INSTITUTE OF BIOLOGY
SRI LANKA

BIOLOGICAL INNOVATIONS FOR FOOD SECURITY AND SUSTAINABLE GREEN ECONOMY

Proceedings of the 45th Annual Sessions

25th September 2025

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PROCEEDINGS OF THE 45TH ANNUAL SESSIONS

Theme

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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. It was established in 1981 by a group of Sri Lankan biologists led by the late Prof. B.A. Abeywickrama, Emeritus Professor of Botany at the University of Colombo. In 1984, it was formally incorporated as an organization through Act of Parliament No 22.

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 currently has around 637 members engaged in research, education and industry. The institute also awards Fellowships and the status of Chartered Biologist for eligible members. Membership is offered under seven categories, with the opportunity to transfer to other higher categories over time. 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), Chartered Members are eligible to use C. Biol (Sri Lanka), and Members may use M.I. Biol (Sri Lanka). The designation 'Chartered Biologist' endorses the high professional 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 also works to promote public interest in biology by regularly conducting forums and discussions on current topics. The annual national Biology Olympiad competition organized and administered exclusively by the IOBSL, is a hallmark event in the country. The Sri Lankan Biology Olympiad competition provided students with the opportunity to explore their interest in the field of biology and challenge their knowledge and skills. 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 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 among undergraduates of universities in Sri Lanka in biology and interdisciplinary studies.

The Institute also recognizes and celebrates excellence in research and creativity. The prestigious 'Young Scientist Award' recognizes outstanding contributions and achievements in research by early-career corporate members of the IOBSL. In addition, the biology photography competition offers professional, amateur, and young photographers across Sri Lanka the opportunity to capture the hidden wonders of biology, helping to communicate scientific themes to the general public.

To strengthen scientific communication, the IOBSL publishes two major platforms: 'BIO-NEWS' its official e-newsletter featuring the activities conducted by the institute, research updates, feature articles, art and creative writing, and contributions from for young biologists; and the Sri Lankan Journal of Biology (SLJB), a biannual, peer-reviewed, open access journal that provides a platform for disseminating the findings of biology-related research under a Creative Commons Attribution 4.0 International License. The Institute also maintains active outreach through its Facebook and LinkedIn pages, which share updates on activities, competitions, and research news, thereby bridging the gap between researchers and the general public.

The Annual Sessions of the IOBSL provide a forum for both senior and junior biologists to communicate their research findings to a multifaceted audience. This year marks the 45th Annual Sessions, continuing the Institute's long-standing tradition of advancing the frontiers of biology in Sri Lanka.

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PRESIDENTIAL ADDRESS

Biological Innovation for Food Security and a Sustainable Green Economy: Sri Lankan Perspective of Postharvest Technology

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Food security in Sri Lanka is shaped by multiple and interconnected pressures, including fluctuating global markets, climate change, degradation of natural resources, and socio-economic instability. Although the agriculture sector contributes only 7.7% Sri Lankan GDP, agriculture remains a cornerstone of the economy and contributes significantly to rural livelihoods. The sector is dominated by smallholder farmers, who cultivate rice, fruits, vegetables, field crops, and spices, accounting for over 70% of domestic food production. However, productivity is often constrained by outdated practices, high postharvest losses, poor market linkages, and limited access to modern technologies.

The concept of a sustainable green economy underscores the need to enhance agricultural productivity without compromising environmental integrity. The transition to a sustainable green economy is therefore critical. According to UNEP, green economy is defined as one that is required *low-carbon, resource-efficient, and socially inclusive* system. Therefore, it seeks to achieve economic growth without depleting natural resources or harming ecosystems growing wealth without destroying the very systems that sustain life. Sri Lankan green economy requires boosting productivity while conserving ecosystems, reducing greenhouse gas emissions, preventing biodiversity loss, and improving energy efficiency. However, barriers such as high initial investment costs, weak policy enforcement, limited technical capacity, and resistance to change among stakeholders slow this transition in the country. Industries and stakeholders often hesitate to embrace new approaches, despite their long-term benefits. In this context, the adoption of innovative agricultural practices is crucial for enhancing food security, particularly in developing regions where smallholder farmers face systemic challenges.

Biologically innovative technologies and practices that leverage biological processes and organisms provide a strategic pathway to achieving both food security and environmental sustainability. Innovative postharvest technologies that extend the shelf life of produce, minimize losses, and enhance quality can significantly reduce waste while improving resource efficiency. Controlled and modified atmosphere storage methods, improved packaging materials, and solar-powered cold chains are additional solutions that can cut postharvest losses and reduce carbon footprints.

The FAO estimates that approximately 1.3 billion tons of food are wasted globally each year, underscoring the urgent need for innovation across all sectors of agriculture. In Sri Lanka, cutting postharvest losses even by 10% could save hundreds of thousands of tons of food annually, directly strengthening food security and farmer incomes.

Rice, the staple food in the country, occupies about 34% of cultivated land and supports nearly 1.8 million farm families. Annual paddy production averages 4.3 million MT, but postharvest losses of around 12% (equivalent to 516,000 MT) are reported due to poor harvesting, drying, milling, and storage practices. Fruits and vegetables, which are vital sources of nutrition and income for farmers, experience postharvest losses of 30–40%, equivalent to nearly 684,566 MT annually, resulting in financial losses of approximately Rs. 88,000 million in recent years. However, current postharvest losses have declined to 15–20% for fruits and 20–30% for vegetables, reducing the associated economic loss to around Rs. 32,000 million annually. This reduction has been achieved primarily through the introduction of innovative R&D initiatives in the country. By 2021, total fruit exports generated approximately US$ 38.0 million in revenue. As an example, in 2023, nearly 19,500 MT of bananas were exported to various countries and gained earnings US$ 17.7 million. But these figures remain small compared to the potential due to high domestic losses during ripening, handling, and storage of banana. Cinnamon, pepper, cloves, and cardamom account for about 30,000 MT of agricultural exports annually, generating export earnings of US$ 462 million in 2024, reflecting strong global demand. However, quality deterioration during drying, storage, and packaging often reduces competitiveness in international markets, which remains a key challenge to be addressed through modern biological innovations.

Sri Lankan R&D initiatives have demonstrated the effectiveness of postharvest interventions in reducing losses across a range of commodities. Rice stored in hermetically sealed PVC tanks and airtight bags maintained moisture stability, suppressed insect infestation, and preserved head-rice yield, with mass losses as low as 0.4% over several months of storage. Hermetic storage of pulse grains has proven effective in significantly reducing storage losses while preventing the development of hard-to-cook characteristics in mungbean and cowpea. Inefficient drying and poor storage conditions accelerate undesirable chemical changes in grains, promoting the formation of mycotoxins. In this context, aflatoxin contamination in maize is a significant concern in Sri Lanka due to the growth of *Aspergillus flavus*, the primary aflatoxin-producing fungus, posing serious risks to human health. Proper drying, optimal storage management, modified atmosphere storage systems, and innovative fumigation methods such as ozone treatment are effective strategies to control fungal proliferation and reduce aflatoxin contamination in maize.

The adoption of IPM management strategies in warehouses, such as early detection methods except pheromone traps, natural insecticide-incorporated storage polybags, modified atmosphere storage techniques, and biological control has been shown to significantly reduce pest damage. In addition, plant-based fumigants derived from various botanical sources, together with ozone and irradiation treatments, have proven effective method of controlling common stored-product pests such as *Sitophilus spp*., *Sitotroga cerealella*, and *Callosobruchus chinensis*, etc. These approaches not only minimize dependence on synthetic chemical fumigants but also align with global trends toward safer, eco-friendly, and residue-free storage technologies, thereby enhancing the competitiveness of agricultural commodities in international markets.

Controlled atmosphere storage, when combined with cold storage, retard ripening process, reduces fungal decay, insect damage, and significantly extends the shelf-life of fruits and vegetables. Modern postharvest management encourages the use of controlled ripening chambers that utilize ethylene for proper ripening of fruits and optimized storage conditions to maintain both quality and safety. Rather than relying on chemical treatments for fruit

ripening, innovative and safe ripening methods such as ultrasound treatment, ethylene-releasing natural agents, and plant-based coatings can be used to induce fruit ripening. These methods ensure uniform ripening of fruits while preserving nutritional quality, preventing spoilage, and minimizing health risks. The implementation of modern dehydration techniques, including vacuum microwave drying, heat pump drying, solar tunnel dryers, and other solar drying techniques, enhance microbial safety, preserve the nutritional, biochemical, and sensory quality of fruits and vegetables, and improve their marketability. These types of drying techniques add value to export products and facilitate the development of ready-to-use fruit and vegetable products, thereby contributing to economic growth and food security in the country. Solar-based technologies, in particular, provide energy-efficient and environmentally friendly solutions that are well-suited for small and medium-scale producers. The use of solar-powered cold rooms, evaporative cooling chambers, and natural wax or biofilm coatings effectively reduces microbial spoilage and optimizes energy efficiency in postharvest storage of fruits and vegetables.

The fruit and vegetable sector produces substantial amounts of waste throughout harvesting, transportation, processing, and consumption. If this waste is not managed properly, it can lead to significant environmental challenges. Implementing effective valorization strategies can help reduce pollution, improve food security, generate income, and support a sustainable green economy. Especially fruits, vegetables and grain wastes can be transformed into animal feed, organic fertilizers, bioenergy, bioactive compounds, industrial products, and innovative food items. Cleaning vegetables with contaminated water may cause significant public health hazards. This is more crucial in areas of upcountry vegetable production. Therefore, washing vegetables with potable water, combined with innovative postharvest handling techniques, is essential to ensure food safety and protect consumer health.

The future of biological innovation in Sri Lankan agriculture depends on enabling regulatory frameworks, investment in research and development, and robust public-private partnerships. Strengthening extension services, capacity building, and aligning postharvest innovations with global market standards will be essential. By adopting these technologies, Sri Lanka can ensure food security, enhance export competitiveness, improve rural livelihoods, and mitigate climate change, ultimately positioning agriculture as a driving force in the sustainable green economy.

FELICITATION OF

Emeritus Professor Jeevanthi De Silva Amarasinghe

Citation Presented by

Professor K.B. Suneetha Gunawickrama, F.I. Biol. (Sri Lanka)
Chair Professor, Department of Zoology, University of Ruhuna, Sri Lanka

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Institute of Biology, Sri Lanka is delighted to felicitate Emeritus Professor Nallahandi Jeevanthi De Silva Amarasinghe for her lifelong contribution to Biology, Zoology, and Aquatic Biology in teaching, research and institutional development, and for many other services rendered in respect of Biology education, science dissemination and national development at its 45th Annual Sessions held on September 25, 2025.

