control, showed varying pathogenicity across different inoculation methods with the highest DI value observed in leaves co-inoculated with *C. siamense* and *P. simitheae* under wounded conditions. *Daldinia eschscholtzii* effectively controlled both *C. siamense* and *P. simitheae*, with PIRG% over 50%. *Trichoderma* sp. showed limited control, inhibiting *P. simitheae* in two out of three replicates with PIRG% above 50%. In conclusion, newly emerged leaf fall disease (LFD) in rubber plantations is caused by *C. siamense*, *N.saprophytica*, and *P. simitheae*, with *D. eschscholtzii* showing potential as a biocontrol agent for managing the disease.

Keywords: Biological control, Collectotrichum, Leaf Fall Disease, Pseudopestalotiopsis, Rubber

Acknowledgement: The authors acknowledge the University of Kelaniya research grant (RP/03/02/01/01/2023) for the funding.

Genome-wide identification and characterization of nodulation-related genes in soybean (*Glycine max*)

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Nitrogen fixation is a key component of the nitrogen cycle and essential for the stability of the ecosystem. Nodule development is an important component of this process and identifying the genes and molecular mechanisms underlying nodule development is important to understand the interactions between nitrogen-fixing bacteria and the plant. However, a comprehensive bioinformatic analysis of nodulation-related genes is only performed on the peanut genome. Soybean, an important legume crop, could benefit from such an analysis, leading to the development of new varieties with better nitrogen fixation efficiency. Therefore, in this study, a full-scale genome-wide analysis and bioinformatics characterization of nodulation-related genes of the soybean genome was performed using several bioinformatics tools such as BLAST, TBtools, MEGA11, Meme Suite, and WoLF PSORT server. Known nodulation-related gene sequences from peanut (*Arachis hypogaea),* barrel medic (*Medicago truncatula)*, and chickpea (*Cicer arietinum)* were used to search the soybean Wm82.a2.v1 genome. This unraveled 54 soybean nodulation-related genes that were unevenly distributed on 18 chromosomes except the 3rd and 13th chromosomes. According to the phylogenetic tree and synteny analyses, a majority of the identified soybean genes were highly homologous to peanut genes. The comparison of domain and motif patterns with phylogenetic trees revealed that members of the same clades have similar domain architectures. The cis-acting element analysis revealed that the expression of these nodulation-related genes is regulated by phytohormones and biotic and abiotic stresses, and these genes may modulate plant responses associated with various stages of nodulation. Gene ontology analysis revealed potential gene functions, which were directly or indirectly associated with the nodulation process. To our knowledge, this is the first instance of a full-scale genome-wide analysis of all nodulation-related genes is performed on soybeans. Therefore, these results can be used for crop improvement, sustainable agriculture, and genetic improvement of soybeans focusing on nodulation.

Keywords – Soybean, Nodulation-related genes, Symbiotic, Model legumes, Bioinformatics tools

Genome-wide analysis and characterization of the LysM-RLK gene family in *Oryza sativa*

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Rice (*Oryza sativa*) is a vital crop, feeding over half of the global population. Its role in food security is crucial, especially amid rising population pressures and climate change. Microbes significantly impact rice plants through both pathogenic and symbiotic interactions, affecting plant health, growth, and yield. Among the key gene families involved in plant-microbe interactions are LysM receptor-like kinases, which recognize microbial signals and initiate plant responses. Despite their importance, a comprehensive genome-wide analysis of LysM-RLKs in rice has not been conducted, leaving a gap in understanding their role in rice defense and symbiosis. Through a bioinformatics analysis, we identified 10 LysM-RLK genes in the rice genome, located on six different chromosomes. Comparative genomic analysis with *Arabidopsis thaliana*, *Medicago truncatula*, *Zea mays* and *Triticum aestivum* revealed homology relationships. Phylogenetic analysis grouped these genes into four clades. The subcellular localization analysis revealed that all LysM-RLK genes were localized to the plasma membrane, which confirms their roles in pathogen recognition and signal transduction. The gene ontology enrichment highlighted roles in signal transduction, molecular binding, receptor activity and immune responses. The gene structure analysis revealed significant variations in intron and exon distributions among LysM-RLK genes. Motif analysis revealed four common (motifs 1, 3, 5, and 6) among the rice LysM-RLK sequences. The GRAVY index of some proteins was negative, indicating their hydrophilic status. The cis-acting regulatory element (CREs) analysis revealed 64 putative CREs besides common CREs such as TATA-box and CAAT-box. Most of these CREs belonged to light and hormone-responsive elements. Overall, this study enhances the understanding of the structural, functional, and regulatory aspects of the LysM-RLK gene family in rice suggesting their crucial roles in rice defense mechanisms and stress resilience, which will be beneficial for crop improvement focusing on rice-microbe interactions.

Keywords: LysM-RLKs, plant-microbe interactions, genome-wide analysis, crop improvement, bioinformatics

An assessment of the phytochemical, antioxidant, and anti-Inflammatory properties of *Tamarindus indica* fruit by *in vitro* bioassays

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Tamarindus indica, is a plant with a variety of health benefits and the fruit is often used in Sri Lankan curry dishes. This study set out to ascertain the tamarind fruit with seeds photochemical makeup, antioxidant content, and anti-inflammatory properties using six distinct extraction techniques. Previous studies have not comprehensively explored Tamarind fruit's bioactivity using all six extraction techniques. The tamarind fruit was collected from the Puttalam district and was air dried, powdered, and sieved and was extracted by six different methods: as a hot water extract (HWE) at 100°C for 3h and 1.5h; at 60°C for 1.5h; as a macerated extract with water and ethanol for 72 h; and as an autoclaved extract at 115°C. Out of which the hot water extracts have been used traditionally as a medicine. All six samples were subjected to various bioassays; total phenolic content (TPC), total flavonoid content (TFC), antioxidant assays: DPPH, (2,2-diphenyl-1-picryl-hydrazyl-hydrate), ABTS (2,2'-azino-bis(3-ethylbenzothiazoline-6-sulfonic acid)), anti-inflammatory assays: human red blood cell (HRBC) membrane stabilization and protein denaturation assays. The macerated ethanol sample demonstrated the highest values for TPC (25.10 mg GAE/g extract) and TFC (329.38 mg QE/g extract) out of all extracts. The ethanol sample had the most radical scavenging for ABTS (59.12%), whereas the HWE at 3h sample had the highest radical scavenging for DPPH (63.72%) at 1mg/ml. The ethanol sample had a marginally lower value of 55.24% at 1 mg/ml for DPPH. The ascorbic acid positive control demonstrated 81.84% for ABTS and 82.76% for the DPPH test at 1mg/ml. In the HRBC assay, the ethanol sample demonstrated the greatest anti-inflammatory inhibition at 64.20%, whereas the positive control, ibuprofen, displayed a value of 83.52±0.56% at 1mg/ml. In the protein denaturation assay, the ethanol sample demonstrated an inhibition of 72.74% (Ibuprofen, 83.20±0.10%) at 1mg/ml. This study demonstrates that the ethanol extract of tamarind fruit seeds exhibits the most potent bioactivity across multiple assays, highlighting the need for further investigation.

Keywords: Tamarind fruit, Plant-based traditional medicine, Bioassays, Antioxidant activity, Anti-inflammatory activity.

Acknowledgement: The authors would like to thank the National Research Council (Grant Number MPG 21-10) of Sri Lanka for their financial support.

SNP marker diversity in black pepper (*Piper nigrum* L.)

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Single nucleotide polymorphism (SNP) markers play a key role in understanding genetic diversity and enhancing crop traits, particularly in non-model crops, such as black pepper (*Piper nigrum* L.), which is globally valued as one of the most important spices. This study aimed to assess SNP marker diversity in black pepper using publicly available next-generation sequence datasets. A total of 30 raw sequence read files, comprising 16 derived from RNA sequencing (RNA-seq) of Chinese black pepper accessions and 14 from restriction site-associated DNA sequencing (RAD-seq) of Sri Lankan black pepper accessions, were retrieved and mapped to the black pepper genome. Using BCFtools, Genome Analysis Toolkit (GATK) with soft-filtering, and GATK with hard-filtering pipelines, a total of 498128, 396003, and 312153 SNPs were identified, respectively. Of these, 260,026 SNPs were commonly identified across all pipelines. Further, this revealed an uneven distribution of variants across the 45 scaffolds of the genome. The highest average SNP density was observed on pseudo-chromosome Pn25 (0.86 SNPs/kb), followed by Pn8 (0.74 SNPs/kb), and Pn7 (0.72 SNPs/kb). Most of the SNPs (32.54%) were in downstream regions of genes, followed by upstream (22.52%) and exonic (16.20%) regions. Among the identified SNPs, the most abundant substitution type was transitions (57.42%), with an average transition-to-transversion ratio of 1.36. Furthermore, SNPs were classified as synonymous (43.91%) and non-synonymous (56.09%), with the majority being missense mutations (53.59%). Interestingly, some of these non-synonymous variants were mapped to genes associated with alkaloid biosynthesis, highlighting their potential utility in genome-wide mapping and marker development for black pepper improvement. Collectively, the catalog of SNP markers reported in this study could aid in understanding genetic diversity and enhancing desirable traits in this important spice crop.

Keywords: SNPs, black pepper, BCFtools, Genome Analysis Toolkit

Comparative analysis of blood indices in pancreatic cancer patients with and without diabetes: a preliminary study

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Several decades of research have established a relationship between pancreatic cancer and Diabetes Mellitus. In more than 66% of pancreatic cancer patients, diabetes or impaired glucose tolerance can be seen. Hematological parameters may be used as early indicators of pancreatic cancer-associated diabetes. Therefore, this study aimed to assess the impact of diabetes mellitus on hematological parameters of patients diagnosed with pancreatic cancer. After obtaining ethical clearance from the ethics review committee of the IOBSL, a total of 15 pancreatic cancer patients were recruited for this study from the National Cancer Institute (NCI), Maharagama, so that the test group consisted of 10 pancreatic cancer patients with diabetes and the control group consisted of 5 pancreatic cancer patients without diabetes. The sample size calculation was done using available statistical data for the prevalence of pancreatic cancer patients in Sri Lanka. However, due to the limited availability of patients and limited amount of time, the maximum possible number of patients was recruited. The total WBC count, neutrophil count, lymphocyte count, monocyte count, RBC count, platelet count and amount of Hemoglobin were collected as the cell blood count (CBC) parameters, using clinical data from the NCI of the patients recruited for the study. CBC-derived parameters were also calculated and analysed similarly. The Mann Whitney U test was used to compare the total WBC counts and the two sample t-test was used to analyse the other CBC and CBC-derived parameters between the two groups. XLSTAT software (version 2023 5.2.1413.0) was used for all statistical analyses. All the parameters did not show a significant difference between the two groups. These parameters serve as valuable tools that may be used to diagnose and monitor patients by observing the alterations that may occur due to pancreatic cancer-associated diabetes. However, the stage of chemotherapy of the patients should be taken in to consideration in such analyses. Further studies with higher sample numbers and additional test groups are required to explore the role of these parameters in the development of pancreatic cancer-associated diabetes, for early diagnosis and better prognosis of this cancer.

Keywords: pancreatic cancer, diabetes mellitus (DM), pancreatic cancer-associated diabetes, hematological parameters, complete blood count (CBC)

Effect of polyamine seed priming in chlorophyll content of *Vigna radiata* L. seedlings under water stress

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Mung bean (*Vigna radiata* L.) yield potential is significantly hampered by water stress due to impaired photosynthetic efficiency from chlorophyll degradation. Polyamines (PAs) are plant growth regulators that contribute to various development processes and enhance tolerance to stresses. Exogenous application of PAs offers a prospective approach to enhance plant resistance against water stress. This study aimed to investigate the effect of priming *V. radiata* seeds with PAs on the chlorophyll content of plants under water stress. About 120 *V. radiata* seeds from the “MI 6” variety were primed for 1 hr with PAs putrescine (Put), spermidine (Spd), and spermine (Spm) separately, each with 50 µM,100 µM, and 200 µM (3 replicates each) and with distilled water (control). The 200 µM exhibited the highest germination indices of 130.67, 140.00, and 150.00 for Put, Spd and Spm, respectively. Three-week-old seedlings obtained from seeds primed with 200 µM PAs along with distilled water primed seeds were subjected to two levels of water stress; watering to half (0.5×FC) and a quarter (0.25×FC) of the field capacity (FC). A control group was maintained at FC. After imposing water stress for one week, the total chlorophyll content of the youngest fully expanded leaves was quantified spectrophotometrically from five replicates for each treatment. Statistical analysis with one-way ANOVA revealed that the chlorophyll content was significantly reduced in control plants at 0.25×FC and 0.5×FC as 0.14 and 0.19 mg/g tissue, respectively compared to plants at FC with 0.24 mg/g tissue. At 0.5×FC, plants from Put, Spd, and Spm treatments showed significantly higher total chlorophyll content of 0.27, 0.29, and 0.31 mg/g tissue respectively, compared to the control with 0.19 mg/g tissue. At 0.25×FC only Spd and Spm treatments showed a significant increase in chlorophyll content of 0.18, and 0.20 mg/g tissue respectively, compared to the control with 0.14 mg/g tissue. The results show that seed priming with PAs positively impacts the chlorophyll contents of water-stressed *V. radiata* plants.