Family background and education

Prof. Jeevanthi De Silva hailed from a respectable family in Ambalangoda. She was born on February 18th, 1956, and is the eldest daughter of the family of eight siblings. Her late father Mr. N. Sumanadasa De Silva retired as an electrical engineer Ceylon Transport Board, and her late mother Mrs. Gayini Nandawathie De Silva was an Agriculture-specialized teacher trained at the Kundasale Agriculture Training School and retired from Karandeniya Central college as a vice principle. Prof. Jeevanthi received her primary and secondary education from G/ Dharmashoka College at Ambalangoda from 1961 to 1974. After passing GCE (A/L) in 1974, she got admission to then the Faculty of Natural Sciences of the University of Sri Lanka,

Colombo Campus in 1975. She graduated from the University of Colombo, securing a Special Degree in Zoology with Second Class Honours in August 1979.

Academic career

After a brief period serving as a temporary demonstrator at Department of Zoology, University of Colombo, she started her academic career when joining the Department of Zoology of then Ruhuna University College as a Probationary Assistant Lecturer in Zoology on 20th March 1980. While shouldering a huge responsibility in teaching as a pioneering academic in a newly established university, young Ms. Jeevanthi De Silva was fortunate to win a postgraduate scholarship in Namur, Belgium at Faculties Universitaires Notre Dame De La Paix. On successful completion of her doctoral studies in three years' time, she was awarded the Doctor of Science in Zoology Division in October 1985. Her doctoral education provided the path to specialize in Limnology, Fish Biology, Aquatic pollution and management, the required areas to be developed in the department during that time. Dr. Mrs. Jeevanthi De Silva Amarasinghe returned to Sri Lanka having the PhD, when Ruhuna is already a fully pledged, University of Ruhuna, with a well-developed Department of Zoology under the leadership of the late Professor Sena De Silva, then Chair Professor, and Dr. Celine De Silva. Dr Jeevanthi was promoted to the Grade of Lecturer in Zoology and got her confirmed in the academic career in November 1985. She climbed the academic career ladder as a Senior Lecturer from January 1988 to November 2007, and then served as Professor in Zoology since November 5th November 2007 to November 4th, 2015, and became a Senior Professor in Zoology on 5th November 2015. After completing uninterrupted service record of 41 years seven months and 10 days, Senior Professor Jeevanthi Amarasinghe retired from the University of Ruhuna on September 30, 2021 leaving an unprecedented service record at the University of Ruhuna. Recognizing her dedicated service to the University of Ruhuna, Dr. Jeevanthi was awarded the title of Emeritus Professor in October 2021.

Service to University of Ruhuna

The Department of Zoology, Faculty of Science and the University of Ruhuna were nourished through her unparallel dedication and lifelong commitments in academic and administrative matters. She was a born talented and passionate teacher loved by several thousands of students over 41 years of uninterrupted career. She has served as the Head of the Department of Zoology for five occasions, including one term when she was elected as the Dean of the Faculty of Science. Prof. Jeevanthi was the Dean of the Faculty of Science, rendering an unparallel leadership to the faculty from 8th December 1998 to 18th June 2001. Her representation at the Senate spanned more than 27 years. She served the Council of the University of Ruhuna for an unprecedented duration from December 1998 to June 2001 as the Dean of the Faculty of Science, and thereafter for three consecutive terms as the elected Senate Representative to the Council from 9th August 2011 to 8th August 2020. Her academic contribution was significant in shifting the older curriculum into Credit-based Course unit system of curriculum during 2002-2004, where her Zoology and Environmental education was fundamental, giving leadership for

preparing an initial thorough curriculum for the General degree and Special Degree courses in Zoology. Even after retirement, she continues to be involved in maintaining the standards of education we provide students with.

Service to other higher education institutes

Her academic service in Zoology and Biology education did not limit to Ruhuna premises. She was often invited to be a visiting teacher or a consultant at other universities. She was a visiting lecturer for BSc Degree programme in the Open University of Sri Lanka - Regional Center, Matara from 1st February 1995 to 31st May 2012. Dr Jeevanthi joined Senior Lecturer Grade I in Zoology at Open University's Regional Center at Matara on contract basis from 15th April 1996 to 14th August 1997 during the sabbatical leave and also worked as a Senior Consultant there from 15th August 1997 to October 2001. Furthermore, she was a Consultant Academic Coordinator of the Faculty of Natural Sciences at the Matara Regional Centre, The Open University of Sri Lanka from 1st February 2011 to 31st July 2011 as well as from 15th November 2012 to 14th May 2013. Prof. Jeevanthi served as an External Member of the Faculty Board of the Faculty of Natural Sciences, Open University of Sri Lanka, nominated by the said Faculty Board since November 2013 to September 2019.

Professor Jeevanthi rendered a great service as a visiting fellow for the Department of Biological Sciences, of the Rajarata University of Sri Lanka as a young university of the state higher education, for several areas for which they did not have the human resources. She was a Professor on contract basis at Department of Biological Sciences, Rajarata University of Sri Lanka from 16th August 2010 to 30th June 2012 (during the sabbatical leave), relieving a huge academic burden off their department. Again, she was a visiting Lecturer for ZOO 4309 - Fish health management and ZOO 4306 - Aquaculture Engineering at the Department of Biological Science, Faculty of Applied Sciences, Rajarata University of Sri Lanka, Mihinthale from November 2012 to October 2016. She was a question paper Setter, Moderator & Second Marking Examiner of number of course units conducted by the Department of Biological Science, from August 2010 until retirement.

Contributions to administration

It is worth mentioning at least a few instances when Prof Jeevanthi contributed as an administrator. She was a brilliant and prolific leader wherever she took the leading position at the University of Ruhuna. She was the first female Dean of the Faculty of Science for one term as mentioned above, and the Director of the Centre for the International Affairs (CINTA) of University of Ruhuna, from 15th May 2007 to 30th June 2010. She also served as the Acting Director of the Centre for Modern Languages and Civilizations (from 01.08.2007 to 25.09.2008). She served as the Programme Coordinator of the MA Degree in Conflict, Peace and Development Studies (CPDS) jointly conducted by the Tribuvan University in Nepal and University of Ruhuna in Sri Lanka from 1st September 2008 to 30th June 2010. She was a member of the Staff Development Centre (SDC) of University of Ruhuna, and Coordinator of

Higher Education for the Twenty-first Century (HETC) project University Development Grant (UDG) from 25th February 2010 to 31st May 2011). She served as the Chairman of the Progress review sessions of the grant scheme Transforming University of Ruhuna to International Status (TURIS) over many years and helped the university to achieve the targets of internationalization through those research grants. Being a student counsellor, patron, advisor, senior treasurer and a member of many university and faculty level committees and student-based societies, she contributed to enhance the extra-curricular activities of the faculty and the university.

Research career

Prof. Jeevanthi De Silva Amarasinghe has supervised more than 20 undergraduate students, 15 postgraduate students who led to PhDs, MPhils and MSc degrees. She has published three book chapters, five national reports, and authored or coauthored more than 85 research communications including research journal articles and scientific conference abstracts. She has also served as editorial board member of the Ruhuna Journal of Science, the only Web of Science research journal of the university of Ruhuna for many years since its inception in 2006. She was an essential referee/reviewer for all research conferences organized by the university and other higher education institutes, and a journal reviewer on numerous occasions.

Contribution to national services

Prof. Amarasinghe extended her service for nationally important matters in numerous occasions. She had been a Chief Examiner in Zoology/Biology for G.C.E. (A/L) examination since 1990 until last year, and she continued to involve in this national service with enthusiasm for several years even after retirement. She was a member of many national level committees. To name a few, the member of the Editorial committee – Freshwater Fauna of Sri Lanka (1987), of the technical Review committee of wetland site Report and Conservation Management Plan (1994), and a member of the Oil Spill Contingency Management Project (2003). Her service extended to improve the quality of the education system in Sri Lanka by serving as a member of the Standing Committee of Science (1999-2001), Special Committee on Science communication, at NSF 2002-2003 and a member of the IRQUE project evaluation team, Ministry of Tertiary Education and Training.

Consultancies in her expertise area

As a consultant, Prof. Amarasinghe had worked on many projects, and to name a few, Fishery Harbour Project at Hikkaduwa (1997), 'Rakewa, Kalamatiya and Ussangoda coastal conservation project implemented by IUCN, and the Project on paddy cultivation within Katagamuwa Sanctuary.

Awards

She was the recipient of Postgraduate Scholarship offered by the Kingdom of Belgium to pursue higher studies, Academic Exchange Fellowship 1989/1990 awarded by the Association of Commonwealth Universities, and ACU Development Fellowship 1992-1993 awarded by the Association of Commonwealth Universities. For her excellence in service rendered to the University of Ruhuna, she was awarded by the Ruhuna university service Award 'Threeshath Purna Sewa Upahara'. For her active contribution to the field of education of the southern Province, she was awarded the 'Dakshina Lanka Wanitha Pranama' at the international women's day organized by Southern Province Council of Sri Lanka.

Memberships in professional bodies

Prof. Jeevanthi De Silva Amarasinghe is a Chartered Biologist awarded by the Institute of Biology, Sri Lanka since 2008, while she was a full member of the Institute of Biology, Sri Lanka since September 2001. She is a life member of the Field Ornithology Group of Sri Lanka (FOGSL) since 1978, and of Sri Lanka Association for the Advancement of Science (SLAAS) since 1993. Professor Jeevanthi is a full founder member of Sri Lanka Association for Fisheries and Aquatic Resources (SLAFAR) established in 1994. She is also a member of a several international societies, including, Asian Fisheries Society (AFS) since 1987, Societie International Limnologique (SIL) since 1989, and Inland Fisheries Society of India (IFSI) since 1990.

Contributions to the science related societies/ institutes of national significance

Prof. Jeevanthi De Silva Amarasinghe served in many national level committees. She was an elected Council member of the Institute of Biology in 2002/2003, the Editor of the Council of IOB for the year 2003/2004. Further, she was an active member of the SLAAS involving in leading and contributing to national tasks in various capacities. Prof. Jeevanthi Amarasinghe was a member of the Executive Committee of SLAAS Section D in 1997, and a Member of the General Research Committee of the SLAAS in 2000, and the Rapporteur of SLAAS Section D in 1998 and 1999. She served as the Joint Secretary of the Science Education Committee, SLAAS 2005, and the Coordinator of the Science Education committee (SEC/SLAAS) activities at the Southern Province, from 2000 to 2006, including the School Science project in 2001. In addition, she was an Executive Committee Member of SLAFAR in 1994/95, and 1995/96.

Government appointed committees

Professor Jeevanthi Amarasinghe also served in government appointed committees, to name a few, she was a member of the Sectorial Committee on Fish and Fishery Products - Sri Lanka Standards Institution, Colombo (from 1992 to 1995), a member of the Curriculum Development committee for G.C.E. (A/L) Biology New Syllabus (appointed in January 1994) appointed by NIE, Maharagama, and a member of the Governing Board of the Post Graduate Institute of Science, Peradeniya from January 1999 to June 2001. She was also served as a

member of the Coordinating Committee, Progress of Implementation of National Action Plan for Haritha Lanka Programme, appointed by the Secretary, Ministry of Environment.