Keywords: *Vigna radiata*, water stress, polyamines, seed priming, total chlorophyll

Evaluation of genotoxic effects of food flavour enhancer, monosodium glutamate (MSG) on the root meristem cells of *Allium cepa* L.

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Monosodium glutamate (MSG) (E621) is a food flavour enhancer frequently used in the food industry to improve the taste of food. However, research indicates that food flavour enhancers may pose potential health risks, including risk of cancer, and genetically inherent diseases due to their potential genotoxicity. This study was aimed at investigating the genotoxic effects of MSG by using *Allium cepa* L. as a plant model. Roots of *A. cepa* bulbs were treated with 1000 ppm, 2000 ppm, and 3000 ppm concentrations of MSG considering the Acceptable Daily Intake values of MSG which were established by the Joint FAO/WHO Expert Committee on Food Additives, distilled water as negative control for 24 h, 48 h and 72 h exposure periods. Five replicates of *A. cepa* bulbs per treatment were used. For each MSG concentration of each exposure period, a total of 30 root tips were excised from five replicates of *A. cepa* bulbs. By staining the roots, Mitotic Index (MI) which is the ratio between the number of cells undergoing mitosis to its total number of cells and percentage chromosomal aberrations in root tip cells were investigated microscopically. The total number of cells scored from one root tip was 1000. The General Liner Model and Tukey's test were applied with 95% confidence limit (significance at $P \leq 0.05$) for results analysis. The microscopic investigations revealed a significant ($P \leq 0.05$) reduction in MI and occurrence of chromosomal aberrations compared to the respective negative control with the increase of MSG concentration and exposure period. After 72 h exposure, MI of root tips in the negative control was 51.44%, whereas MI of root tips treated with 1000 ppm and 3000 ppm MSG concentrations were 40.31% and 38.05% respectively. Chromosomal aberrations, c-mitosis, distorted metaphases and anaphases were observed in all MSG concentrations. At 2000 ppm and 3000 ppm of MSG anaphase and telophase bridges, multipolar anaphase, and stickiness were observed. The highest percentage of chromosomal aberrations of 2.43% was induced by 3000 ppm MSG after 72 h. The reduction of MI and the presence of chromosomal aberrations indicate that MSG can cause chromosomal mis-segregation and genomic instability. The present investigation demonstrates that MSG exhibits significant genotoxic effects on the chromosomes of *A. cepa*.

Keywords: Genotoxicity, MSG, Mitotic Index, Chromosomal aberrations, *Allium cepa*

Assessing employee knowledge and awareness of the need for carbon reduction before and after implementing carbon reduction measures in a shoe manufacturing facility

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Global warming and climate change have become the most threatening global environmental issues over the past few decades. Many industries have taken measures to reduce emissions and become carbon neutral using different methodologies. This study was carried out to assess the level of understanding and responsiveness of 37 employees before and after the introduction of specific carbon reduction initiatives and awareness creation of the need for reducing carbon footprint of a shoe manufacturing company in the Colombo district. The methodology involved a questionnaire covering knowledge of global warming, climate change and carbon footprint, knowledge of low Greenhouse gas (GHG) emissions, causes of carbon footprint and willingness to reduce carbon footprint. Questionnaires were administered before and after awareness creation and implementation of the carbon reduction measures. The carbon footprint of the process was calculated using the Intergovernmental Panel on Climate Change (IPCC) 2006 methodology. According to the results, the carbon footprint was reduced by 35.58%. There was no significant change in the score of employees' general recognition of global warming, climate change, and carbon footprint ($p = 0.079$). The score improvements were analyzed with independent sample t-tests. However, knowledge on low carbon consumption ($r = 0.001$), understanding of the causes of carbon footprint ($r = 0.000$), and willingness to reduce carbon footprint ($r = 0.000$) showed a significant change. The age and gender did not significantly influence carbon footprint reduction ($r=-0.036$). According to the one-way ANOVA test, a significant difference was observed after implementation ($p = 0.013$), with the management section showing a significantly lower score compared to the executive and operation sections. One of the efficacious ways of reducing carbon footprint is by making employees aware of the consequences of the carbon reduction process. Therefore, raising awareness among employees leads to a more cost-effective and economical approach to reducing GHG emissions in the process.

Keywords: Carbon footprint, Employee awareness, Global warming, Greenhouse gas (GHG) emission, Shoe manufacturing

Optimizing indoor growth conditions for Gotukola *(Centella asiatica)* and Peppermint *(Mentha piperita* L.) using light spectrum experiments

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With the growing world population, the demand for food is increasing rapidly. The crop-growing techniques have taken a positive turn with improved hydroponics techniques and successful attempts at indoor plant cultivation in urban areas around the world. This research focuses on optimizing growth conditions for two economically important crop varieties in Sri Lanka, Gotukola and Peppermint. The objective is to determine the most suitable light combination for optimal growth of hydroponically cultivated Gotukola and Peppermint in an indoor setting. In the experiment to determine optimum light conditions, 5 different light spectra (white light, blue: red=1:1, blue: red: white= 1:1:1 using LED light, indoor sunlight, and outdoor sunlight as controls) were tested. Treatments were arranged in a randomized design with 3 replicates each with 6 plants illuminated at equal photon flux density (PFD) of 150µmolm^{-2} s^{-1} for a daily photoperiod of 16 h during the experiment. A deep-water culture system was used, EC was maintained at 1400 µS/cm, and pH values within 5.5 to 6.5. Different vegetative growth data were measured for Gotukola and Peppermint separately. The obtained results were analyzed using R software. One-way ANOVA and Duncan's multiple range test were performed to identify the optimum treatment. Considering the Gotukola data, leaf length, number of leaves, leaf width, root length, fresh weight, and dry weight were significantly higher in white light followed by outdoor control > blue: red: white= 1:1:1 > blue: red=1:1 in all weeks. Considering Peppermint data, plant height, number of leaf pairs, leaf width, root length, fresh weight, and dry weight were significantly higher in white light followed by outdoor control > blue: red: white= 1:1:1 > blue: red=1:1 in all weeks. Hence, it can be concluded that white light conditions can be used to grow indoor leafy vegetables, Gotukola and Peppermint successfully.

Keywords: Hydroponics, Peppermint, Gotukola, White light, Indoor cultivation

Microalgae *Chlorella sorokiniana* and *Scenedesmus* sp. as a sustainable source of beneficial bioactive compounds

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Microalgae biomasses are natural sources rich in diverse bioactive compounds, including lipids, polysaccharides, proteins, amino acids, carotenoids, vitamins, and many other secondary metabolites. Functional ingredients from microalgae can enhance the nutritional value of foods and have many biotechnological, industrial, pharmaceutical and cosmetic uses. This study aimed to investigate two freshwater microalgae isolates, *Chlorella sorokiniana* and a *Scenedesmus* sp., for their total protein, phenolic, flavonoid, and carotenoid contents and for antioxidant and antimicrobial properties. The microalgae species were isolated from local freshwater samples using serial dilution and streak plate methods. Isolated species were morphologically identified using microalgae identification guides. Molecular identification was done for *C. sorokiniana* isolate. Isolates were cultured and scaled-up in Bold's Basal Medium (BBM). Biomasses were harvested using flocculation, and centrifugation, air-dried, suspended in methanol or ethanol (0.1 g/ml), and sonicated to obtain the extracts, which were then concentrated by evaporating the solvent. Total protein content, total phenolic content (TPC), total flavonoid content (TFC), and total carotenoid content of each extract, and their antioxidant and antimicrobial properties were determined using standard analytical methods. Total protein content of *C. sorokiniana* extract was 350.38±5.01 µg/mL while it was 86.10±18.08 µg/mL in the *Scenedesmus* sp. extract. For *C. sorokiniana*, the TPC, the TFC and the Total Carotenoid contents were 52.80±0.80 µg Gallic Acid Equivalent (GAE) /mg Dry Extract (DE), 362.00±3.14 µg Rutin/mg DE and 5.34±0.21 µg/mg DE, respectively. For *Scenedesmus* sp., those were 50.05±4.00 µg GAE/ mg DE, 99.06±5.46 µg Rutin/mg DE, and 4.02±0.12 µg/mg DE. *C. sorokiniana* extract showed a higher DPPH radical scavenging activity (IC_{50}: 227.40 µg/mL) compared to that of the *Scenedesmus* sp. extract (IC_{50}: 652.19 µg/mL), and additionally, showed antimicrobial activity against *Staphylococcus aureus*. It can be concluded that both isolates have shown the presence of beneficial bioactive compounds investigated and may have potential antioxidant properties.

Keywords: Microalgae, *Chlorella sorokiniana*, *Scenedesmus* sp., bioactives compounds, antioxidant

Impact of plant growth regulator combinations and half-strength MS medium on *in vitro* shoot proliferation in two *Aloe vera* cultivars

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Aloe vera, renowned for its high medicinal value, is a succulent plant primarily propagated through offshoots in nature. Due to its slow propagation rate relative to demand, alternative methods such as *in vitro* micropropagation have been explored. This study focuses on developing a micropropagation protocol for two *Aloe vera* cultivars: *Aloe barbadensis* Miller and *Aloe vera* L. var. *chinensis* (Haw.) Berger*.* The effect of different plant growth regulator combinations on shoot proliferation across the two cultivars, as well as the feasibility of using a half-strength Murashige and Skoog (MS) medium for shoot proliferation were determined. Surface sterilization of *Aloe vera* shoot tips was achieved using 50% ethanol for 7 minutes followed by 30% Clorox for 25 minutes. Explants consisting of shoot tips with two (2) leaves were utilized. Four treatments supplemented with 1.5 mg/L, 2.0 mg/L, 2.5 mg/L, and 4.0 mg/L6-Benzylaminopurine (BAP) with 0.5 mg/L Naphthalene acetic acid (NAA) were employed in 10 replicates to assess their impact on shoot proliferation, revealing that the highest number of shoots per explant for *A. barbadensis* Miller (0.70 ± 0.47) occurred with the 1.5 mg/L BAP and 0.5 mg/L NAA treatment ($P \leq 0.05$) after six weeks of incubation. Conversely, plant growth regulator combinations did not significantly affect shoot proliferation in *A. vera* L. var. *chinensis* (Haw.) Berger during the six weeks of the study period. The study underscores the cost-effectiveness of utilizing a half-strength MS medium ($^1/_2$MS) for propagating these *Aloe vera* cultivars. Rooting *in vitro* was achieved for both cultivars using a plant growth regulator-free MS medium, followed by successful acclimatization (80%) using steam-sterilized sand and soil mix (1:1). In conclusion, this study provides an economical protocol for scaling up *A. vera* cultivation in Sri Lanka, by determining the effect of different plant growth regulator combinations, feasibility of using a ½MS medium for shoot proliferation, as well as using a plant growth regulator-free MS medium for root induction, ensuring a sustainable supply of planting material for future propagation efforts.