Felicitation

Her list of contributions to Biology education in Sri Lanka and other contributions to institutional and national level matters are well beyond the list of services that are mentioned here. In concluding this citation, it was a timely nomination by the Council of the Institute of Biology Sri Lanka to felicitate Professor Jeevanthi De Silva Amarasinghe at this serene juncture of her retired life. Considering her lifelong contribution to Biology, Zoology and Aquatic Biology in teaching and research and institutional and national services rendered over 45 years of her academic career in connection to Biology education and dissemination, Council of the Institute of Biology Sri Lanka is pleased to felicitate and honour Emeritus Professor N. Jeevanthi De Silva Amarasinghe. The IOBSL council wishes her a long and healthy life.

ABSTRACTS – ORAL PRESENTATIONS

Parallel Session 1: Microbiology and Chemical Biology

In-vitro evaluation of synergistic antibacterial effects of three Sri Lankan medicinal plants against selected skin-infecting bacteria

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Skin infections pose a significant global public health challenge due to the increasing resistance of pathogenic microorganisms to conventional antibiotics, which has increased focus on developing natural-based antimicrobial treatments. The present study aims to investigate the synergistic antibacterial potential of three medicinal plants, i.e., *Dillenia retusa* (Godapara: bark, leaves, and fruit), *Alpinia malaccensis* (Kaluwala: rhizome), and *Mimosa pudica* (Nidikumba), traditionally used in Sri Lankan herbal medicines, against selected skin-infecting bacterial strains. Plant materials were air-dried, processed to produce 50% ethanolic extracts via maceration, and concentrated using a rotary evaporator. Five main extracts were tested along with their eleven synergistic combinations. Phytochemical screening was conducted qualitatively to identify bioactive compounds. The antibacterial activities of the extracts against *Staphylococcus aureus* (DSM 20231), *Escherichia coli* (DSM 30083), and *Salmonella typhimurium* (ATCC 14028) were assessed using the agar well diffusion method on Mueller–Hinton agar with 6 mm wells, 0.5 McFarland. Assays were triplicated, and results expressed as mean±Standard Error of the Mean. The broth microdilution method was used to determine the minimum inhibitory concentrations (MICs) with an eight-concentration series of two-fold dilutions. Phytochemical analysis confirmed the presence of polyphenols, tannins, flavonoids, terpenoids, glycosides, steroids, and coumarins in the selected plant extracts. Among tested extracts (200 mg/ml), *A. galanga* showed the highest inhibitory zone of 31.1 mm with a MIC value of 12.5 mg/ml against *S. aureus*, and its synergistic combinations also exhibited strong inhibitory activity with zone of inhibition ranging 23.7-27.3 mm, while exhibiting MIC values between 50 and 12.5 mg/ml. Identified phytochemicals may contribute to the observed antibacterial activity. The other two bacterial strains were not inhibited by any of the tested extracts. MIC was determined only for the ABST-positive strain. In conclusion, selected plant extracts and combinations demonstrated notable *in-vitro* antibacterial efficacy against *S. aureus*, necessitating comprehensive mechanistic and pharmacological investigations.

Keywords: Antibacterial, medicinal plants, skin infections, phytochemicals

Acknowledgement: This study was supported by the Biomedical Science degree programme conducted by the Department of Life Sciences, Faculty of Science, NSBM Green University.

Enhancing the biodegradation of nylon-based textile waste using microbial consortia

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The continuous expansion of the textile industry has led to the accumulation of synthetic polymer waste, where nylon has emerged as a major environmental problem due to its extreme resistance to natural degradation. Conventional disposal methods are either energy-intensive or environmentally harmful. To the best of our knowledge, this study is the first to investigate textile waste degradation using microbial consortia in Sri Lanka, despite several related studies being reported globally. Therefore, the main aim of this study was to find out the possibility of nylon biodegradation using newly developed microbial consortia. Microorganisms were isolated from the Karadiyana municipal waste site and the Department of Plant Sciences culture collection. Microbes, including *Bacillus cereus*, *Pseudomonas aeruginosa*, *Aspergillus niger*, *Trichoderma* spp., *Fusarium* spp., and two unidentified fungal and bacterial strains, were used for the experiment. All the isolates were subjected to testing of their ability to secrete enzymes, cellulase, and laccase (indicating degradative potential). The selected microbes were tested for their ability to form consortia through compatibility testing. Three microbial consortia: *B. cereus* + *P. aeruginosa*, *Trichoderma* spp. + *Aspergillus* spp., and *Fusarium* spp. + unidentified fungi were selected and applied to sterilized, pre-weighed nylon fabric samples. Over a 12-week incubation, gravimetric analysis and Fourier-transform infrared spectroscopy (FTIR) were conducted every three weeks to quantify weight loss and detect polymer structural changes. Scanning electron microscopy (SEM) was employed to visualize surface morphological alterations. The consortium of *B. cereus* and *P. aeruginosa* showed the highest weight loss percentage (19.33%) after 12 weeks, followed by *Trichoderma* spp. *A. niger* (14.07%) consortia. FTIR revealed significant shifts in the amide and carbonyl functional groups, while SEM confirmed the progressive physical deterioration of the nylon fibers. These findings demonstrate that properly selected microbial consortia, particularly bacterial combinations, can significantly enhance the biodegradation of nylon.

Keywords: Nylon degradation, microbial consortia, textile waste**,** weight loss

Bioactivities of termite nest-derived actinomycetes

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Termite nests represent a unique but underexplored ecological niche harbouring diverse microbial communities capable of producing novel bioactive metabolites. This study aimed to isolate and evaluate termite nest-derived actinomycetes for antimicrobial, antioxidant, and enzymatic activities. Eight morphologically distinct isolates (A1–A8) were obtained using selective pre-treatment and enrichment methods. The combined physico-chemical pretreatment methods involve calcium carbonate enrichment followed by plating on starch casein agar (SCA) and actinomycete isolation agar (AIA) supplemented with antibiotics. Antibacterial screening demonstrated that isolate A2 exhibited strong inhibition against *Escherichia coli* (37 mm) and *Pseudomonas aeruginosa* (22 mm), while no conspicuous activity was observed against *Staphylococcus aureus* and *Bacillus cereus*. Isolate A5 displayed antifungal activity against *Candida albicans* (15 mm). Antioxidant activity, assessed by the DPPH assay, showed low radical scavenging potential compared with the standard ascorbic acid (IC_{50} = 5.31 µg/mL). L-asparaginase production, a clinically significant enzyme used in leukemia treatment, was detected in several isolates, with A3 and A7 showing the highest quantitative activity. Thin Layer Chromatography (TLC) of A2 extract indicated the presence of chemically diverse metabolites, though detailed profiling is ongoing. All experiments were conducted in triplicate to ensure reproducibility. The results highlight termite nests as promising reservoirs of actinomycetes with antimicrobial and enzymatic potential, particularly isolates A2, A3, A5, and A7, which demonstrate significant bioactivities of pharmaceutical relevance.

Keywords: Actinomycetes, antibacterial, antifungal, L-asparaginase, bioactive metabolites

Preliminary assessment of the enzyme activity of wild mushrooms collected from Baduraliya, Sri Lanka

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Wild mushrooms are a largely untapped natural resource with significant potential for food, medicine, sustainable agriculture, and industrial applications. However, their diversity and bioactive properties remain underexplored specially in Sri Lankan context. This study focused on identifying wild mushrooms collected from Baduraliya, Western Province, Sri Lanka, based on their morphological characters, and screening them for the enzymatic activities. Morphological and microscopic characters of ten wild mushrooms were compared with published keys and guides for the identification. Accordingly, the ten specimens were identified as *Termitomyces microcarpus*, *Lentinus* sp., *Lentinus strigosus*, *Coprinus disseminatus*, *Tramella fuciformis*, *Pycnoporus* sp., *Auricularia* sp., *Ganoderma* sp., and *Schizophyllum* sp. 1 & 2. Biochemical assays were conducted to assess the enzymatic activities (laccase, amylase, cellulase, phosphatases, L-asparaginase, and L-glutaminase) of the fungal mycelium isolated from the above 10 specimens. All enzyme assays were performed as agar plate-based assays in triplicate to ensure reproducibility. Four isolates, *Lentinus* sp., *L. strigosus*, *C. disseminatus*, and *Ganoderma* sp., exhibited laccase activity, with *C. disseminatus* showing the highest mean zone diameter (7.51 ± 0.05 cm). Three isolates, *T. fuciformis*, *Pycnoporus* sp., and *Lentinus* sp., produced extracellular amylase. All isolates except *T. microcarpus* and *C. disseminatus*, demonstrated cellulase activity, with *L. strigosus* exhibiting the highest cellulase index (1.96 ± 0.11), indicating lignocellulose degradation potential. Phosphate solubilization was observed in one *Schizophyllum* isolate, while L-asparaginase activity was detected in *T. microcarpus*, from mycelium grown in asparagine-supplemented Modified Czapek Dox's broth media, with an enzyme activity of 12.123 units/mL (defined as the amount of ammonia released in µmol per minute at 37 ± 2 °C), suggesting potential applications in anticancer therapy and industrial enzyme production. None of the isolates produced L-glutaminase under the experimental conditions, which may reflect species-specific gene regulation or the need for further optimization of culture parameters. These findings provide foundational insights into the enzymatic capabilities and bioactive potential of underutilized wild mushrooms in Sri Lanka, paving the way for further research on their sustainable use in biotechnology and medicinal applications.

Keywords: Amylase, cellulase, laccase, L-asparaginase, wild mushrooms

Preliminary investigation of plant-growth promotion and bioremediation of diesel by fungal endophytes associated with salt marsh plants in Kalpitiya, Sri Lanka

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Salt marshes are part of the coast representing a dynamic habitat with characteristics of both marine and terrestrial ecosystems. These ecosystems host diverse plant species and provide a habitat for fungal endophytes that reside within plant tissues, contributing significantly to plant health. However, the diversity and bioprospecting potential of fungal endophytes in Sri Lankan salt marshes remain largely unexplored. This study aimed to address this knowledge gap by investigating bioactivities of fungal endophytes associated with selected salt marsh plants in Kalpitiya, Sri Lanka. Fungal endophytes were isolated from four salt marsh plant species, including *Suaeda maritima, Suaeda monoica, Salicornia brachiata,* and *Sesuvium portulacastrum*. Immature and mature root and shoot tissues were surface sterilized and initially cultured on PDA medium supplemented with salt, followed by preparation of pure cultures. The obtained isolates were subjected to different bioassays to evaluate their plant growth-promoting properties. *In vitro* tests included phosphate solubilization, ammonia, and Indole-3-acetic acid production. Bioremediation potential was assessed by inoculating fungi into Bushnell-Haas media supplemented with diesel as the carbon source and observing the colour change of the redox indicator 2,6-DCPIP after 2 weeks. Kruskal–Wallis test was performed for the statistical analysis of results. A total of 22 fungal endophytes were isolated from the halophytic plants. Among them, four isolates exhibited varying levels of phosphate solubilization. Detectable level of ammonia was produced by 13 isolates with isolate SMMR2 (4.503 ± 0.936 $\mu molml^{-1}$) yielding the highest concentration. Eleven isolates produced Indole-3-acetic acid with isolate SBIS1 being the highest producer (16.210 ± 8.59 ppm). Ten fungal isolates were able to degrade diesel under aerobic conditions demonstrating their potential for bioremediation. The ability of these fungal isolates to produce plant growth-promoting compounds suggests their potential for sustainable agriculture while their capacity to degrade diesel indicates their applicability in bioremediation of hydrocarbon-contaminated environments.

Keywords: Ammonia, hydrocarbon, indole-3-acetic acid, phosphate solubilization

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In vitro antimicrobial and antioxidant activity of some mangrove-derived fungi isolated from Kalpitiya, Sri Lanka

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Mangrove ecosystems harbor rich microbial diversity, offering significant potential for biotechnological applications. Mangrove fungi, adapted to harsh environmental conditions, produce a diverse array of bioactive secondary metabolites. This study aimed to explore the antifungal, antibacterial, and antioxidant potential of fungal isolates from the Kalpitiya mangrove, Sri Lanka. Fifty fungal isolates, obtained from different sources in the Kalpitiya mangrove, were coded for convenience and screened for antifungal activity against three phytopathogenic fungi: *Colletotrichum musae*, *Fusarium oxysporum,* and *Rhizoctonia solani* using a dual culture plate assay. None of the isolates were effective against *R. solani*. Six isolates exhibiting clear inhibition zones against *C. musae* and *F. oxysporum,* were subjected to ethyl acetate extraction and their crude extracts were evaluated using disc diffusion and spore germination inhibition assays. Isolate DC2 demonstrated strong antifungal activity in both dual culture and modified disc diffusion assays against *C. musae* and *F. oxysporum*. It was revealed that crude extract of DC2 inhibited *F. oxysporum* spore germination by 97.59% while completely inhibiting *C. musae* spore germination. When tested against the human pathogenic fungus *Candida albicans*, DC2 showed antifungal effects. All six fungal crude extracts demonstrated antibacterial activity against *Staphylococcus aureus* in the disc diffusion test, with ciprofloxacin serving as the positive control. Among the six extracts, the strongest antioxidant activity, with an IC_{50} of 43.92 µg/ml, was exhibited by DC2 in the DPPH radical scavenging assay, using ascorbic acid as the standard. All tests were performed in triplicate. Thin-layer chromatography indicated the presence of multiple secondary metabolites, and further compound identification through NMR is ongoing. The isolate DC2 was identified via morphology and molecular techniques. Fungal genomic DNA was isolated following a standard extraction protocol, and forward primer ITS1 and reverse primer ITS4 were used to amplify the internal transcribed spacer (ITS) region of the fungi using polymerase chain reaction. According to the BLAST results of the consensus sequence, the DC2 isolate showed a 99.64% similarity (100% query coverage) compared to *Aspergillus* sp. (MH141270). This study highlights mangrove fungi, such as DC2, as valuable sources of natural bioactive compounds, emphasizing their potential for eco-friendly biocontrol agents and pharmaceutical development while underscoring the need to conserve mangrove ecosystems as reservoirs of novel biological resources for sustainable agriculture and food security.

Keywords: Mangrove fungi, antifungal activity, antibacterial activity, dual culture, Kalpitiya

Understanding the influence of environmental factors on cyanobacterial dynamics in Nuwara Wewa, Sri Lanka

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Seasonal cyanobacterial proliferation in Nuwara Wewa, a multipurpose dry zone reservoir in Anuradhapura, Sri Lanka, poses significant ecological and public health concerns. This study assessed the spatiotemporal variability in physicochemical parameters and cyanobacterial composition during the dry (August) and wet (December) seasons of 2024. Field data from 20 sites revealed that in August, the reservoir experienced elevated temperatures (up to 33.79 ± 0.2 °C), lower water clarity (Secchi depth ~71.3 ± 1.15 cm), and higher conductivity (0.751 ± 0 mS/cm) and salinity (0.37 ± 0 psu). In contrast, December conditions were cooler (25.07 ± 0.02 – 28.52 ± 0.18 °C), with greater transparency (up to 153 ± 1 cm), lower conductivity (0.562 ± 0.0 mS/cm), and salinity (0.28 ± 0.005). Nutrient enrichment was evident, with high concentrations of dissolved nitrate (6.43 ± 0 ppm), phosphate (0.601 ± 0 ppm), and chlorophyll a (12.63 ± 0 mg/L) in August compared to December. Total cyanobacterial cell densities were significantly higher in August, exceeding 2,000,000 cells/mL at peripheral sites, while December values declined to below 1,500,000 cells/mL, with a significant decrease confirmed by t-test (t-value = 6.67, p = 0.000). The dominant cyanobacterial genera included *Microcystis*, *Dolichospermum*, and *Aphanocapsa*, while *Cylindrospermopsis* and *Aphanizomenon* were absent in December. The Total Trophic State index (TTSI) shifted from predominantly eutrophic in August (TTSI up to 5.43) to mesotrophic in December (TTSI – 3.63), indicating improved water quality. Spearman's correlation revealed strong positive associations between cyanobacterial cell density and temperature, pH, salinity, conductivity, nitrate, and chlorophyll a in August ($p \leq 0.05$). In December, all correlations remained significant except for conductivity. Redundancy analysis for both months accounted for ~41.5% of the species composition variation, with *Microcystis* strongly associated with salinity, temperature, and pH, while *Dolichospermum* was positively linked with water transparency, and *Aphanocapsa* was associated with conductivity. MANOVA indicated no significant spatial variation but confirmed a significant temporal shift in cyanobacterial composition (F-value = 3.395, p = 0.027). These findings highlight the influence of seasonally driven environmental factors in shaping cyanobacterial composition and emphasize the need for seasonal monitoring to mitigate cyanobacterial bloom-related health and ecological risks.

Keywords: Cyanobacteria, eutrophication, spatiotemporal variation, Nuwara Wewa, multivariate analysis

Isolation of algicidal bacteria from Beira Lake to control bloom-forming *Microcystis aeruginosa*

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Cyanobacterial harmful algal blooms (CyanoHABs), particularly caused by *Microcystis aeruginosa*, pose a serious threat to freshwater ecosystems and public health. Beira Lake in Colombo, Sri Lanka, frequently experiences such blooms due to eutrophication, causing severe water quality degradation and ecological imbalance. This study aimed to isolate and characterize native algicidal bacteria from Beira Lake as potential biological control agents against *M. aeruginosa*. Water samples were collected from two distinct sites, Floating Market (FM) and Gangaramaya Temple (GT) areas. *M. aeruginosa* was isolated and cultured in BG-11 medium, and chlorophyll-a was used as an indicator of algal biomass. Physicochemical analysis revealed eutrophic conditions in the Lake with high nitrite and phosphate levels. From 25 preserved bacterial slants, 16 pure colonies were obtained, and four isolates (FMA1, FMC6, FMB1, GTC3) demonstrated algicidal activity. Chlorophyll a analysis revealed that FMB1 and GTC3 reduced chlorophyll levels from day one, with mean values of 0.1852 ± 0.21 mg/L and 0.0483 ± 0.05 mg/L, respectively. FMA1 and FMC6 showed delayed reductions but ultimately reduced chlorophyll a by 75% and 68% after seven days, while controls showed increased levels. Light microscopy confirmed inhibition zones. Both intracellular enzymes and extracellular metabolites contributed to algicidal effects, with FMA1 exhibiting stronger intracellular activity and FMC6 being highly effective extracellularly. Biochemical characterization showed catalase and urease activity in all four isolates. Gram staining identified FMA1 and FMC6 as Gram-positive cocci and FMB1 and GTC3 as Gram-negative rods, demonstrating their adaptability and roles in algicidal activity. These findings highlight the potential of native bacterial strains from Beira Lake as eco-friendly alternatives to chemical algicides. Future research, including molecular identification, is recommended to assess safety and optimize application strategies for sustainable CyanoHAB control.

Keywords: Algicidal bacteria, Beira Lake, harmful algal blooms, biological control, chlorophyll a

ABSTRACTS – ORAL PRESENTATIONS

Parallel Session 2: Molecular Biology and Biotechnology

Do life history traits and ecological features shape up MHC diversity? The patterns of selection and polymorphism in exon 3 of the avian MHC

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The Major Histocompatibility Complex (MHC) is a vital component of the vertebrate immune system. The α2 domain of MHC I, a component of the peptide-binding groove, the functionally critical part of MHC, is encoded by exon 3. MHC I, especially the exon 3, is known for its high polymorphism and stronger balancing selection. Birds exhibit a broad distribution over different ecosystems from the tropics to the poles, with different behavioral patterns, and variable susceptibility to various infectious diseases. Population density, mating systems, environmental interactions, and anthropogenic activities could be key factors governing the risk. MHC diversity is considered maintained through balancing selection, driven by heterozygote advantage and pathogen pressures. Birds show greater MHC variations than other fauna. This study examined MHC I exon 3 sequences from GenBank, encompassing 65 passerines and 37 non-passerines across a diverse range of phylogenies, ecologies, biogeographies, and behaviors. The potential impact of six selected traits is examined in this study: Aggregation, Long-term Monogamy, Cavity Nesting, Breeding-Site Fidelity, Human Association, and consumption. Nucleotide diversity (π) and the ratio between synonymous and nonsynonymous substitutions (dN/dS) are key metrics for inferring polymorphism and selection. Major findings suggest more pronounced sequence polymorphism in passerines than non-passerines. However, selection analyses imply that high sequence diversity does not necessarily reflect functional diversity, especially in non-passerines. Alongside phylogeny, ecology, and behavior could be considered in MHC selection studies. Aggregation indicates a positive association with selection in passerines, manifesting enhanced functional diversity in dense populations, potentially by high pathogen-driven selection pressure. Non-passerines claim a negative association with human consumption, probably due to the pattern that bigger birds tend to be hunted more by people. The slower metabolic rate due to larger body sizes might also influence this pattern. This study highlights the value of functional genomics to better understand how genetic variation drives adaptation across species.