Keywords: *Aloe vera*, Micropropagation, Shoot tip, *In vitro*

A preliminary taxonomic study of some selected *Sargassum* species in Sri Lanka

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Sargassum C. Agardh (1820) is the most species-rich genus in the family Sargassaceae, with about 80% of recorded taxa. In Sri Lanka, it is known as one of the most common seaweed genus. However, the current status of the genus *Sargassum* in Sri Lanka remains unknown as there is a six-decade gap in the taxonomy of the genus *Sargassum* in Sri Lanka due to the lack of validly published taxonomic literature. Therefore, the main aim of this study is to address the six-decade gap in the *Sargassum* taxonomy, by studying some of the selected *Sargassum* species in Sri Lanka. Some selected localities in Southern, Northern, Western and Eastern coastal areas of Sri Lanka were explored for the sample collection process, and nine (09) *Sargassum* specimens were collected. For each collected specimen the geographic distribution was recorded and photographs of the thallus morphology were taken. Moreover, for each collected specimen a voucher herbarium specimen was prepared. Among the collected 09 specimens, seven (07) were identified and differentiated using their morphology as they all have distinct morphological characters. Those 07 species are, *Sargassum aquifolium* (Turner) C. Agardh, *S. cymosum* C. Agardh, *S. vulgare* C. Agardh, *S. siliquosum* J. Agardh, *S. oligocystum* Montagne, *S. carpophyllum* J. Agardh and *S. natans* (Linnaeus) Gaillon. The other two specimens were similar in morphology and could not be differentiated using their morphological characters. Therefore, for the identification of those two specimens, a molecular study was performed by amplifying the nuclear ITS1 region. However, the molecular study of those two specimens was not successful due to the low quality of the extracted DNA caused by the polyphenolic compounds. Therefore, for more accurate identification of the *Sargassum* species, further molecular characterization is needed.

Keywords: ITS1, Morphology, *Sargassum*, Sri Lanka, Taxonomy

Understanding the relationship between water stress and stomatal conductance using an AI-based method

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Stomatal conductance (g_s), the capacity of the stomatal aperture to control gas exchanges from or into the leaf, significantly impacts the growth and productivity of plants. More open stomata allow greater conductance, resulting higher rates of photosynthesis and transpiration. Since g_s is a measure of the degree of stomatal opening it can be used as an indicator of plant water status. This study aimed to develop an Artificial Intelligence (AI) model to predict the relationship between water stress and g_s (expressed as the ratio of Closed/Total stomata). *Peperomia pellucida* plants were grown under controlled environmental conditions in a soil-less medium prepared with a concentration series of the Albert's nutrient solution (NS) to provide the plants with varying levels of water stress. Photographs of leaf lower epidermal peels were taken under the x100 magnification of the compound light microscope. These images were used to train an Artificial Neural Network (ANN) using the Yolov5-m AI object detection platform to count the open and closed stomata. The ANN was trained for 20000 epochs. The ratios of Closed/Total stomata predictions were generated by the ANN. The Closed/Total stomata ratio was determined for all treatments using the model. *P. pellucida* plants showed optimal growth in the 2 g/l of NS. Those grown in high concentrations (4.5-8.0 g/l) of the NS dried quickly, while those in the low concentrations (0.05-1.5 g/l) rotted within a week. Linear regression results showed an increasing Closed/Total stomata ratio with increasing concentration levels up to 3.5 g/l of the nutrient solution, indicating a drop in the g_s. The AI model results showed a significant correlation between water stress severity and g_s. Furthermore, the developed model performed with a high accuracy of 97.8% which showed potential for future applications.

Keywords: Stomatal conductance, Peperomia pellucida, Artificial Intelligence, Artificial neural networks

Comparative analysis of antioxidant accumulation in rice callus and rice seed extracts

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Plant tissue culture technology offers a standardized, contaminant-free solution for producing bioactive compounds, allowing for easy industrial expansion. Rice (*Oryza sativa* L.) is a highly nutritious staple food, with different varieties demonstrating varying bioactivity levels that offer diverse health benefits. Callus cultures of rice can also serve as an alternative and sustainable source of antioxidants. This study aimed to induce callus formation from seeds of traditional and improved rice varieties, examining the antioxidant potential of calli and comparing them with rice seeds. Eight rice varieties, namely Kalu Heenati, KuruluThuda, Pachchaperumal, Pokkali, Radhal, At 362, Bg 450, and Bg 250, were cultured on MS medium supplemented with 2 mg/L of 2,4-Dichlorophenoxyacetic acid (2,4-D), 1 mg/L of 1-Naphthalene acetic acid (NAA), and 1 mg/L of 6-Benzylaminopurine (BAP). Four replicates of each ethanolic extract of dried calli (1 mg/mL) were analysed for Total Phenolic Content (TPC), Total Flavonoid Content (TFC), DPPH radical scavenging activity (DPPH), and potassium ferricyanide reducing power assay (PFRAP) and compared with ethanolic extracts from milled rice grains (1 mg/mL). The data were analysed using a one-way ANOVA in RStudio (version 4.3.3). The traditional red rice type Pachchaperumal showed the highest levels of TPC (14.94 mg GAE/g), DPPH radical scavenging activity (19.47 %), and PFRAP activity (5.65 mg AAE/g) among the callus extracts. Meanwhile, the highest TFC (13.04 mg RE/g) was found in the callus extract of the At 362. Among rice seed extracts, Kalu Heenati exhibited the highest values for TPC (204.57mg GAE/g), TFC (179.90 mg RE/g), and PFRAP activity (86.57 mg AAE/g), while the KuruluThuda showed the highest DPPH radical scavenging activity (93.73 %). All rice seed extracts contain significantly($p \leq 0.05$) higher levels of TPC, TFC, DPPH radical scavenging activity, and PFRAP activity compared to rice callus extracts. Therefore, further research is necessary to enhance the antioxidant accumulation of callus cultures of rice. This study provides valuable insights for future research on the antioxidant properties of rice callus.

Keywords: *Oryza sativa* L., Antioxidant, Total phenolic content, Total flavonoid content, DPPH radical scavenging activity

Evaluating *in-vitro* response of *Passiflora edulis* var. Horana Gold using internodal and leaf segments

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Passiflora edulis (passion fruit) holds a significant economic value as the fruit is enjoyed fresh and confectionary. An improved variety *P. edulis* "Horana Gold", with higher yield and better qualities, was developed in Sri Lanka. *In-vitro* propagation techniques are crucial for preserving these enhanced characteristics. Since *in-vitro* propagation protocols using shoot tips have been investigated, this study focused on the potential of internodal and leaf explants for *in-vitro* plant regeneration. Internodes (1 cm) were cultured in vertical and horizontal orientations on MS medium supplemented with varying BAP levels (0.0, 1.5, 2.0, and 2.5 mg/L), determined based on previous literature. Eight treatments were arranged in a completely randomized design (CRD), each replicated 10 times with four explants per replicate. Leaf explants (1 cm^2) were cultured in abaxial and adaxial orientations, with and without midvein, on MS medium supplemented with different BAP concentrations (0.0, 1.5, 2.0, and 2.5 mg/L). Sixteen treatments were arranged in a CRD, each replicated ten times, containing four leaf segments per Petri Dish. Almost all internodal explants responded by forming callus at the cut surfaces after three weeks of incubation. Interestingly shoot bud formation was observed only in explants cultured on MS medium with BAP in both orientations. According to One-Way Analysis of Variance, the highest shoot bud formation frequency in explants placed horizontally (87.50%) was observed on MS medium with 2.0 mg/L BAP. For vertical orientation, the highest bud formation frequency (79.17%) was observed with 2.5 mg/L BAP. Leaf explants produced callus and/ or protuberances after two weeks. At each BAP level, callus induction frequency was significantly higher ($p \leq 0.05$) in leaf explants with midvein (68 – 95%) than in explants without midvein (5 – 61%). In explants with midvein, neither the orientation nor BAP concentration significantly affected the callus induction frequency. Anatomical studies indicated that callus was initiated from procambium and parenchyma cells of leaf tissue. Regeneration of shoots/buds from internodes shows promise for the rapid multiplication of *P. edulis*. However, the regeneration protocol for leaf segments needs further improvement.

Keywords: Passiflora edulis, Horana Gold, Internode, Leaf segment, Regeneration

Extending the vase life of *Chrysanthemum indicum* (magenta colour) cut flowers with natural and artificial preservatives

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Consumers are increasingly seeking eco-friendly methods to extend the vase life of cut flowers. This study evaluated the efficacy of several natural and artificial substances to increase the vase life of *Chrysanthemum indicum* (magenta colour) flowers. There were three concentrations with three replicates for the sucrose solutions (50%, 30%, and 10% w/v), citric acid (30%, 10%, and 1% v/v), and bleach (10%, 1%, and 0.1% v/v). The experiment also used *Aloe vera* leaf extract (20 % v/v), coconut water (20 % v/v), *Calotropis gigantea* (wara) leaf extract (20 % v/v), and tap water as the control. Flowers were placed in the test solutions and regular stem end trimming to keep the end open was allowed for consistent water uptake. The wilting angle of the flower stem's droop was measured with a protractor, and petal colour changes were recorded daily throughout bloom until flowers became unusable aesthetically. Vase life increased in all treatments compared to the 7±1.15 days of the control; in the 30% w/v sucrose solution flowers showed the standard withering angle after 13±1.15 days. Solutions of citric Acid at 1 % w/v and bleach 0.1 % v/v were able to maintain the aesthetic quality for 10±1.15 and 11±1.15 days respectively. Likewise, natural extracts such as *A. vera* leaf extract and coconut water also extended the vase life compared to the control. Flowers in both solutions retained aesthetic value for 11 ± 0.00 days. These results provide evidence that of the treatments used in this experiment 30% v/v sucrose solution could prolong the vase life of cut *C. indicum* (magenta color) flowers most. *A. vera* whole leaf extract (20% v/v) and coconut water (20% v/v) can be used as natural substitutes for conventional preservatives.

Keywords: *Chrysanthemum indicum* (magenta color), Natural preservatives, Vase life

Effect of *Aloe vera* (L.) Burm. f. aqueous extract on seed germination and seedling growth of *Abelmoschus esculentus* (L.) Moench

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Among the various botanical seed germination stimulators, *Aloe vera* is an eco-friendly and cost-effective option to improve seed germination. This study aimed to evaluate the effect of *A. vera* aqueous extracts on the seed germination and seedling growth of *Abelmoschus esculentus* (Okra). The effects of 20%, 40%, 60%, 80%, and 100% (v/v) *A. vera* aqueous extractions were tested, while distilled water served as the control. Healthy *A. esculentus* seeds from a same seed lot were surface sterilized using 2% NaOCl and placed on petri dishes lined with filter papers, each moistened with 2.5 mL of *A. vera* extract for treatments and water for the control. Six replicates (120 seeds/each) were conducted for each treatment and control. Seeds were incubated to germinate at 27 ^{0}C temperature and 83% relative humidity. Number of germinated seeds was counted daily. The Mean Germination Time (MGT), Mean Germination Index (MGI), Mean Germination Energy (MGE), and Mean Coefficient of Velocity of Germination (MCVG) were calculated from the daily seed germination data. Hypocotyl and root length of seedlings were measured at the end of the experiment. All the calculated data were subjected to one-way ANOVA and Turkey pairwise comparison tests at $\alpha = 0.05$ using “R” statistical software. The 60 % *A. vera* extract recorded significantly highest values for MGI (8.2 ± 1.2), MGE (96.7 ± 5.8 %), and MCVG (72.3 ± 1.1 %). Treatments with 20 %, 80 %, and 60 % *A. vera* aqueous extracts significantly decreased the MGT indicating a rapid growth than the control ($p < 0.05$). The 20% treatment significantly enhanced root length (4.2 ± 0.7 cm) while the highest hypocotyl length (1.98 ± 0.5 cm) was recorded for the 60% treatment. Therefore, 60% *A. vera* aqueous extraction was more effective than the control in enhancing *A. esculentus* seed germination.