Keywords: Birds, ecological variables, functional genomics, MHC polymorphism, selection

Dual regulatory role of the Mycobacterium xylanase Regulator (MxyR): a promising drug target in drug-resistant tuberculosis

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Transcriptional regulators play a crucial role in bacterial adaptation and survival, allowing for dynamic control of gene expression in response to environmental stimuli. In *Mycobacterium tuberculosis* (MTb), these regulators orchestrate complex transcriptional networks that govern virulence, metabolism, and stress responses. Mycobacterium xylanase regulator (MxyR), a member of the MarR family of transcriptional regulators, was initially characterized as a ligand-responsive repressor that binds specifically to the *mxyO* intergenic region. However, promoter sequence similarity analyses have identified additional putative MxyR-binding regions in the MTb genome that harbour genes essential for DNA replication (*dnaA*, *dnaN*, *gyrA*, *gyrB, rpmH*), cell wall biosynthesis (*embA*, *embB*, *embC*), stress response (*sigE*, *htrA*), and oxidative stress management (*katG*). To investigate the effect of ligand binding on MxyR-regulated expression of the genes mentioned above, MTb samples were treated with 0.2% of ligands, including beechwood xylan, corncob xylan, and arabinose, during their mid-exponential growth. MTb cells were lysed, total RNA was extracted, and cDNA was synthesized, then subjected to RT-qPCR using gene-specific primers. Relative expression levels were determined using the comparative cycle threshold ($2^{-\Delta\Delta C}$T) method, with 16S rRNA as the internal control. Exposure to beechwood and corncob xylan resulted in a marked downregulation of nearly all target genes, with Ct values exceeding 37. In contrast, arabinose induced a gene-specific response: dnaN expression was upregulated by 160%, embB showed no significant difference at approximately 100%, and other genes exhibited variable levels of downregulation. These observations challenge the original hypothesis that ligand binding would generally relieve MxyR-mediated repression and instead suggest that MxyR may function as both a repressor and activator in a context-dependent manner. This dual regulatory behaviour is consistent with other MarR family proteins, where ligand-induced conformational changes modulate DNA-binding activity and transcriptional outcomes. The study highlights the potential of xylan-based ligands to modulate MxyR activity and suppress MTb pathogenic pathways, reinforcing MxyR as a novel drug target. Further studies, including knockout and ChIP-based assays, are warranted to confirm the direct regulatory roles of MxyR.

Keywords: MxyR, ligand-responsive transcriptional regulation, MarR family regulators, drug-resistant tuberculosis

Feasibility of designing a CADMA-based real-time PCR assay for the detection of the R248Q & R273C *TP53* mutations

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Among the most frequent and functionally significant cancer mutations are R248Q and R273C of the *TP53* (tumor protein p53) gene. Detecting them with high sensitivity requires advanced and expensive platforms. CADMA (Competitive Amplification of Differentially Melting Amplicons) based real-time PCR is a relatively new and cost-effective technique that detects as few as 0.5% of mutant alleles in a primarily wild-type background. It uses a three-primer system that concurrently amplifies both wild-type and mutant alleles, where the mutation-specific primer is designed to reduce the melting temperature (Tm) of the mutant amplicon compared to that of the wild type. Alleles are distinguished using high-resolution melting (HRM) analysis based on this difference in melting behaviours. However, due to the sequence-specific constraints, CADMA assay design is not feasible for all mutations. The current study aimed to assess the feasibility of designing a CADMA-based qPCR assay to detect R248Q and R273C mutations in *TP53*. Primers were designed using the SNPgen online tool to generate a product of ≈51 bp, to facilitate optimal discrimination between alleles during HRM. The potential primer dimer formation was evaluated with the OligoAnalyzer™. Melting temperatures of the amplicons were calculated with the Blake and Delcourt algorithm from the uMelt online tool. For the R248Q SNP, mutant-specific primers were shortened (22 bp) and designed with 'A' nucleotide mismatches (5'-CATGCATGAGCGGCATGAACCA-3') to lower the amplicon Tm (80°C), while wild-type primers (25 bp) included 'G/C' mismatches (5'-GTTCCTGCATGGGCGGCATGAACCG-3') to yield a higher Tm (82.5°C). Common-reverse primer 5'-TGTGATGATGGTGAGGATGGGCCTC-3' wasn't modified. For the R273C SNP, mutant-specific primer (22bp) included 'T' mismatches (5'-TGACTGAACAGCTTTGAGGTGT-3') to lower the amplicon Tm (78.75°C), while wild-type primers (25bp) used 'G/C' mismatches (5'-CTGGGACGGAACAGCTTTGAGGTGC-3') to yield a higher Tm (81.5°C). The common reverse primer was 5'-TCTCTCCCAGGACAGGCACAAACAC-3'. The ΔG values for both homodimer and heterodimer formation were < -10 kcal/mol in all instances and occurred only at the 5' end, indicating a low probability. Self-complementarity index of ≤ 8.00 and Self-3'complementarity index of ≤3.00 further ensured their functional utility, while off-target primer binding potential was analyzed with NCBI-primer BLAST, and SNPgen confirmed their specificity. These results suggest that CADMA-based qPCR can be successfully utilized for the detection of the R248Q and R273C mutations of the *TP53* gene.

Keywords: CADMA, HRM, qPCR, R248Q, TP53

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Association of *TERT* rs2736100 gene polymorphism with interstitial lung disease and its prognostic significance in a Sri Lankan cohort

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Interstitial lung disease (ILD) refers to a heterogeneous group of about 200 distinctive lung disorders classified based on their shared clinical, pathological, physiologic, or radiographic factors. Mutations in the telomerase reverse transcriptase (*TERT*) gene and other telomere-related genes have been found to occur frequently in types of ILD. The study sought to investigate the association of the *TERT* rs2736100 C/A polymorphism with ILD along with its correlation with disease severity, becoming the first of its kind conducted in Sri Lanka. Genotyping of 14 ILD patients (cases) and 13 age, sex and ethnicity-matched healthy controls (controls) using peripheral blood-derived DNA was performed via a newly designed in-house PCR-RFLP assay that amplifies a 516 bp region flanking the polymorphic site (Forward primer: 5'-CTTCATCTGTGCATCATAAGC-3'; Reverse primer: 5'-TTAGTAGAGATAGGCTTTCACC-3'). Restriction digestion with *SfcI* cleaved the C allele into 197 bp and 319 bp fragments, while A allele was kept intact. The genotyping results resolved using 2% agarose gels were statistically analysed using Graphpad Prism (Version 10.4.2). The allele frequencies observed with respect to the major C allele were 0.6429 for cases and 0.5769 for controls, and with respect to the minor A allele were 0.3571 for cases and 0.4231 for controls. The heterozygotes were more frequent in both groups (cases: 0.5714; controls: 0.6923). The polymorphism exhibited conformance to Hardy-Weinberg equilibrium in both cases and controls. Analysis of the genotyping results failed to reveal a statistically significant association of any of the alleles with ILD (p-value > 0.05), with the 95% confidence intervals of the Odds Ratio (OR) and the Relative Risk (RR) falling within the ranges 0.4395 – 4.110 and 0.7225 – 1.759, respectively. Correlational analysis between the polymorphism and the Gender/Age/Physiology (GAP) index employed to assess disease severity demonstrated no statistically significant correlation (p-value > 0.05). The results of the study largely oppose the findings of similar studies conducted in other ILD cohorts and therefore warrants further research conducted in larger, representative cohorts stratified according to ILD subtype for validation.

Keywords: Interstitial lung disease, genotyping, rs2736100, Sri Lanka, *TERT*

Comparative evaluation of the anti-gastric activity of *Eclipta prostrata*, *Tinospora cordifolia*, *Acrostichum aureum*, and their polyherbal formulation using *in vitro* antacid assays

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Gastroesophageal reflux disease (GERD) is commonly treated with antacids, but conventional therapies can have adverse effects; therefore, herbal alternatives with fewer side effects are of interest. This study compared the antacid and antioxidant activities, cytotoxicity, and physicochemical properties of aqueous leaf extracts of *Eclipta prostrata*, *Tinospora cordifolia*, *Acrostichum aureum*, and their combined polyherbal formulation. The polyherbal blend was formulated in ratios based on LC_{50} values obtained from the zebrafish embryo assay, which measured embryotoxicity (LC_{50}). Acid-neutralizing capacity was assessed by Fordtran's titration model, and a modified version of Vatier's artificial stomach model monitored the neutralization time. Antioxidant capacity was evaluated via DPPH assay, and GC-MS analysis profiled phytochemical constituents. The cytotoxicity assay showed dose- and time-dependent embryotoxicity for all extracts. The LC_{50} values were 521.72 ± 1.02 µg/mL for *T. cordifolia*, 464.15 ± 0.05 µg/mL for *E. prostrata*, and 412.30 ± 0.72 µg/mL for *A. aureum*, indicating *T. cordifolia* was the least toxic and *A. aureum* the most toxic. All extracts elevated gastric pH, confirming antacid activity. The polyherbal blend exhibited a significantly higher acid-neutralizing capacity ($p<0.05$) and the longest buffering duration at all concentrations, ranging from 200 µg/mL to 1000 µg/mL. In the DPPH assay, antioxidant potency ranked highest for *T. cordifolia* (298.12 ± 25.33 µg/mL), followed by *E. prostrata* (375.78 ± 28.10 µg/mL), the polyherbal mix (466.42 ± 47.02 µg/mL), and *A. aureum* (480.35 ± 48.11 µg/mL). The polyherbal blend also had the highest total extractive yield (36.03 ± 3.99 mg/g), reflecting maximal phytochemical content. GC-MS profiling confirmed sesquiterpenes and polyphenolic compounds in all extracts. Overall, *T. cordifolia* exhibited the highest antioxidant potency and lowest toxicity, whereas *A. aureum* showed the highest toxicity. The polyherbal formulation demonstrated a synergistic buffering effect and potential gastric protective activity, which requires validation in additional animal models before therapeutic application in GERD.

Keywords: Antacid activity, antioxidant activity, embryotoxicity, gastroesophageal reflux disease, medicinal plants

Molecular insights into the regulation of copper detoxification in pathogenic *Leptospira*

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Leptospira interrogans, a pathogenic spirochete that causes global zoonosis leptospirosis, is facing various external environmental stress conditions in its lifetime including metal stress. Though copper is an essential element in leptospiral growth, it is also toxic at high levels. Thus, metal ion homeostasis in *Leptospira* is vital for survival and virulence. Characterization of copper-regulated expression in *L. interrogans* is important to determine copper tolerance level. Our study focused on a leptospiral operon consisting of a conserved metal-sensitive transcriptional regulator (A6J42_RS08895, Gene ID: 61142862) and other metal-binding genes including heavy metal-translocating p-type ATPase (A6J42_RS08885) cation transporter (A6J42_RS08890), and DUF-domain exotoxins (A6J42_RS08900). Two *L. interrogans* serovar Canicola and serovar Icterohaemorrhagiae, were grown and treated with increasing levels of $CuSO_4$ (10 µM, 50 µM, and 100 µM) for one hour in the mid-logarithmic growth phase. RNA was extracted, purified and reverse-transcribed into cDNA for RT-PCR analysis of gene expression analysis. Results revealed a clear upregulation of genes encoding the transcriptional regulator, ATPase, and cation transporter in response to increased copper levels, most notably in the Canicola strain. Interestingly, the genes encoding the DUF1561-domain exotoxins were significantly downregulated under copper stress, possibly an energy-saving and self-protective measure. Comparative analysis across both serovars identified different expression profiles for the ATPase gene, possibly caused by minor sequence differences in regulatory regions. These results confirm the hypothesis that metal detoxification and regulation of virulence are closely related and strain-specific in *L. interrogans* and are controlled by subtle genetic variation. The research highlights the significance of transcriptional regulation in *Leptospira* metal homeostasis to metal stress and implies that the metal-sensitive regulator is a central regulator in copper homeostasis. These results not only deepen our understanding of *Leptospira* pathogenesis but also suggest potential molecular targets for antimicrobial therapy.

Keywords: *Leptospira interrogans*, copper stress, gene expression, transcriptional regulation, metal detoxification

Acknowledgement: Financial assistance from the University of Colombo undergraduate research grant.

Evolutionary analysis and host state reconstruction of rust fungi (Pucciniales; Basidiomycota), with emphasis on the morpho-molecular characterization of coffee rust (*Hemileia vastatrix*) in Sri Lanka

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Rust fungi are among the most complex and economically significant phytopathogens within Basidiomycota, including over 7,800 known species with a global distribution, particularly on cultivated crops. The causal agent of coffee leaf rust, *Hemileia vastatrix*, has posed serious threats to cultivation in Sri Lanka since the 19th century. Despite its significance, little research has been done on the evolutionary history of Pucciniales and the morpho-molecular characterization of *H. vastatrix* using samples from Sri Lanka. This study investigated morpho-molecular variation in *H. vastatrix* and reconstructed ancestral host traits within Pucciniales to understand key evolutionary events. Infected coffee leaves were gathered from the Matale and Balangoda regions. Urediniospores were morphologically analyzed through microscopic observation, with special focus paid to their shape, size, and wall ornamentation. Following genomic DNA extraction, pathogen-specific primers were used to amplify the LSU and SSU regions. The phylogenetic analysis was performed via maximum likelihood (ML), and divergence times were estimated using Bayesian analysis in BEAST. Morphologically, urediniospores were ellipsoidal, thick-walled, and echinulate, with no significant variation between regions. Phylogenetic analysis resolved the evolutionary relationship among species of 17 families of the order Pucciniales and verified the position of *H. vastatrix* within the family Zaghouaniaceae. According to divergence time estimation, the Pucciniales originated approximately 163 million years ago (MYA), which corresponds to the late Jurassic period, a time of gymnosperm prominence. Rust fungi species expanded rapidly during the mid-Cretaceous period, aligning with angiosperm diversification. The Zaghouaniaceae family, which includes *Hemileia* species, diverged around 132 MYA during the early Cretaceous. However, *H. vastatrix* diverged ~107 million years after the divergence of the family Zaghouaniaceae suggesting its recent adaptation to coffee hosts. These findings introduce new evidence for the evolutionary history of rust fungi and host association to support both co-evolution and host jump as principal drivers of Pucciniales diversity.

Keywords: Rust fungi, phylogenetic analysis, co-evolution, divergence time estimation, coffee leaf rust

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Characterization of Xylariales diversity in the Kanneliya forest reserve

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A diverse and ecologically significant group of fungi, the Xylariales order (Phylum Ascomycota) is found mainly in tropical forests and primarily functioning as saprophytes. Although Xylariales fungi have been thoroughly researched worldwide, their diversity in Sri Lanka remains largely undocumented, particularly within the Kanneliya forest reserve. This study aimed to characterize Xylariales species morphologically and molecularly across three distinct zones within Kanneliya: Natural Forest Reserve, Restoration site, and *Dicranopteris linearis*-invaded site. Both macroscopic and microscopic features were utilized in the morphological characterization. A modified CTAB (cetyltrimethylammonium bromide) method was used to extract genomic DNA from fungal isolates acquired using a multi-spore isolation technique on Malt Extract Agar (MEA) media. Molecular characterization involved the amplification of the ITS gene region utilizing ITS5/4 primers. A phylogenetic analysis of the ITS gene regions provided robustly supported resolution of the isolated species, as evidenced by high bootstrap values. Site-dependent variations in Xylariales species diversity were found in this study. The highest diversity was found in the Natural Forest Reserve, which included nine species identified from *Xylaria*, *Daldinia*, *Graphostroma*, and *Annulohypoxylon* genera. The Restoration site included four species from *Xylaria* and *Annulohypoxylon* genera, indicating a moderate diversity. In contrast, the *Dicranopteris linearis*-invaded site showed the lowest diversity, with only three species identified from *Hypoxylon*, *Biscogniauxia*, and *Xylaria* genera. *Annulohypoxylon areolatum, A. moriforme var. moriforme, A. stygium var. stygium, A. viridistratum, Graphostroma platystomum, and Xylaria fanglanii* were all identified morphologically. Furthermore, the phylogenetic analysis confirmed the identities of *Xylaria laevis*, *Hypoxylon hypomiltum*, and *Daldinia eschscholtzii*. These findings demonstrate the high level of Xylariales diversity in the Kanneliya forest reserve and the different degrees of Xylariales diversity found within the unique and diverse microclimates of Kanneliya.

Keywords: Morphology, phylogeny, taxonomy, Xylariales

Acknowledgement: The authors acknowledge the University of Kelaniya Research Grant - RP/03/02/01/01/2023 for the funding.

Uncovering the transcriptional factors of *Cocos nucifera*: a genome-wide study

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Coconut (*Cocos nucifera*) is a perennial crop with immense agricultural, economic, and ecological significance, found especially in tropical countries. Despite its significance, genomic resources for coconut remain limited compared to other major crops. Transcription factors (TFs) act as master regulators of gene expression and are critical to understanding plant development and stress responses. With the growing importance of computational tools in TF prediction, this study focused on identifying all TF-encoding genes in the coconut (*Cocos nucifera* L.) genome. Using HMMER software, the researchers utilized Hidden Markov Model (HMM) profiles of conserved DNA-binding domains from 60 TF families to systematically scan the coconut proteome. The analysis led to the identification of 1999 candidate genes encoding transcription factors in the coconut genome, accounting for approximately 7.14% of the total protein-coding genes in the coconut genome. The most abundant TF families included MYB, bHLH, NAC, C2H2, and ERF. Physicochemical profiling revealed neutral pI values and hydrophilic tendencies, while subcellular localization predicted approximately 80% of these TFs were localized to the nucleus, a few were also located in plastids, and the cytoplasm. Structural analysis of AP2, C3H, Dof, and Trihelix families revealed diverse exon-intron structures and untranslated regions (UTRs) and chromosomal mapping revealed an uneven but specific distribution of TFs across the 16 coconut chromosomes. Most abundant families can be found in all chromosomes, while smaller TF families were restricted to single/few chromosomes. Promoter analysis of the TFs identified *cis*-regulatory elements (CRE) that act as hormone, stress, and light-responsive elements. Among the aforementioned TF families, under salt stress C3H family exhibited the highest and most dynamic expression. These findings offer new information on the transcription factors and serve as a valuable reference for future molecular and functional studies, thereby supporting the development of effective genetic improvement strategies in coconut.

Keywords: Transcription factors, coconut, genome, HMMER

Evaluating the dietary impact of cooking – induced changes in Essential Trace Elements in Sri Lankan rice (*Oryza sativa* L.)

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Essential Trace Elements(ETEs) are a group of minerals considered essential for numerous physiological functions within living organisms. Many cereals, including the Sri Lankan dietary staple, rice are known sources of ETEs that contribute towards their Recommended Daily Allowances(RDA). A total of fifty-four husked, raw rice samples of most commonly consumed varieties in Sri Lanka were purchased from Dedicated Economic Centers and pooled in to twenty-five analytical composites that underwent a standardized domestic cooking procedure where raw and cooked grains were lyophilized, powdered, digested and quantified for ETEs; Zinc(Zn), Selenium(Se) and Manganese(Mn) using Inductively Coupled Plasma Mass Spectrometry(ICP-MS). Results were expressed as mg kg^{-1} dry-weight and mg $100g^{-1}$ wet-weight basis, respectively and inferred with RDA for each ETE using recommended daily portions of cooked rice (min-max: 520-845 $gDay^{-1}$) for Sri Lankan adults. The Mean(±SD) of Zn, Se and Mn in raw rice grains were 32.02±6.82, 0.05±0.02 and 13.71±3.86 mg kg^{-1}dw, respectively. The cooking process significantly decreased all ETEs (p<0.001), corresponding to 17.42–60.26% net loss from levels available in raw grains. The %reduction was higher in white pericarp grains than red (p>0.05), non-parboiled rice than parboiled (p<0.05) and improved rice than traditional and imported rice (p>0.05). Daily intake of Zn, Se and Mn through rice consumption ranged; 2.33-13.81, 2.77×10^{-3}–2.99×10^{-2} and 0.75-8.22 mg, respectively. The %fulfilment of RDA by rice consumption were therefore, for Zn: 21.2-125.5%, Se: 5.0-54.5% and Mn: 32.7-357.6%. Consumption of red-rice over white provided 9.56%, 28.08% and 24.01% dietary advantage for Zn (p>0.05), Se (p<0.05) and Mn (p<0.05) respectively while consumption of parboiled rice provided a similar advantage of Zn: 26.18% (p<0.001), Se: 41.32% (p<0.001) and Mn: 25.23% (p<0.05) over Non-parboiled rice. Moreover, traditional rice provided 12.64%, 36.25% and 33.14% more dietary advantage of Zn (p>0.05), Se (p<0.05) and Mn (p<0.05) over improved rice varieties. Cooked rice from all Sri Lankan rice varieties is a reliable source for daily intake of ETEs and consuming red pericarp, parboiled traditional rice would provide substantial dietary advantages.

Keywords: Essential elements, Essential Trace Elements, beneficial elements, cooked rice, Sri Lankan rice

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Full genome annotation of polythene-degrading fungus *Phlebiopsis flavidoalba*

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White rot fungi are strong degraders with great potential in biotechnology. One such example is polyethylene degradation ability, and previous research has shown that the white rot fungus, *Phlebiopsis flavidoalba* harbors such potential. This study aimed to annotate the full genome of *Phlebiopsis flavidoalba*, to identify genes and metabolic pathways relevant to polymer biodegradation. Genomic DNA of the fungus was subjected to full genome sequencing using Illumina MiSeq platform. Sequences were subjected to preliminary processing and genome assembly was done. The assembled genome, comprising 224 contigs, was annotated using the GenSAS 6.0 pipeline. Structural and functional annotation involved repeat masking, *ab initio* gene prediction, evidence-based refinement, and domain analysis. Functional annotation incorporated protein similarity searches, InterProScan, and KEGG-based pathway mapping. The analysis revealed 5,641 predicted genes, with 5,623 protein-coding sequences and 5,895 repeat elements, suggesting a compact and efficient genome. Benchmarking Universal Single-Copy Orthologs (BUSCO) analysis identified 61 complete single-copy genes, confirming partial genome completeness. KEGG pathway analysis indicated genes associated with primary metabolism, secondary metabolite biosynthesis, and xenobiotic degradation, including pathways for benzoate, aminobenzoate, toluene, and naphthalene degradation. Notably, genes encoding oxidative enzymes such as laccases, manganese peroxidases, and alkane hydroxylases were identified, highlighting their potential role in breaking down polyethylene and other hydrocarbons. Additionally, secondary metabolite biosynthesis pathways, including streptomycin and phenylpropanoid biosynthesis, suggest antimicrobial potential. These results provide genomic insights into the biodegradative and biosynthetic capacities of *P. flavidoalba*, supporting its application in bioremediation of plastic and hydrocarbon-contaminated environments.