Keywords: Aloe vera, Abelmoschus esculentus, Seed germination enhancers, Coefficient of velocity of germination, Germination index

Comparison of soil properties in space open and closed dry-mixed evergreen forest ecosystems in a human-impacted forest landscape in the dry zone, Sri Lanka

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Re-establishment of forest canopy through restoration of degraded forests optimizes ecosystem services and functions. Soil plays a vital role in achieving restoration success.
This study compared key soil properties of three habitats of varying canopy cover; open area with 0% canopy (OA), adjoining 40-50% closed-canopy habitat dominated with shrubs (SH) and 70-80% closed canopy forest (TH) in a degraded dry-mixed evergreen forest in Thuppitiyawa, Anuradhapura. Soil texture, organic carbon, pH, electrical conductivity, water holding capacity and total nitrogen were analysed in litter-free topsoil from composite samples collected in both dry and wet seasons. Soil bacterial counts and fungal morphotypes were observed in the wet season. Analysis of Variance followed by post hoc test identified significant differences in soil properties among habitats. Hierarchical cluster analysis was done to identify habitats of similar soil properties. RStudio software was used for data analysis. Higher contribution of leaf litter from the closed canopy forest significantly increased percentages of soil organic carbon [3.25 ±0.53 and 2.72 ± 0.21 in wet and dry seasons respectively], total nitrogen (0.26 and 0.25 in wet and dry seasons respectively), and electrical conductivity (140.22 µS/cm ± 21.34 and 113.77 ± 54.47 µS/cm in wet and dry seasons respectively) compared to other habitats. A positive correlation between soil organic carbon and water-holding capacity was noted. No significant differences in soil pH was noted. High amount of clay and silt were reported in wet season probably due to inflow of storm water and subsequent flooding. SH had the highest clay content (23.6%) compared to OH (9.6%) and TH (3.2%) in wet season while amounts were almost the same in dry season with averages varying 10-12.5%. In the wet season TH had the highest silt (36.6%) than SH and OH (19.7% and 25.8% respectively), but in dry season OH reported the highest percentage (22.5%) than SH (21.7%) and TH (19.2%). The sand percentage varied 64.51% (OH)> 60.6% (TH)> 56.57% (SH) irrespective of the season. Highest bacterial colony count (22520 ± 6689 per gram) was reported in OA in both seasons. Seven fungal common morphotypes were observed in soil with one being limited to TH. Findings reflected habitat specific seasonal dynamics of soil properties, which could assist in designing further improvements to the site during restoration practices initiated in the degraded forest.

Keywords: Soil, restoration, dry-mixed evergreen forests

Comparison of floristic changes and carbon sequestration in areas of varying canopy covers in a degraded dry-mixed evergreen forest, Sri Lanka

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Forest restoration work attempts to optimize forest health and ecosystem services. In this regard, it is vital to understand the vegetation characteristics at the initial stages of restoration and quantify the carbon sequestration capacity that would yield with the improvement of the canopy re-establishment. In this study we compared vegetation composition and structure in wet and dry seasons, and carbon sequestration capacity in the areas of varying canopy cover. The study site was a 25 ha degraded open spaced area, intact shrub dominated area and dry-mixed evergreen dense forest patch in Thuppitiyawa, Anuradhapura. We reported species composition, life form spectrum, and importance value index (IVI) of vegetation in three areas; open area (OH) without canopy establishment having only saplings recently planted, adjacent shrub-dominated area (SH) with 40-50% canopy cover and tree dominated forest area (TH) with 70-80% canopy cover. We also compared the plant diversity among habitats using Shannon-Weiner and Simpson's diversity indices and estimated each area's carbon sequestration capacity using available allometric equations for tropical trees. The richness of plant species varied OH (16) <TH (22) <SH (31) totalling 41 plant species from 18 families. In the dry season, OH had a higher abundance of *Panicum maximum, Mimosa pudica,* and *Lantana camara*, but was heavily dominated with *Basilicum polystachylon* during the wet season. A high herbaceous cover was also noticed in SH in the wet season whereas species richness was almost the same throughout in TH. Higher values of Simpson (0.906) and Shannon-Wiener (2.8) indices supported high richness in SH. Plant life-form analysis showed a remarkable change in SH between seasons adding many hemicryptophytes in the wet season. The importance Value Index (IVI) of TH revealed higher values for *Glycosmis angustifolia* and *Drypetes sepiaria whereas* in SH, *Flueggea leucophyrus* and *Syzygium cumini* exhibited high IVI values. Timber trees, on average, had a lower Importance Value Index (IVI). The Carbon sequestration capacity in ton/ha varied TH (26358.9)>SH (8073.0) >OA (1599.1). The minimum changes in species richness over the wet and dry seasons and the highest carbon sequestration capacity obtained from TH reflected the importance of ecosystem stability and the potential increase in carbon sequestration capacity of the land could result in future canopy cover improvement via restoration.

Keywords: Carbon sequestration, Dry Forest, vegetation, restoration

Temporal distribution of salt marsh species in the Kalpitiya, Northwestern province of Sri Lanka

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Salt marshes are diverse coastal wetlands found in low-energy coastal areas associated with bays, inlets, estuaries, and soft substratum foreshores. The present study aimed to analyse the spatiotemporal distribution of halophytes in a selected salt marsh coastal ecosystem of the northwestern province of Sri Lanka. The study site was selected along the coastal line of Kalpitiya, in Norochchalei town (8°02'15.0"N 79°44'24.2"E). Randomised Study plots were carried out in the selected study site. Analysis of vegetation surveys conducted in November 2023 and February 2024. Plant specimens were collected, identified, and herbarium sheets were created. The Braun-Blanquet percentage cover of each plant species was estimated visually using 2x2 meter plots. There was no observed decrease in the percentage cover for *Salicornia brachiata*; however, there was a corresponding increase in *Sesuvium portulacastrum*. This suggests a possible dominance shift between these two species, potentially driven by environmental changes or competition. The presence of *Suaeda monoica* was variable, suggesting localized differences in habitat suitability or ecological disturbances. Grasses and mangrove species exhibited relatively stable percentages, indicating less susceptibility to short-term fluctuations. However, a significant increase in grasses was noted, possibly reflecting seasonal variations or ecological succession. Environmental factors such as salinity, waterlogging, and nutrient availability are hypothesized to be influencing the competitive dynamics between *S. brachiata* and *S. portulacastrum*. Changes in these factors may favour one species over the other. The patchy distribution of *S. monoica* could be due to localized disturbances like grazing or trampling. The increased abundance of grasses might be a result of seasonal growth patterns or changes in grazing pressure. These observations suggest that competitive interactions, facilitative relationships, and environmental factors are shaping the plant community composition at the Kalpitiya study site. Further investigation is needed to determine the specific drivers of these observed changes.

Keywords: Salt marsh, plant community, Kalpitiya, *Salicornia brachiata*, *Sesuvium portulacastrum*

An investigation of the effect of selected plant extracts on plant growth of *Capsicum annum* seedlings

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Aloe vera extract, coconut water, and rice rinsed water are proven for their efficacy in promoting plant growth, root elongation, shoot elongation, leaf development, etc., and have applications in horticulture and tissue culture. Those materials are known to carry various growth-promoting substances including plant hormones. This study mainly focused on the comparative analysis of selected plant extracts in terms of their efficacy on the growth of *Capsicum annum* (Chili pepper) seedlings. Two weeks old potted *C. annum* seedlings were treated for 15 consecutive days with diluted coconut water (Coconut water: water, 1:4), red rice (BW 364) washed water, and freshly prepared *A. vera* gel extract (Aloe gel: water, 1:4) separately, in triplicate (with three pots with 5 plants in each, for each treatment), using tap water as the control. When treating the plants, a volume of 10 ml was used for each plant from the relevant plant extract solutions and tap water for initial 7 days. The experiment was conducted for another 8 days by increasing the treatment volume to 20 ml. Root length, shoot length, and leaf area were measured using ImageJ software and statistically analysed using Minitab (21.2.0). As per the results analysed by the two-sample t - test, rice rinsed water positively affects shoot length (5.504 ± 0.236 cm; P-value 0.012), and leaf area (1.634 ± 0.105 cm^2; P value 0.015) in chili seedlings while *A. vera* gel extract had significant effects on root length (10.859 ± 0.983 cm; P value 0.010) and leaf area (1.046 ± 0.046 cm^2; P value 0.023), compared to the control. Coconut water had no significant effect on the growth of *C. annum* seedlings, under the experimental conditions. The rice water significantly increased shoot length and leaf area of *C. annuum* seedlings, while *A. vera* extract significantly increased both root length and leaf area, with a marginal effect on shoot length. Coconut water yields varied outcomes. Future research could explore the constituents in these extracts which are responsible for the effects shown and their concentration dependencies individually and synergistically on plant growth.

Keywords: *Capsicum annum,* Coconut water, rice water, *Aloe vera*

Changes in pigment composition during the development of *Mesua ferrea* leaves

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Leaf pigments chlorophylls, and carotenoids absorb the blue and red wavelengths of light essential for photosynthesis, while reflecting green wavelengths. Anthocyanins absorb light in the blue-green wavelengths, allowing the red wavelengths to be scattered to make the organs visibly red. Carotenoids and anthocyanins in leaves are crucial for regulating leaf temperature, preventing photoinhibition of photosynthetic apparatus, and combating oxidative stress. *Mesua ferrea* ('Na' or Ceylon Ironwood; family Calophyllaceae) is characterized by a prominent pink to red flush of drooping young leaves, and grayish-green mature leaves. The main objective of the study was to identify the changes in pigment composition during the development of *M. ferrea* leaves. Healthy leaves were selected and categorized into 8 specific age stages using pre-observations of leaf development. To extract chlorophyll, 2.00±0.05 g of leaves was ground in 20.00±0.05 ml 80% (v/v) acetone, followed by centrifugation at 3000 rpm for 10 minutes. For anthocyanin extraction, 2.00±0.05 g of leaves and solution mixture of methanol, water, and hydrochloric acid (6:4:0.06) with chloroform (10.00±0.05 ml) was ground and then centrifuged at 3000 rpm for 15 minutes. Absorbance of the resulting supernatants from each age stage was measured using UV-Visible spectrophotometer at 663 nm and 645 nm for chlorophyll extract and at 530 nm and 675 nm for anthocyanin extract. Pearson correlation test was conducted using Minitab software to check the correlation between age stage and the anthocyanin to chlorophyll ratio. The total chlorophyll content (mg/g) from age stage 1 to 8 ranged from 0.25±1.26 to 3.90±1.26, while the anthocyanin content (mg/g) from age stage 1 to 8 were 0.94±0.19, 0.96±0.19, 0.42±0.19, 0.59±0.19, 0.58±0.19, 0.60±0.19, 0.46±0.19, 0.71±0.19, respectively. The total chlorophyll content increased with the age. The anthocyanin content decreased, but not significantly. Both content changes were analysed using polynomial regression curves. Anthocyanin to chlorophyll ratio was obtained to show the change of pigment composition as one variable. At 5% significance level, there is a negative correlation between anthocyanin to chlorophyll ratio and the age stage of the leaf, with a r value of -0.808, p value of 0.015. When the *M. ferrea* leaf develops anthocyanin to chlorophyll ratio decreases, reflecting that mature leaves contain increased chlorophyll content for efficient photosynthesis while younger leaves contain higher anthocyanin content, most likely to prevent photo-damage of the immature leaf tissue.

Keywords: *Mesua ferrea*, pigment composition, chlorophyll, anthocyanin, age stage

Development of an organic liquid fertilizer to replace commercial hydroponic solution (Albert solution) to cultivate "Kangkung" plants

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Hydroponics is an extremely popular method of crop cultivation. Here, the crops are grown in an inorganic nutrient solution and the extensive use of these nutrients are coupled with many direct and indirect economic, environmental, and health problems. This study aimed at developing an organic liquid fertilizer to replace Albert Solution (Commercial Inorganic fertilizer) in a hydroponic Kankung cultivation. Moringa (*Moringa oleifera*) and Gliricidia (*Gliricidia sepium*) leaves were used as the main material to obtain Nitrogen (N), Phosphorus (P), Potassium (K) along with cow dung for essential micronutrients. Before treatment preparation, chemical analyses were conducted to analyze NH_4^+, NO_3^-, and PO_4^{3-} concentrations of Fermented Moringa Extract (FME) and Fermented Gliricidia Extracts (FGE). Different ratios (FME:FGE: 2:3. 3:2, 1:4, 4:1) in different treatments were added with a constant volume of cow dung solution. Treatments were arranged in a randomized design with three replicates, and growth data (mean shoot length, number of leaves, chlorophyll content, plant fresh weight, root length) were obtained for five weeks. Plant extracts had sufficient NPK levels to be used in the experiment. NH_4^+, NO_3^-, and PO_4^{3-} concentrations of FME and FGE ranged from 125.25-195.15 ppm, 149.57-242.40 ppm, and 116.25-118.00 ppm respectively. There was no statistically significant difference between the growth parameters of the organic fertilizer and Albert solution (12.4 cm and 14.0 cm respectively) in the 2:3 ratio during the first two weeks. However, in next two weeks, only a few plants of the ratio 2:3 showed similar growth to Albert solution but with an exponential development in 5-6 weeks. In conclusion, prepared organic liquid solution can support Kangkung plant growth without hindering its growth and a 2:3 ratio was selected as the best treatment.