Keywords: *Phlebiopsis flavidoalba*, genome annotation, polyethylene degradation, xenobiotic metabolism, bioremediation

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Characterization of *Sclerotinia sclerotiorum* isolates collected from cabbage fields in Sri Lanka, with insights into mycovirus-associated hypovirulence

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Despite the global emergence of mycovirus-mediated hypovirulence as a promising biocontrol strategy for *Sclerotinia sclerotiorum*, no single study has explored the mycovirus and their diversity of *S. sclerotiorum* populations since its first report in 2014 in Sri Lanka (SL). This study aimed to characterize *S. sclerotiorum* isolates and investigate the presence of mycoviruses in SL. Sclerotia were collected from commercial cabbage fields in Pattipola, Ambewela, Seetha Eliya and Kandapola area in 2024. Morphological characterization using mycelial linear growth, colony morphology and sclerotia production were determined. When abnormal colonies were present, BLASTn searches of β-tubulin gene sequence was used in species identification. Detached cabbage leaf assays were conducted to evaluate the virulence of each slow growing isolate with abnormal phenotypes. Oxalic acid production was also determined among the isolates. Molecular detection of DNA virus, targeting *Sclerotinia sclerotiorum* hypovirulence-associated DNA virus 1 (SsHADV-1) was carried out by PCR amplification of the coat protein (CP) gene. RNA mycovirus detection was done by reverse transcription PCR targeting the RdRp region using degenerated primers. Significant variation in mycelial linear growth was observed ($p \leq 0.05$), with isolate P1_2 exhibiting the lowest radial growth and reduced sclerotia production. β-tubulin sequencing confirmed its identity as *S. sclerotiorum*. Pathogenicity tests showed varying lesion sizes, ranging from 1.317±0.56 cm^2 to 6.47±1.16 cm^2 and the isolates P1_2, and AW5 were non-pathogenic. A significant positive correlation ($r = 0.672$, p-value = 0.0085) was observed between oxalic acid concentration and lesion size. Even though isolate P1_2 produced moderate level of oxalic acid (112.985± 38.51 µg/mL), it was non-pathogenic suggesting the possibility of harbouring hypovirulence mycoviruses. An extrachromosomal band (~2000 bp) was detected in the abnormal isolate P1_2, and PCR yielded expected 332 bp with SsHADV-1-specific primers along with non-specific bands suggesting the possibility of the presence of mycoviruses in Sri Lankan *S. sclerotiorum* populations. These findings suggest morphological and pathogenic diversity among local isolates and indicate potential mycovirus presence, warranting further molecular characterization.

Keywords: *Sclerotinia sclerotiorum*, mycovirus, hypovirulence, SsHADV-1, mycelial compatibility

Integrating morphological characterization and DNA barcoding for the identification of *Aporosa* species in Sri Lanka

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Accurate species identification of species of the genus *Aporosa* Blume. (S: Kebella) (family Phyllanthaceae), medicinally important plants in Sri Lanka are complicated by taxonomic ambiguity. This is mainly due to sharing morphological similarities and overlapping vernacular names that result in misidentification. These limitations affect botanical research and herbal medicinal validations, leading to drug adulteration in traditional therapeutic systems. This study aimed to clarify the species identities of six *Aporosa* specimens, including *A. cardiosperma* (Gaertn.) (Ac) and *A. lanceolata* (Tul.) Thwaites (Al) collected from different geographical locations. The four specimens coded as MT_1, MT_2, MT_3, and MT_4 exhibited taxonomic uncertainties. Therefore, an integrative approach combining morphological characterization and DNA barcoding was applied. Fifteen qualitative morphological characters were analyzed using cluster analysis. The internal transcribed spacer (ITS) region in nuclear DNA was sequenced to infer evolutionary relationships, and a phylogenetic tree was constructed with the neighbor-joining method. Cluster analysis produced a phenogram with three main clusters, indicating distinct patterns of morphological variation. The integrated approach of morphological and molecular characterization enabled the inference of their relationships, thereby resolving the ambiguity in identification. Subsequently, MT_1, MT_2, and MT_3 were identified as morphotypes of *A. cardiosperma,* while MT_4 was identified as a morphotype of *A. lanceolata.* Moreover, this study provides novel DNA barcoding data for six *Aporosa* species in Sri Lanka, representing the first such records in global sequence databases. Incorporating plastid markers (e.g., rbcL or whole plastid genomes) alongside nuclear markers would support assess phylogenetic incongruence and reveal potential reticulate hybridization events within genus *Aporosa*. These findings underscore the importance and effectiveness of integrating morphological characters with molecular systematics to resolve taxonomic ambiguities, particularly within a genus characterized by high morphological plasticity.

Keywords: *Aporosa* spp., morphotypes, DNA barcoding, morphological and molecular characterization

In silico analysis of non-synonymous single nucleotide polymorphisms in the human *HNF1A* gene

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Mutations in the *Hepatocyte Nuclear Factor-1 Alpha* (*HNF1A*) gene have been associated with various disorders, most notably Maturity-Onset Diabetes of the Young (MODY). This study aimed to identify high-risk single non-synonymous nucleotide polymorphisms (nsSNPs) in HNF1A and evaluate their potential impact on protein structure, stability, and function using a comprehensive in silico approach. A total of 1,546 nsSNPs in the *HNF1A* were retrieved from the dbSNP database and analysed using sixteen computational tools: SIFT, PolyPhen, MutationTaster, MetaSVM, MetaLR, MutPred, FATHMM, MetaRNN, LRT, CADD, AlphaMissense, M-CAP, PROVEAN, PhD-SNP, SNPs&GO, and PANTHER-PSEP. This integrative approach identified 24 high-confidence deleterious nsSNPs, of which 11 variants (rs19392260, rs771108132, rs193922604, rs1057520504, rs1249563793, rs1225814280, rs765432081, rs193922603, rs779184183, rs886039386, rs886039544) were consistently predicted as damaging across all tools. Protein stability predictions using I-Mutant, MUpro, INPS, INPS3D, and DynaMut2 indicated that variants E172G (rs901689962), V264F (rs193922604), F268S (rs193922605), and R271Q (rs779184183) significantly destabilize the protein. Conservation profile analysis using ConSurf revealed that most deleterious nsSNPs occurred at highly conserved residues of HNF1A. Moreover, structural and functional assessments predicted that these variants could alter secondary structure, solvent accessibility, and post-translational modifications such as phosphorylation, methylation, and glycosylation. Three-dimensional modeling and structural alignment further confirmed that several mutations caused conformational changes, with R203C (rs1180119907) showing the highest structural deviation. In addition, gene-gene and protein-protein interaction network analysis revealed functional associations between HNF1A and key metabolic regulators, including Hepatocyte Nuclear Factor 4 Alpha (HNF4A), Forkhead Box A3 (FOXA3), and Pyruvate Kinase, Liver and Red Blood Cell (PKLR). These interactions highlight HNF1A's role in hepatic function and glucose metabolism, suggesting that deleterious nsSNPs could disrupt broader regulatory pathways critical for metabolic homeostasis. Overall, this study provides valuable insights into the structural, functional, and regulatory consequences of SNPs in HNF1A and establishes a foundation for future experimental validation and disease association studies.

Keywords: HNF1A, nsSNPs, *in silico* analysis, protein stability, non-coding variants

Antioxidant properties of the methanolic crude extract, beta-carotene, and carrageenan from *Hypnea* sp. (Rhodophyta)

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Marine macroalgae, particularly species within the genus *Hypnea* J.V. Lamouroux (1813), are recognized for their diverse bioactive compounds with notable pharmaceutical, nutraceutical, and cosmetic applications. The antioxidant potential of specific components derived from *Hypnea* sp. remains insufficiently explored. The objective of the present study is to investigate the antioxidant properties of three distinct extracts from *Hypnea* sp., the methanol fraction of the crude extract, beta-carotene, and carrageenan. *Hypnea* sp. was collected in June 2024, from the Koggala shoreline 5.98544° E, 80.32838°N, and the identity was confirmed based on morphological characteristics and biochemistry. Morphological features that were used in the confirmation included quantitative traits such as length, width, height of thallus and qualitative traits such as color, shape of holdfast, fruiting structures, constriction at base, shape of tip, thallus description, and branching pattern. The methanolic extract, isolated beta-carotene, and carrageenan were tested for antioxidant activity by DPPH (2,2-dipheyl-1-picrylhydrazyl) radical scavenging assay. Each extract was tested across a concentration range from 1.9531 µg/mL to 1000 µg/mL. Ascorbic acid served as the standard antioxidant reference. The assay was triplicated, and absorbance was measured at 517 nm to determine radical scavenging activity. The percentage inhibition and IC_{50} values (concentration required to inhibit 50% of DPPH radicals) were calculated for all three extracts. Statistical analysis was performed at a 95% confidence level, and the P value was calculated using one-way ANOVA and subsequent Tukey's test for pairwise comparison. The IC_{50} values observed for the methanolic extract, beta-carotene, and carrageenan were 1022.59 µg/mL, 52.08 µg/mL, and 256.05 µg/mL, respectively. Accordingly, beta-carotene exhibited the most potent antioxidant activity, falling into the category of moderate antioxidants, and in contrast, the methanolic crude extract and carrageenan showed weaker antioxidant activity, compared to the reference drug ascorbic acid (IC_{50} of 11.26 µg/mL) ($p \leq 0.05$). These findings suggest that beta-carotene from *Hypnea* sp. holds moderate antioxidant potential and could be a promising candidate for natural antioxidant development.