Keywords: Hydroponics, Organic fertilizers, Kangkung, Moringa, Gliricidia, NPK Analysis

Investigating the effect of selected plant extracts on polyphenol oxidase activity in *Annona muricata* L. fruit extract

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Enzymatic browning can cause significant economic losses in fruits and vegetables. When fruit or vegetable tissues are damaged, their polyphenols are oxidized upon exposure to atmospheric oxygen transforming into quinone which is subsequently polymerized into melanin with the catalytic action of polyphenol oxidase (PPO) enzyme, causing fruit browning. This enzymatic browning leads to loss of quality in fresh fruits and vegetables, hence there is much effort to develop methods to prevent it. This study investigates the inhibitory effects of *Ananas comosus* (pineapple), *Averrhoa bilimbi* (bilin), *Averrhoa carambola* (star fruit), *Citrus aurantiifolia* (lime), and *Zingiber officinale* (ginger) extracts on enzymatic browning in *Annona muricata* L. (katu anoda / soursop) fruit extract. All were aqueous extracts prepared by blending the chilled plant tissue, with subsequent centrifuging to obtain the supernatant. The *A. muricata* L. fruit extract was mixed with each plant extract (2:1 ratio), and absorbance readings were taken at 525 nm immediately, after 3 hours, and after one day, using a UV/Vis spectrophotometer. Data underwent one-way ANOVA analysis. Results indicate *C. aurantiifolia* extract as highly effective, showing 72% inhibition after 3 hours and 92% after one day at 525 nm, while *A. bilimbi* extract had the lowest inhibition: 4% after 3 hours and 11% after one day. *C. aurantiifolia* emerged as the most cost-effective natural anti-browning agent of the selected plant extracts. All extracts significantly inhibited polyphenol oxidase activity at 525 nm over 3 hours and 1 day. This research advances circular and sustainable bio-economy by employing natural plant extracts with anti-browning capacity to extend shelf life of fruit extracts, reduce food waste, and offer a safe, economically viable alternative to synthetic chemicals in food preservation.

Keywords: Polyphenol oxidase, anti-browning, *Annona muricata* L.

Habitat preference of *Panthera pardus kotiya* in the Kumana National Park, Sri Lanka

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The Sri Lankan leopard (*Panthera pardus kotiya*), the island's sole apex predator, is poorly studied in some of its strongholds. This research investigated the leopard's habitat preferences in the Kumana National Park (KNP) in southeastern Sri Lanka. Records of 865 direct sightings over a four-year period (2020-2023) linked to 61 individually identified leopards were used to assess habitat preferences. The study area covered 113.00 km^2, encompassing the surveyed region of KNP where accessibility was facilitated by the road network. Seven distinct habitat types—Dry-mixed Evergreen Forest, Scrub Forest, Grassland, Rock, Waterbody, Villu, and Beach—were identified within KNP and delineated using ArcMap 10.8. The extent of each habitat type was quantified using GIS measurement tools. Habitat preferences were assessed using two methodologies: a comparison of the percentage availability (A) of habitat types with their usage by the leopard as indicated by the percentage of sightings (O) in that habitat type, and the Jacob's preference index. Results revealed a marked preference for grasslands (A=6.42%, O=23.47%) and rocky habitats (A=11.91%, O=13.06%), with occurrences exceeding availability. This preference persisted across both wet (W) and dry (D) seasons. Additionally, a slight increase in preference for waterbodies (A=3.50%, O_D=3.55%, O_W=1.22%) and villu (A=1.51%, O_D=1.68%, O_W=0.91%) was noted during the dry season. These observations were confirmed by the Jacob's preference indices. The preference for grasslands is due to their suitability as hunting grounds, providing visibility and attracting ungulates. Rocky habitats offer cover, cooler microclimates, and shelter year-round. Increased preference for waterbodies during the dry season is likely due to the need for water and the higher prey concentration near these areas. Accordingly, no major seasonal shift was observed in the preferred habitat types, indicating a consistent habitat selection by the leopards throughout the year. The study provides information useful for maintaining suitable habitats for the leopards within KNP which would also be beneficial in terms of tourism.

Keywords: Sri Lankan leopard, habitat preference, seasonal fluctuations, Kumana National Park, GIS analysis

Acknowledgement: Department of Zoology and Environment Sciences, University of Colombo

Morphological characterization of marine ponyfish species (Family Leiognathidae) on the west coast of Sri Lanka

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Ponyfish, or '*Karalla*', is renowned for its high nutritional value and immune-boosting properties, particularly when used in soup. Those species can be categorized under three genera *Leiognathus*, *Gazza* and *Secutor* which have some specific morphological characteristics endemic to the genera. At the same time, they possess some doubtful traits which make the species differentiation more complex. The current study aimed at morphological characterization of Family Leiognathidae, to which ponyfish belong, with the intention of confirming their phylogeny in the future. A total of 15 species were purchased from fish landing sites on the west coast of Sri Lanka extending from Negombo to Beruwala and were identified based on their morphological features according to the FAO guidelines. Observations confirmed that the genus *Gazza* is characterized by the presence of caniniform teeth and a forward-projecting mouth, while the genus *Secutor* has an upward-protruding mouth. Within *Gazza*, *G. minuta* is recognized by its elongated rhomboidal body with anterior scales, contrasting with *G. achlamys*, which is deep-bodied. *Secutor* species are laterally compressed, with *S. ruconius* displaying vertical bars on its upper flank, and *S. insidiator* showing spots and dashes. The genus *Leiognathus* exhibits considerable variability. *L. berbis* is elongated with irregular upper body margins. *L. fasciatus* and *L. leuciscus* have elongated second dorsal spines, a trait also found in *L. smithursti*, which additionally has an elongated second anal spine. *L. equulus* is notable for its breast scales and dark brown saddle on the caudal peduncle. *L. splendens* features a black-dotted snout tip and dorsal fin. *L. daura* is identified by a black dorsal fin blotch and a yellow longitudinal body line, while *L. dussumieri* has similar features with added yellow coloration. *L. brevirostris* is unique for a yellow spot below the pectoral fin, though this is often faint and complicates identification. Given these complexities, molecular methods are recommended for accurate phylogenetic confirmation within the Leiognathidae family, as morphological identification alone proves insufficient.

Keywords: Leiognathidae, Morphological characterization, Ponyfish

Acknowledgement: Financial assistance from the Faculty Research Grant-2023, Grant No. FC/362/27 provided by The Open University of Sri Lanka is highly acknowledged.

Validation of vessel monitoring system records with logbook data of multiday fishery vessels: a case study in the Southern and Southwestern exclusive economic zone of Sri Lanka.

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Vessel Monitoring Systems (VMS) are satellite-based surveillance systems frequently used for fishery enforcement. In Sri Lanka, VMS provides regular reports (i.e., every four hours) of fishing vessels' locations, speeds, events, and other information on a per-vessel basis as message alerts to the Fisheries Monitoring Centre (FMC) of the Department of Fisheries and Aquatic Resources (DFAR). Due to the scarcity of studies on the accuracy and reliability of using logbook data, the present study investigates VMS to validate logbook data based on a case study in the Southern and Southwestern exclusive economic zone (EEZ) of Sri Lanka. Thus, the study primarily relies on secondary data, such as logbook data and VMS data obtained from relevant authorities, analyzed using the R statistical programming language. VMS, which was installed on only 900 vessels in the study area by the end of 2022, was subjected to analysis. VMS and logbook data were merged at different degrees of precision by matching the vessel ID, fishing date, and fishing locations. The optimal precision level for further analysis was identified by considering the average vessel speed (3.74 knots) and the area a vessel could cover (a region with a radius of 27.72 km) within the four-hour interval between alerts. The optimal precision level of 0.25 degrees indicated validation rates of 85.6% for the number of fishing vessels, 770 out of 900. However, among the 770 fishing vessels, only 636 fishing trips out of 3240 were validated using VMS records. These trips were categorized into three types of gear, and based on the results, fishing locations using ring nets were recorded most accurately, followed by gillnets and longlines. The validated data enhances the accuracy and reliability of further analyses, such as identifying species' key fishing grounds, annual and seasonal variations, and the influence of oceanographic parameters on species distribution. The study also highlights the necessity of proper awareness and implementation of relevant policies to encourage the efficient utilization of VMS.

Keywords: EEZ of Sri Lanka, R programming language, Vessel monitoring system, Validation, Offshore fisheries

Acknowledgment: Department of Zoology and Environment Sciences, Faculty of Science, University of Colombo, Department of Fisheries and Aquatic Resources and National Institute of Oceanography and Marine Sciences, National Aquatic Resources Research and Development Agency.

Assessment of anthropogenic influence on blue carbon stocks of tidal salt marshes in Northwest coast, Sri Lanka

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Recent global attention has been drawn to blue carbon ecosystems due to their high rates of carbon sequestration potential and their significant contribution to climate change mitigation. Out of those ecosystems, salt marshes have been given the least attention, and large knowledge gaps remain. Despite the value of these ecosystems, they are heavily exploited. Salt marshes along the Northwest coast of Sri Lanka, especially those close to the Puttalam lagoon area, are being degraded rapidly due to intense anthropogenic activities. Therefore, the current study aims to assess any anthropogenic influence on blue carbon stocks of salt marshes on the Northwest coast of Sri Lanka. 140 vegetation and 24 soil core samples were collected from two different salt marsh sites in Norochcholai, one was a natural undisturbed site, while the other was a site disturbed due to anthropogenic influence. Vegetation carbon stock was estimated by developing species-specific allometric relationships. Soil samples were taken from 1m depth and loss on ignition technique was used to assess the soil carbon stocks. The estimated total carbon stock of the natural salt marsh site was 162.874±38.58 MgCha^{-1} while the total carbon stock of the disturbed salt marsh site was 118.01±23.47 MgCha^{-1}, indicating that the natural salt marsh sites hold higher carbon stocks than the disturbed sites. Furthermore, an alkaline pH was observed at the natural salt marsh site. Also, the 0-30 cm layer of soil at the disturbed site showed low (acidic) pH, very low electrical conductivity, and lower total dissolved solids and salinity values whereas, the soil parameters were not significantly different in the lower soil layers of the two sites. The study results reveal the vulnerability of these ecosystems and highlight the urgent need for conservation efforts to protect and preserve their carbon sequestration potential.

Keywords: blue carbon, carbon sinks, salt marsh, soil organic carbon, anthropogenic influence

Acknowledgement: Department of Zoology and Environment Sciences, University of Colombo

Feasibility of implementing a circular economy for plastic waste management in Fast Moving Consumer Goods (FMCG) industry in Sri Lanka

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Plastic waste management is critical in Sri Lanka, with the FMCG (Fast Moving Consumer Goods) sector contributing significantly to plastic waste generation. Understanding the role of this industry, along with the influence of gender and community perceptions, is essential for developing effective waste management strategies. This study investigated the feasibility of implementing a circular economy model for plastic waste management in Sri Lanka, focusing on the FMCG industry, gender dynamics, and community perceptions. The research utilized a quantitative approach, collecting data through surveys from a diverse range of stakeholders, including industry professionals (N=50) and community members (N=50), using systematic sampling. The results reveal a high level of awareness and understanding of plastic waste management and circular economy principles among respondents, with 68% demonstrating substantial knowledge. Additionally, 66% of participants expressed willingness to adopt circular economy practices, and 74% considered the transition moderately feasible. Industry statistics indicate significant plastic consumption, with the FMCG sector using materials like PET, LDPE, and HDPE extensively, yet recycling efforts remain minimal. Despite a predominantly male participant sample (84%), the variety in age and occupational backgrounds reflects broad sectoral involvement in managing plastic waste. The study identified several challenges, including high initial investment costs, inadequate recycling infrastructure, regulatory obstacles, and a lack of community incentives. Collaborative efforts among government, industry, and communities are crucial to overcoming these barriers. Recommendations include providing financial incentives for businesses, enhancing public awareness through targeted educational initiatives, and investing in recycling infrastructure. Emphasizing gender-inclusive strategies and increased community engagement is also essential to garner widespread support for circular economy initiatives. In conclusion, while the transition to a circular economy for plastic waste management in Sri Lanka presents challenges, there is cautious optimism about its feasibility. Addressing the identified barriers and leveraging opportunities for innovation and collaboration will be crucial for advancing towards a sustainable and circular bioeconomy.

Keywords: Circular Economy, Fast Moving Consumer Goods Industry, Waste Management, Recycling, Sustainability

Are odonates sensitive to agrochemicals? A comparison of odonate diversity in an agricultural vs natural habitat

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Agrochemical contamination is a severe environmental issue in many parts of the world. With high sensitivity to environmental stresses, Order Odonata, damselflies and dragonflies are considered as bioindicators of environmental quality. The present study was conducted in an agricultural field in Kosgama- Boralugoda village in the Seethawaka division, in Colombo district with reference to Waga- Indikada muklana forest in the Western province. The objectives of the study were to identify the species diversity and abundance of odonates in the area, and to correlate the physicochemistry of the sites with the diversity and abundance of odonate species, with an aim of identifying a bioindicator to predict the aquatic pollution in agriculture associated habitats. Pretested structured questionnaire was administrated to identify the commonly used agrochemicals in the field and to identify the awareness of the farmers about the Odonate species. Water quality parameters including temperature, pH, electrical conductivity, salinity, biological oxygen demand (BOD), nitrate, phosphate, total hardness, and sulfates were determined. NPK, TDM (Top Dressing Mixture) and urea were the commonly used agrochemicals in the study sites, used with frequency of 3 to 4 times per cultivating season. Weedicides such as Gulliver (Azimsulfuron), Marshall 20 (Carbosulfan) and MCPA 60 (2-methyl-4-chlorophenoxyacetic acid) were found to apply with a frequency of 3 to 4 times per a cultivating season. Though, statistically not significant, the odonate diversity in the farming area is 0.76 which was lower than the diversity of 0.96 in the natural habitat. Most abundant species of both sites were Pied Parasol (*Neurothemis tullia tullia*). Coenagrionidae and Libellulidae families which seemed to have high tolerance to the environmental stresses showing higher abundance in the polluted site, suggesting their resistance against pollution. However, further studies are warranted to validate their role as bioindicators of aquatic pollution.

Keywords: Water quality, Odonates, Bioindicator, Sensitivity, Agrochemicals

Spatial distribution of the macrobenthic community, relative to sediment dynamics and hydrodynamic regimes in Negombo Lagoon

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Understanding macrobenthic distribution in coastal lagoons is vital for ecosystem management, as these communities indicate environmental changes and contribute to nutrient cycling. The present study examines the combined effect of hydrodynamic regimes and sediment dynamics on macrobenthic distribution patterns of the Negombo Lagoon. Field sampling was conducted twice across the lagoon, from December 2023 to April 2024, at 40 sites. Sediment samples were collected using a sediment core sampler. Macrobenthic species were identified using standard identification guides and databases. pH, conductivity, total dissolved solids, water depth, color, and texture of sediment and seagrass distribution were measured. QGIS, Euclidean Distance Dendrograms, and Pearson Correlation Coefficient analyses were performed to identify clusters and correlations. The study observed 3,898 individuals belonging to 52 species, with *Obtusella macilenta* being the most abundant. Shannon-Wiener index showed higher diversity in the northern-middle than the southern region ranging from 1.673 - 2.453 vs. 0.563 - 1.569 respectively. This pattern is linked to two clusters that result from the Euclidean Distance Dendrogram. Counterclockwise circulation of nutrient-rich seawater, driven by the Coriolis effect, into the lagoon along the northwest side, promoting a salinity gradient conducive to seagrass growth in those regions, creating heterogeneous habitats. Conversely, the southern part experiences high freshwater input and sedimentation, leading to significant environmental fluctuations and lower species diversity. This is compounded by its shallow depth and lower pH levels, unlike the deeper and more neutral pH conditions in the northern areas. Sediment analysis revealed sandy textures near the lagoon mouth due to tidal activity, and clay-silty textures towards the lagoon head due to sedimentation, which shaped the spatial distribution of macrobenthic organisms. Thus, the findings of the present study offer valuable insights into biodiversity conservation strategies, while highlighting the necessity of considering both hydrodynamic regimes and sediment dynamics in ecological assessments.

Keywords: Macrobenthic community, dendrogram analysis, lagoon hydrodynamics, tides, ecological assessments

A preliminary study on soil arthropod diversity in Karadiyana, a solid waste dumping site, Western province, Sri Lanka

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Soil pollution due to solid waste disposal is a global issue of major concern. As the soil performs many functions to maintain environmental quality and agricultural productivity, indicators of soil pollution is a main concern in environmental management. Arthropods as a main group, involved in the decomposition process, are used as bioindicators to evaluate the level of pollution in the soil environment. This study aimed to identify the suitable indicator species of arthropods to evaluate solid waste pollution. Karadiyana Dumping site (polluted site) and Halgahawaththa (reference site) were selected for this purpose and the soil samples were collected from June to November in 2021. Soil pH, soil temperature and soil moisture were determined as the physicochemical parameters. Litter and soil Arthropods were collected using quadrat sampling method in twelve sampling points at each site to observe species diversity in the study sites. A total of 5248 individuals of Arthropod species belonging to 8 orders were recorded in the polluted site. Collembola sp. belonging to order Coleoptera was the most abundant (53%) species followed by isopods (%) in this site. 3268 individual species belonging to 15 orders have been recorded in the reference site showing higher diversity compared to the polluted site. The weaver ant (*Oecophylla smaragdina*) belongs to order Hymenoptera was the most abundant (20%) species and the decomposers such as millipedes, centipedes, termites were also recorded as common species in this site. The study revealed the involvement of Collembolans and isopods as pollution indicators suggesting their involvement in the solid waste decomposition as they are abundant in Karadiyana site. In contrast, ants and other soil decomposers such as millipedes, centipedes, termites are abundant in the natural site. With further extensions this study may provide a valuable insight to develop bioremediation tool for solid waste pollution.

Keywords: Solid waste, decomposition, collembolan, bioindicator, arthropods

Hot spots of mangrove habitat transformation in selected coastal wetlands in the Southern Province of Sri Lanka: A spatiotemporal approach

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Mangrove ecosystems, known for their high productivity, are facing significant threats both natural and anthropogenic, yet a detailed analysis of the extent and specific nature of these threats is lacking. This study employed remote sensing to assess changes in mangrove cover in Rekawa Lagoon, Attaragoda Wetland, and Madampa Lake along the South coast of Sri Lanka. Satellite images were analyzed for 2003 and 2023 to assess the change in mangrove cover extent. Land cover and land use maps were generated using supervised classification, and the changes in the extent of mangrove cover were evaluated. Areas experiencing more than a 20% decline in mangrove cover extent were identified as 'hot spots', where 32 semi-structured interviews with stakeholders were conducted to explore community perceptions of mangrove ecosystems. During the period analyzed, the mangrove cover extent in Rekawa lagoon has increased by 26.7%, while in Attaragoda, it has decreased by 9.1% and in Madampa Lake, it has decreased by 53.3%. Madampa Lake was identified as a hot spot. The semi-structured interviews with people in Madampa revealed that 81.25% of the community is aware of the degradation of mangroves in the region and implied the lack of conservation efforts to restore mangroves sustainably. There was no significant difference between the awareness levels of interviewees based on their age groups, gender or education level. The community believed that land reclamation, changes in the lake's salinity, garbage buildup, commercial cinnamon growing, and illegal cutting were the main causes of mangrove degradation; factors which were not identified by satellite image analysis. This study emphasizes the significance of integrating a bottom-up approach that complements scientific findings with community perspectives essential for effective management and conservation of natural ecosystems.

Keywords: Remote sensing, Mangrove ecosystems, Land cover classification, Change detection, Satellite imagery

The impact of mangroves on environmental wellbeing, socioeconomic importance and economic status in Sri Lanka

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Mangroves are unique salt-tolerant plants forming distinctive coastal ecosystems that provide numerous economic and environmental benefits. However, studies on the environmental, socioeconomic, and economic status of Sri Lankan mangroves are limited, particularly those incorporating perspectives of on-the-ground conservationists, and field experts. Therefore, this study aimed to investigate whether mangroves have a positive impact on environmental wellbeing, socioeconomic and economic status in Sri Lanka for creating a more holistic approach to managing mangrove ecosystem services. The research utilized qualitative methods via interviewing two participants heading renowned mangrove conservation and restoration initiatives in Sri Lanka and compiling a scientific letter to highlight key findings. A reflexive thematic analysis was employed on interview transcripts, categorizing coded excerpts under overarching themes with sub-themes and sub-themes. Themes consisted of 1) 'environmental importance'; 2) 'economic and socioeconomic importance' with 'fisheries', 'challenges' and 'solutions' as sub-themes; 3) 'threats' and 4) 'the importance of conservation and restoration' with 'ecological connectivity', 'challenges' and 'solutions' as sub-themes. Sub-themes included 'stakeholder involvement' and 'temporal aspects' under theme 2 and 'human nature' under theme 3. Findings stressed the environmental, economic and socioeconomic importance of healthy mangroves to both coastal communities and Sri Lanka, underscoring the need for effective mangrove management, conservation, and restoration. Furthermore, the study identified challenges and recommended solutions under respective themes, contributing to a comprehensive approach to mangrove management in Sri Lanka and offering valuable insights for policymakers and stakeholders in this field. Future research could explore mangrove regeneration in a Sri Lankan context and investigate sustainable utilization of blue carbon financing for economic growth opportunities.

Keywords: Mangroves, Mangrove conservation and restoration, Ecosystem services, Economic importance, Socioeconomic importance

The impact of vehicle collisions on macro-invertebrate fauna adjacent to the protected area network of southern wildlife region Sri Lanka.

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The rapid expansion of roads and highways leads to direct roadkill of wildlife and indirectly affects ecological processes. Invertebrate fauna plays a crucial role in tropical biodiversity. A plethora of studies have focused on vehicle collisions of vertebrates, but the data related to invertebrates is sparse. This study assessed vehicle impacts on invertebrates in the road network adjacent to the Udawalawa-Lunugamwehera protected areas in Sri Lanka. Data were collected over six months from September 2023 to February 2024 along 25 km stretches of the B427 (R-01), B528 (R-2), and A2 (R-03) roads using a Honda 100cc scooter travelling nearly at 20 km/h. Vehicle traffic and roadkill counts were manually recorded, along with ambient and surface temperature and humidity. Spatial variations of road traffic, road killing, and environmental variables were statistically analysed using one-way ANOVA. Vehicle traffic significantly changed ($p < 0.05$) among three roads and fluctuated following the order, R-03 > R-01> R-02 order in every sampling event. A total of 868 invertebrate roadkill was recorded, and they changed significantly over the study period. The most noticeable roadkill observed was on three roads were: R-01, termites (72.33% September), molluscs (62.31% November), butterflies (42.92% October); R-02, butterflies (80.88% October), beetles (40% September) and molluscs (27.78% December and January); R-03, beetles, (55.56% February), butterflies (53.42% October and 50% September), and molluscs (27.27% December). The study observed exceptionally high mortalities of termites, butterflies, molluscs, annelids, and orthopterans during the rainy season, likely due to breeding periods. Results show a strong correlation between road killings and ambient temperature ($p < 0.05$), and intermediate vehicle traffic was found to have the highest impact on invertebrate mortalities. The present study provides solid evidence of the adverse effects of vehicles on invertebrates and legitimate mitigatory measures in road networks in protected areas.

Keywords: Vehicle collisions, Invertebrates mortalities, Udawalawa-Lunugamwehera, vehicle traffic

Acknowledgement: Department of Wildlife Conservation is acknowledged for permitting research in wildlife areas.

Seroprevalence and risk factors of toxoplasmosis among antenatal mothers in Kuliyapitiya; A cross sectional study

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Toxoplasmosis, caused by Toxoplasma gondii, is one of the major zoonotic diseases in the world. As the oocysts of the parasite can cross the placenta, the fetuses can be affected severely, when the pregnant mothers catch the infection during or few months prior to the pregnancy. Only few studies have been conducted in Sri Lanka to assess the prevalence, risk factors and awareness about the disease among the pregnant population who are considered as a risk group. The present study was conducted to evaluate the seroprevalence of Toxoplasma specific antibodies and related risk factors to introduce disease control and preventive measures and to make awareness among the community via the risk population, particularly pregnant mothers. This study was a descriptive cross-sectional hospital-based study including 50 study participants who were pregnant women attending antenatal clinics in Kuliyapitiya hospital from January-June 2023. After obtaining consent, sociodemographic and risk behaviour data was gathered using a standard interviewer administered questionnaire. Venous blood samples were collected to test toxoplasma specific antibodies, IgM and IgG with Diapro ELISA kit in manual ELISA method. A total of 11 out of 50 mothers were positive for toxoplasma IgG antibodies in the serum indicating 22% prevalence and none of the mothers were positive for IgM antibodies in the serum. Among the risk factors assessed, Cat litter handling, Cat's diarrheal situation and poor hand washing practices after petting cats were significantly associated ($p<0.05$, multiple regression) with toxoplasmosis in pregnant women. Hence, making awareness among pregnant mothers is recommended to prevent the transmission and the risk of toxoplasmosis in this vulnerable population.

Key words: Toxoplasmosis, Seroprevalence, Pregnant mothers, Pets

Diurnal and nocturnal activities of the Cherry Barb (*Puntius titteya*) inhabiting a shallow stream in the Western Province, Sri Lanka

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Puntius titteya (Cherry barb) inhabiting a shaded, slow-flowing, shallow stream with a muddy and leaf-litter substratum in Diyagama (6°48'34.8"N, 79°59'50.4"E) as a small school of fish was studied from 18th December 2022 to 31st March 2023. The objective of the study was to examine the diurnal and nocturnal behavior of *P. titteya*. Behaviours were quantified using 10-minute scan sampling and short episodes of focal animal sampling conducted from sunrise to sunset (diurnal) and at night. Group composition, nearest neighbor distance (NND), microhabitat occupation and major behaviour patterns were recorded. Behavior patterns recorded were foraging, locomotion, resting, anti-predatory and schooling. Behavioral data were collected on an hourly basis for three times a week during the study period. The group size varied between 12-15 individuals. Sexual dimorphism of adults was evident, and the quaternary sex ratio was 3:5. NND was determined using a photographic method. The microhabitats occupied were open areas (no vegetation cover) and shady areas (covered with vegetation). NND during daytime (1.4±0.2 cm) was significantly lower than that of night (8.4±0.9 cm) (t-test $P<0.05$) indicating that they are clustered during daytime. There was a preference for shady microhabitats (70.6±4.1%) than open microhabitats (29.4±3.8%) during the daytime. An opposite preference was recorded at night, where open microhabitats were preferred (75.6±5.4%) over shady microhabitats (24.4±3.5%). This may be due to the low predatory pressure at night compared to the daytime. Potential predators were herons and kingfishers. There was no diurnal and nocturnal difference in foraging and locomotory behaviour patterns. They preferred slow flow of water (2.2±0.3 m/min) to rapid flow of water (7±1.1 m/min). The most common behavior displayed was foraging, where a feeding preference towards small algal particles was observed. At night, they showed an increased vigilant behaviour (hiding at the slightest disturbance) due to the high abundance of nocturnal catfish who did not predate on them.

Keywords: Behaviors, Focal animal sampling, Focal dynamic area, *Puntius titteya*, Scan sampling

Schedule of the Scientific Sessions

44th Annual Sessions of the Institute of Biology, Sri Lanka
27th September 2024
The Center for Banking Studies, Sri Jayewardenepura Kotte

ORAL PRESENTATIONS

Parallel Session A- Microbiology, Chemical Biology, Molecular Biology and Biotechnology

TIME	ABSTRACT NUMBER	TITLE
1.30–4.00 p.m.	A_01	Investigation of antileukemic enzyme production and antioxidant activities of fungal endophytic communities in *Hellenia speciosa* (J. Koenig) S.R. Dutta (Thebu) of family Costaceae *By K.L.S. Perera, S.S. Ediriweera*
	A-02	Investigating the changes in the microbial composition of Sri Lankan milk microbiota influenced by varying farm sizes *By K.B.M.L. Jayasinghe, S.P.C. Fernando, D.U. Rajawardana, I.G.N. Hewajulige, C.M. Nanayakkara*
	A-03	*Curvularia tuberculata* from a mangrove lichen as a potential antifungal agent against crop pathogens *By C.Y. Amarasinghe, H.A.D.N.N. Happitiya, C.M. Nanayakkara, K.G.S.U. Ariyawansa, S.S. Ediriweera, E.D. De Silva, P.A.N. Punyasiri*

	A-04	Formulation and evaluation of new Ayurvedic polyherbal gargle therapy for promoting oral health *By A.G.L.K. Chandrarathne, I.U. Kariyawasam, P.K. Perera*
	A-05	In silico discovery of antimicrobial peptides of fungal origin *By A.G.T. Nimna, K.G.S.U. Ariyawansa*
	A-06	Optimization of reaction components for a low-cost probe-based quantitative polymerase chain reaction (qPCR) assay to detect the 22q11.2 A-D microdeletion *By T. M. O. D. Tennakoon, N. Warsapperuma, D. M. Ranaweera, D. C. de Silva, N. Perera, G. H. Galhena*
	A-07	Designing low-cost probe-based quantitative polymerase chain reaction (qPCR) assay to detect the chromosome 22q11.2 A-D microdeletion among children with neuropsychiatric phenotypes *By T. M. O. D. Tennakoon, N. Warsapperuma, D. M. Ranaweera, D. C. de Silva, N. Perera, G. H. Galhena*
	A-08	Genome-wide analysis and characterization of Lysin Motif – Receptor Like Kinase (LysM-RLK) gene family in Vigna radiata (Mung bean) *By U.H.B.Y. Dilshan, D.S. Muthmala, P.C. Fernando*
	A-09	Comparative analysis of protein-protein interaction network modules responsible for C3 and C4 photosynthesis: A systems biology approach *By K.Y.G.I. Jayasekara, T.L.S. Tirimanne, P.C. Fernando*
	A-10	Artificial intelligence in crop development: application of deep learning for predicting seed development genes *By S. Ganeshiny, L. Abeywardhana, J. Perera, J.W.J.K. Weeraman, P.C. Fernando*
	A-11	Performance evaluation of tools for predicting transcription factor binding sites *By D.V. Wanniarachchi, S. Viswakula, A.M. Wickramasuriya*
	A-12	Genome-wide analysis of the lipoxygenase gene family in oil palm: insights and implications *By L.W.D.D.V.Lokuwalpola, H.D.D.Bandupriya*

Parallel Session B- Plant sciences and Agriculture

TIME	ABSTRACT NUMBER	TITLE
1.30–4.30 p.m.	B-01	Effects of Low-Density Polyethylene (LDPE) mulching generated microplastics on the shoot growth of Phaseolus vulgaris L. *By P.D.I. Imalka, R. Wimalasekera*
	B-02	The potential of waste flowers as a sustainable source for cosmetic production *By S.V. Withanachchi, P. Saputhanthri*
	B-03	Antioxidant and sun protection capacity of selected medicinal plants in Sri Lanka *By S.V. Withanachchi, P. Saputhanthri*
	B-04	Patterns of phylogenetic diversity of sub and upper montane forest communities in Hatton-Nallathanniya area of the Adam's Peak Wilderness in Sri Lanka *By S.A.C. Harshanie, H. S. Kathriarachchi*
	B-05	Anther culture potential of aromatic rice varieties and their F1 hybrids with local germplasm *By A.M. Senadeera, D.M.R.G. Mayakaduwa, D.M. Withanawasam, G.D. A. Priyantha, N.T. Prathapasinghe*
	B-06	Assessment of carbon sequestration by trees and lianas in Kodigahakanda: a regenerating small forest patch *By W.A.P.U. Ruwanmalie, S.M.W. Ranwala*

	B-07	Molecular characterization of some selected *Madhuca* spp. (Sapotaceae) in Sri Lanka *By H.M.N.D.Herath, H.D.Jayasinghe, I.U.Kariyawasam*
	B-08	Comparative morphological and phytochemical evaluation of *Plectranthus amboinicus* (Lour.) Spreng. (Kapparawalliya) and *Plectranthus barbatus* Andr. (Wal-Kapparawalliya) in Sri Lanka *By K. B. S. Sithara, I. U. Kariyawasam*
	B-09	Floristic analysis of a restoration site and adjacent forest patch in the lowland wet zone of Sri Lanka *By M. S. K. Perera, H.I.U. Caldera*
	B-10	Micropropagation of *Passiflora edulis* var. Horana Gold through shoot tip-derived nodal culture *By U.G.S. Malka, T.D. Silva*
	B-11	Leaf anatomical variation of selected mangrove species on the east coast of Sri Lanka *By R. Krishanthiny, H.I.U. Caldera, T. Mathiventhan, K.G.S.U. Ariyawansa*
	B - 12	Study on the influence of organic mucilage on seed germination, and seedling growth of *Phaseolus vulgaris* L. – A legume crop with high economic potential. *By R.M.C.S. Ratnayake, D.M.H.S.K. Nadungamuwa, T.P.G.N.T. Alvis*
	B - 13	Habitat dissimilarity in a regenerating wet lowland small forest reflects the importance of habitat specific improvements for assisted natural restoration *By W.A.P.U. Ruwanmalie, S.M.W. Ranwala*

Parallel Session C- Zoology and Environment Sciences

TIME	ABSTRACT NUMBER	TITLE
1.30–4.30 p.m.	C-01	Risk factors associated with chronic kidney disease of unknown etiology (CKDu) in Jaffna district, Sri Lanka. *By K. Sithamparapalini, P. J. Jude, B.R. Thangarajah, P. Subramaniam, J. Prabagar, U.A. Jayawardena*
	C-02	Assessment of Tributyltin induced changes in the blood profile of Giant Danio (Devario malabaricus) *By C.H. Uluwaduge, M.R. Wijesinghe, D.K. Weerakoon*
	C-03	A preliminary study on mites associated with solitary bees in Sri Lanka *By K.G.D.P Ariyarathne, W.A.I.P Karunaratne, W. Knee, I.C Perera*
	C-04	Environmental Risk Assessment of Microplastic Pollution on Negombo Beach, Sri Lanka Using Index Models *By C.C.D. Mendis, W.M.D.N. Wijeyaratne, S.R.C.N.K. Narangoda*
	C-05	Environmental transformations along an urban-rural land use gradient from Colombo to Sinharaja Man and Biosphere Reserve *By Ashen Ranaweera, Deepthi Wickramasinghe, V.P.I.S. Wijeratne, Devanmini Halwathura*
	C-06	Effects of environmentally relevant concentrations of Amoxicillin Trihydrate on Hypophthalmichthys molitrix (Silver carp) *By W.A.D. Navodya, M.M.K.I. Marasinghe, V.K. Fernando*

	C-07	Drivers of human-leopard encounters in Ambagamuwa, central highlands of Sri Lanka *By R. N. S. De Zoysa, T. S. P. Fernando, R. Marasinghe, M. De Silva, M.R Wijesinghe*
	C-08	Ecological study of mosquito breeding sites in Dunumdalawa forest, Kandy, Sri Lanka: Implications for mosquito control *By W.M.G.R. Wickramaratne, K.C. Weerakoon*
	C-09	Assessing the embryonic toxicity of Tributyltin, at environmentally relevant concentrations in Sri Lanka, using the Fish Embryo Acute Toxicity (FET) Test *By S.A.P. Dilshan, C.D. Jayasinghe, I.C. Perera, D.K. Weerakoon*
	C - 10	Patterns and variations of diurnal and nocturnal incubation behaviour of a ground-nesting waterbird, the Red-Wattled Lapwings (*Vanellus indicus*) *By Akila S. W. Peiris, H.H.E Jayaweera and Sampath S. Seneviratne*
	C - 11	Assessment of landscape and railway features associated with elephant-train collisions *By W.M.T.L. Karunasena, P. Fernando, V.R. Gunasekara, M.R. Wijesinghe,D.K. Weerakoon*
	C - 12	Preliminary molecular phylogeographical analysis of the endemic freshwater fish *Belontia signata (Anabantoiformes: Belontiinae)* in three river basins of Sri Lanka *By N. A. Liyanarachchi, T.S.P. Fernando, V.R. Gunasekara, D.K. Weerakoon*
	C - 13	Variation of non-volant mammalian communities along a sub-montane elevational gradient in Sri Lanka *By D. Maduranga, A.S. Adikari, S.J. Perera, S.S. Seneviratne*
	C - 14	Spatiotemporal Distribution of Seabirds in the Western EEZ of Sri Lanka determined using eBird: A Global Citizen Science Platform *By D. Meecle, S.S. Senevirathne*

	C-15	Assessment of pollution impacts in selected tributaries reaching lower reaches of Kelani River using physicochemical monitoring and biomarker response of caged Slender Rasbora (*Rasbora daniconius* (Hamilton,1822)) *By W. A. A. N. Wickramasignhe, K.M.S. Ruvinda*
	C-16	Cytogenotoxic effects of tartrazine, a food colouring agent, on *Allium cepa* root meristematic cells *By M.I.F. Imasha, U.A. Jayawardena, G.H. Galhena*
	C - 17	Evaluating the cytogenotoxicity of Stevia, a food sweetener, using *Allium cepa* assay *By T. T. Sithambaram, U. A. Jayawardena, G.H. Galhena*

Parallel Session D- Poster presentations

TIME	ABSTRACT NUMBER	TITLE
1.30–4.30 p.m.	D-01	Exploring laccase producing fungi isolated from freshwater ecosystems in the Anuradhapura and Ratnapura Districts, Sri Lanka *By S.D.M.K. Wimalasena, N.N. Wijayawardene, T.C. Bamunuarachchige, D.Q. Dai, R.G.U. Jayalal, D.J. Bhat, T.M. Dawoud*
	D-02	Physicochemical characterization and evaluation of the antimicrobial activity of silver nanoparticles biosynthesized by marine brown algae *Padina commersonii*. *By R. Ragavi, L.D.C Peiris*
	D-03	Foliose lichens as essential hosts for Lichenicolous Fungi: Insights from Horton Plains, Sri Lanka *By H. Dangalla, C. M. Nanayakkara, R.G.U Jayalal, D. Q. Dai, N. Wijayawardane*

	D-04	Bioactivity profiling of termite-associated fungus *Trichoderma virens* for antibacterial, antioxidant, and anticancer activities *By A.K.O.D. Amarasinghe, C.M. Nanayakkara, E.D. de Silva, P.A.N Punyasiri*
	D-05	Investigation of potential bioactive properties of macrofungi isolated from Anawilundawa wetland sanctuary, Sri Lanka *By K.A.M.R. Premarathne, S.S. Ediriweera*
	D-06	Morphology, phylogeny, and pathogenicity of pestalotioid-like taxa associated with scab disease of guava in the Ratnapura District of Sri Lanka *By M.B.N.S. Medawaththa, C. M. Nanayakkara, N. N. Wijayawardene, K.G.S.U. Ariyawansa*
	D-07	Unveiling and managing pathogens of Leaf Fall Disease in Sri Lankan rubber trees (*Hevea brasiliensis*) *By W.A.L. Wijayarathna, K.K. Liyanage, D.A.D.A. Daranagama*
	D-08	Genome-wide identification and characterization of nodulation-related genes in soybean (*Glycine max*) *By H.D.E.H. Weerasinghe, D.S. Muthumala, P.C. Fernando*
	D-09	Genome-wide analysis and characterization of the LysM-RLK gene family in *Oryza sativa* *By R.M.S.U.D Roland, D.S Muthumala, P.C Fernando*
	D-10	An assessment of the phytochemical, antioxidant, and anti-Inflammatory properties of *Tamarindus indica* fruit by in vitro bioassays *By D. A. D. M Silva, S. B Alahakoon, A.I. Kuruppu*
	D - 11	SNP marker diversity in black pepper (*Piper nigrum* L.) *By H.A. Thanthirige, N.A. Wimalarathna, A.M. Wickramasuriya*

	D – 12	Comparative analysis of blood indices in pancreatic cancer patients with and without diabetes: a preliminary study *By H.T. de Silva, I.C. Perera, D.K. Weerakoon*
	D – 13	Effect of polyamine seed priming in chlorophyll content of *Vigna radiata L*. seedlings under water stress *By W.M.D.A.K Weerasekara, R. Wimalasekera*
	D - 14	Evaluation of genotoxic effects of food flavour enhancer, monosodium glutamate (MSG) on the root meristem cells of *Allium cepa* L. *By V.T.Koggalage, R.Wimalasekara*
	D-15	Assessing employee knowledge and awareness of the need for carbon reduction before and after implementing carbon reduction measures in a shoe manufacturing facility *By P. Hettiarachchi, E. Lokupitiya*
	D-16	Optimizing indoor growth conditions for Gotukola (*Centella asiatica*) and Peppermint (*Mentha piperita* L.) using light spectrum experiments *By J.D.V.M. Obeysekara, T.A. Perera*
	D - 17	Microalgae *Chlorella sorokiniana* and *Scenedesmus sp.* as a sustainable source of beneficial bioactive compounds *By L. A. Udeshika, P. S. Saputhanthri*
	D - 18	Impact of plant growth regulator combinations and half-strength MS medium on in vitro shoot proliferation in two *Aloe vera* cultivars *By N.A.D.K. Deshani, K. Hirimburegama, H.D.D. Bandupriya*
	D-19	A preliminary taxonomic study of some selected *Sargassum* species in Sri Lanka *By D.K. Palihawadana, I.U. Kariyawasam*

	D-20	Understanding the relationship between water stress and stomatal conductance using an AI-based method *By I.R.J.C. Lenagala, T. Kulendran, K.N.M.L.C. Kirindiwatte, P.P.R.K. Fernando, I.S. Gallage, E.G.S.H. Gamage, W.G.G.S.M. Gunarathna, W.N.S. Gunathilaka, D.L.E. Navinda, R.G.S. Anurangi, P.C. Fernando, P.S. Saputhanthri*
	D-21	Comparative analysis of antioxidant accumulation in rice callus and rice seed extracts *By H.A.D.G. Rathnasiri, H.D.D. Bandupriya*
	D -22	Evaluating in-vitro response of *Passiflora edulis* var. Horana Gold using internodal and leaf segments *By U.G.S. Malka, T.D. Silva*
	D-23	Extending the vase life of *Chrysanthemum indicum* (magenta colour) cut flowers with natural and artificial preservatives *By B.S.M.R.I.N. Senevirathna, S.T. Vincent, R.M.A. Yesini, G.A.M. Perera, L.D. Sapuarachchi, W.S.M. Witharama, R.A.P. A. R. Siriwardhana, T.H.J.N. Perera, M. Junkeer, P.S. Saputhanthri*
	D-24	Effect of *Aloe vera* (L.) Burm. f. aqueous extract on seed germination and seedling growth of *Abelmoschus esculentus* (L.) Moench *By R.M.C.S. Ratnayake, R.M.T.K. Ranathunga, K.D.P.V. Sudeshini*
	D-25	Comparison of soil properties in space open and closed dry-mixed evergreen forest ecosystems in a human-impacted forest landscape in the dry zone, Sri Lanka *By S.M Rajapaksha, S.W.M. Ranwala, D. K. Samarathunga, W.P.N. Perera*
	D-26	Comparison of floristic changes and carbon sequestration in areas of varying canopy covers in a degraded dry-mixed evergreen forest, Sri Lanka *By S.M Rajapaksha, S.W.M. Ranwala, D. K. Samarathunga, W.P.N. Perera*

	D-27	Temporal distribution of salt marsh species in the Kalpitiya, Northwestern province of Sri Lanka *By U.D.S.K. Ruwanjana, I.A.J.K. Dissanayake*
	D-28	An investigation of the effect of selected plant extracts on plant growth of *Capsicum annum* seedlings *By B.M.N.S. Balasooriya, B.G.C.I. Bopitiya, R.P.T. Chamuditha, K.P.M.C. Chandrarathna, D.O.S. Chandrasiri, D.B.P. Darshani, A.W.K. De Silva Wijayawickrama, R.G.S. Anurangi, P.S. Saputhanthri*
	D-29	Changes in pigment composition during the development of *Mesua ferrea* leaves *By R.A. Steinwall, J.A.M.Y. Wishwani, J.G.K.N. Sasindi, M.A.D.H. Shehan, K.M.R.K. Somasiri, A.G.N.P. Wickramaratne, U.H.Y. Weeramini, R. M. S. B. Madawala, K.I.L. De Silva, P.S. Saputhanthri*
	D-30	Development of an organic liquid fertilizer to replace commercial hydroponic solution (Albert solution) to cultivate “Kangkung” plants *By T.A. Perera, S.U. Sooriyaarachchi, C.Y. Amarasinghe, A.K.O.D. Amarasinghe, M.B.N.S. Medawaththa, J.D.V.M. Obeysekara, K.A.M.R. Premarathne, A.M. Senadeera, S.V. Withanachchi*
	D-31	Investigating the effect of selected plant extracts on polyphenol oxidase activity in *Annona muricata* L. fruit extract *By S. Rasaiya, R.M.N.T.D Ratnayake, H.M.S. Pieris, R.V. Ranasinghe, N.S.G. Punchihewa, P.H.H.J. Bandara, P.S. Saputhanthri*
	D-32	Habitat preference of *Panthera pardus kotiya* in the Kumana National Park, Sri Lanka *By S.T. Jayakody, J. P. S. Priyankara, D.M.W. Dissanayaka, T.S. P. Fernando, M.R. Wijesinghe*
	D-33	Morphological characterization of marine ponyfish species (Family Leiognathidae) on the in west coast of Sri Lanka *By A.M.P.E.K. Atapattu, W.W.P. Rodrigo, W.A.Y. Chandrani, R.J. Illeperuma*

	D-34	Validation of vessel monitoring system records with logbook data of multiday fishery vessels: a case study in the Southern and Southwestern exclusive economic zone of Sri Lanka. *By W.G.A.U. Dharmasiri, M.M.K.I. Marasinghe, S.S. Gunasekara*
	D-35	Assessment of anthropogenic influence on blue carbon stocks of tidal salt marshes in Northwest coast, Sri Lanka *By E.H.I.C.E. Hewage, S. Udagedara, E. Lokupitiya*
	D-36	Feasibility of implementing a circular economy for plastic waste management in Fast Moving Consumer Goods (FMCG) industry in Sri Lanka *By T. R. Wijayaweera, D. Halwatura*
	D-37	Are odonates sensitive to agrochemicals? A comparison of odonate diversity in an agricultural vs natural habitat *By S.M.D.B.A Mudalige, E.A.D.N.D Edirisinghe, U. A. Jayawardena*
	D-38	Spatial distribution of the macrobenthic community, relative to sediment dynamics and hydrodynamic regimes in Negombo Lagoon *By B.M.D.M. Chandrapala, H.A.S.D. Perera, V.K. Fernando, H.A.S.G. Dharmarathne and M.M.K.I. Marasinghe*
	D-39	A preliminary study on soil arthropod diversity in Karadiyana, a solid waste dumping site, Western province, Sri Lanka *By K.H.W. Kanchana, E.A.D.N.D Edirisinghe, U. A. Jayawardena*
	D-40	Hot spots of mangrove habitat transformation in selected coastal wetlands in the Southern Province of Sri Lanka: A spatiotemporal approach *By F. B. I. Nimeshi, L. Le De, V. K. Fernando, D.D. Wickramasinghe*

	D-41	The impact of mangroves on environmental wellbeing, socioeconomic importance and economic status in Sri Lanka *By A. Marzook, U. Bandaranayake*
	D-42	The impact of vehicle collisions on macro-invertebrate fauna adjacent to the protected area network of southern wildlife region Sri Lanka. *By D.T. Ranaweera, K.M.S. Ruvinda*
	D-43	Seroprevalence and risk factors of toxoplasmosis among antenatal mothers in Kuliyapitiya; A cross sectional study *By A.S.N Jayasinghe, T. Wijerathne, U. A. Jayawardena*
	D-44	Diurnal and nocturnal activities of the Cherry Barb (*Puntius titteya*) inhabiting a shallow stream in the Western Province, Sri Lanka *By I.A.S.R. Ileperuma, P.N. Dayawansa*

ISSN 2012-8924

9 772012 892003

Proceedings of the 44th Annual Sessions
Institute of Biology, Sri Lanka