Keywords: Marine macroalgae, natural antioxidants, seaweed bioactives, beta-carotene, carrageenan

Molecular characterization of *Citrus* species in Sri Lanka using *mat*K and *rbc*L DNA barcode markers

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The genus *Citrus*, belonging to the family Rutaceae, holds significant nutritional and economic value due to the presence of diverse phytochemicals such as alkaloids, tannins, and phenols. Despite its importance, the taxonomic classification of Sri Lankan *Citrus* species remains incomplete. This study aims to molecular characterization of *Citrus* species using chloroplast DNA markers *mat*K and *rbc*L to enhance species identification, improve phylogenetic resolution, and aid in the prevention of biopiracy. Genomic DNA was extracted from young fresh leaf samples using a modified CTAB method. PCR amplification was performed for the *rbc*L and *mat*K gene regions, and the PCR products were sent to Macrogen, South Korea for sequencing. The obtained sequences were analyzed through multiple sequence alignment using BioEdit software. The phylogenetic tree was constructed using the Maximum Likelihood method and Tamura-Nei model of MEGA 11 software to determine the genetic relationship among the species. The phylogenetic tree based on *mat*K DNA sequences revealed three main clusters: Cluster I - Sour orange, Sweet orange, Nas naran, Yak dehi, and Pumelo. Cluster II - Long lemon, Round lemon, Key lime, and Kaffir lime. Cluster III - Sidaran. In contrast, the phylogenetic tree based on *rbc*L DNA sequences formed two main clusters. Cluster I - Sour orange, Sweet orange, Nas naran, Yak dehi, Pumelo, and Sidaran. Cluster II - Long lemon, Round lemon, Key lime, and Kaffir lime. The phylogenetic analysis using both *rbc*L and *mat*K markers revealed a consistent clustering pattern, with Cluster I and Cluster II showing similar grouping across both markers. The only major exception was Sidaran, which formed a separate cluster (Cluster III) in the *mat*K-based tree but was grouped under Cluster I in the *rbc*L-based tree. This overall consistency in clustering highlights the reliability of these chloroplast DNA markers in the classification of *Citrus* species.

Keywords: *Citrus*, *rbc*L, *mat*K, taxonomy, molecular phylogenetic analysis

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ABSTRACTS – ORAL PRESENTATIONS

Parallel Session 3: Plant Sciences and Agriculture

Brontispa longissima (Gestro): an emerging pest of coconut in Sri Lanka

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The coconut leaf beetle (*Brontispa longissima* (Gestro); Coleoptera: Chrysomelidae) was first detected in the Galle district, Sri Lanka, in 2023, and is currently confined to the Southern Province. Globally, this beetle is recognized as a highly destructive pest in palms (family Arecaceae), including coconut. Given its potential threat to coconut cultivation, this study aimed to document key morphological features of the pest for field identification and to describe characteristic damage symptoms on infested palms. Morphological characteristics of different life stages were examined under a stereomicroscope using fifty specimens per life stage, and damage symptoms were recorded from field observations. The pest beetle undergoes complete metamorphosis, with distinct egg, larval, pupal, and adult stages. Adults are dorsoventrally flattened, black in colour, with a distinct square-shaped orange pronotum. Females measured 8.67±0.04 mm in length and males 7.23±0.02 mm. The eggs were brown, flattened, and measured 1.47±0.02 mm in length and 0.54±0.02 mm in width, typically laid in longitudinal rows. The final instar larvae were whitish, measuring 8.88±0.14 mm in length and 1.9±0.04 mm in width, with prominent calliper-like hooks at the posterior end. The pupae were creamy in colour, measured 9.5±0.09 mm in length and 1.98±0.01 mm in width. Damage is caused by both larvae and adults feeding on the spear leaf tissues of the coconut, resulting in characteristic linear brown streaks. When the damaged leaves unfold, leaves display a scorched and ragged appearance. These morphological and damage descriptors provide essential diagnostic information for accurate field identification and for developing management strategies to limit the spread and impact of *B. longissima* in Sri Lanka.

Keywords: *Brontispa longissima*, coconut, life cycle, pest

First identification of *Nigrospora* sp. causing blister blight on tea in Sri Lanka

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Tea (*Camellia sinensis*) cultivation in Sri Lanka faces significant challenges from foliar pathogens, especially with blister blight which is traditionally caused by *Exobasidium vexans*. This study reports the first identification of *Nigrospora* sp. causing blister blight like symptoms on tea in Sri Lanka. Tea leaf samples exhibiting characteristic white blisters protruding from the lower leaf surfaces were collected from five tea estates in the Uva province. To facilitate the isolation of host specific obligate pathogen, *E. vexans*, five different tea extracts (T1; Factory made green tea, T2; Laboratory made green tea, T3; Fresh green leaf, T4; Laboratory made black tea, and T5; Factory made black tea) were tested by altering the potato infusion concentration of home-made potato dextrose agar medium at five different tea: potato ratios (A; 100:0, B; 75:25, C; 50:50, D; 25:75, E; 0:100). Comparatively, 25% of fresh tea leaf infusion incorporated tea extract agar (TEA) medium proved the most effective for targeted pathogen growth and sporulation. Initial morphological observations suggested the presence of *E. vexans* based on characteristic ellipsoid, curved basidiospores, and light green, aseptate hyphae. However, concurrent observation of black, spherical conidia on dark, septate mycelia indicated co-infection. Molecular identification using ITS1 and ITS4 primers and sequencing confirmed the co-infecting pathogen as *Nigrospora* sp. with 100% similarity to GenBank accession number JF909550 (*Nigrospora oryzae*). Koch's postulates were fulfilled through whole plant inoculation, with spore suspensions (1×10^6 spores/ ml) producing blister-like symptoms on healthy tea plants within two weeks, eventually developing into necrotic lesions after three weeks. Temperature profiling revealed optimal growth at 25 °C, with diminished growth at temperature extremes (5 – 40 °C). This represents the first documented case of *Nigrospora* sp. causing leaf blight on tea in Sri Lanka, expanding the known geographic distribution of this pathogen following previous reports from India and China. The successful development of TEA medium provides a valuable tool for future isolation and characterization of tea foliar pathogens, while the identification of *Nigrospora* sp. has important implications for tea disease management strategies in Sri Lanka.

Keywords: Tea, *Nigrospora* sp, Blister blight, Tea disease management, Tea extract agar (TEA) media

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Artificial intelligence in crop development: using protein sequences, structures, and protein-protein interaction networks in deep learning to predict root development proteins

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Accurate prediction of protein function remains a vital challenge in plant biology. While deep learning (DL) models have advanced automated function prediction (AFP), their full potential in plant sciences remains largely untapped. Here, a novel multi-modal DL model that combines protein sequences, structures, and protein–protein interaction (PPI) networks named PlantGO was developed to enhance AFP. PlantGO utilizes dedicated models for each input type: the pre-trained ProteinBERT model for sequences and two variational graph autoencoders for structures and PPI networks. The outputs are combined in a final DL layer to predict Gene Ontology (GO) terms across biological process (BP), molecular function (MF), and cellular component (CC). PlantGO was trained on 10,660 protein chains and 124 PPI networks from the Viridiplantae lineage and benchmarked against the state-of-the-art model DeepFRI. PlantGO consistently outperformed DeepFRI across all GO categories and evaluation metrics recommended by the Critical Assessment of Functional Annotation (CAFA). For instance, PlantGO improved BP-GO micro-Fmax by 50%, MF-GO by 55.9%, and CC-GO by 42.5% compared to DeepFRI. Similarly, micro-AUPR scores increased by 34.36% for BP-GO, 52.8% for MF-GO, and 48.8% for CC-GO. As a biological application, PlantGO was employed to predict potential proteins involved in root development in maize, rice, and soybean—species of agricultural importance. The model identified 33 maize, 32 rice, and 195 soybean proteins lacking previous experimental annotations. Enrichment analysis of the predicted proteins revealed significant associations with auxin signaling, cell wall modification, and root morphogenesis pathways, supporting their potential roles in root development. Overall, these findings underline the advantages of a multi-modal approach over single-modality models in AFP. PlantGO not only establishes a new standard in predictive accuracy but also provides a practical tool for functional genomics in crop species, supporting hypothesis generation for future experimental validation.

Keywords: Automated function prediction, Deep learning, multi-modal, root development, Gene Ontology

Genome-wide identification and comprehensive *in silico* analysis of aspartate aminotransferases in Poaceae crops

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In plant metabolism, aspartate aminotransferases (AspATs) serve as crucial enzymes involved in amino acid biosynthesis and nitrogen metabolism, playing a critical role in linking carbon and nitrogen pathways. AspAT catalyzes the reversible transamination between aspartate and α-ketoglutarate, producing oxaloacetate and glutamate. Although previous studies have examined the roles and evolutionary origins of AspATs, there was a notable gap in a comprehensive, genome-wide identification of AspATs. Therefore, this study analyzed AspATs in Poaceae crops, including *Oryza sativa* subsp*. japonica, Triticum aestivum, Zea mays, Sorghum bicolor,* and *Setaria italica*, which collectively contribute to a major portion of the calories consumed in the human diet. The analysis was performed using a combination of conventional bioinformatics tools such as BLAST, HMMER, and CD-Search, with deep learning tools such as DeepGOPlus and DeepLoc enhancing the overall reliability of the results. The identified AspATs could be classified into two types, eukaryotic and prokaryotic, based on their evolutionary origins, which formed two distinct clades in the phylogenetic tree. The eukaryotic type showed aspartate aminotransferase activity, whereas the prokaryotic type exhibited both aspartate aminotransferase and glutamate/aspartate-prephenate aminotransferase activities. Their distinct evolutionary origins were further supported by the subcellular localizations and synteny analysis, while their expression profiles indicated potential functional divergence. Structural analysis and conserved motif analysis highlighted the differences between the two types. Subcellular localization patterns of AspATs aligned well with the evolutionary origins, as the eukaryotic type was localized in mitochondria, chloroplasts, and cytosol, while the prokaryotic type was located only in chloroplasts. Protein-protein interaction network analysis showed that AspATs interact with proteins in aspartate-related metabolic pathways, and submodule enrichment revealed shared functional profiles between studied plants, suggesting conserved roles. Altogether, the findings of this study lay a foundation for future functional studies and biotechnological applications aimed at enhancing crop productivity through targeted manipulation of aspartate aminotransferases.

Keywords: Aspartate aminotransferase (AspAT), Poaceae, phylogenetic analysis, subcellular localization, genome-wide identification

Developing an AI model for classifying the level of tolerance for iron toxicity in new improved rice lines/varieties

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Iron toxicity is a major abiotic stress in waterlogged lowland rice cultivation, resulting from the accumulation of ferrous iron (Fe^{2+}) in the root zone, under anaerobic soil conditions. This leads to physiological disruptions and characteristic visible symptoms such as leaf bronzing, root damage, and stunted growth, ultimately reducing yield significantly. The development of iron toxicity–tolerant rice varieties offers a sustainable solution to mitigate this issue. However, existing conventional screening methods rely on manual scoring, which are labour-intensive, subjective, and ineffective for high-throughput phenotyping, thus limiting the progress of breeding. This study addresses these limitations by developing a deep learning (DL)-based image classification approach for rapid, and precise assessment of iron toxicity tolerance in rice. A controlled hydroponic experiment using Yoshida nutrient solution was conducted with seven rice varieties representing different iron tolerance levels. Plants were exposed to 0 mg/L and 300 mg/L Fe^{2+} using $FeSO_4 \cdot 7H_2O$ in a two-factor factorial design with a Completely Randomized Design (CRD), which ensured unbiased replication of treatments. Leaf bronzing symptoms (LBS), which were induced under standardized conditions, were assessed using the IRRI Standard Evaluation System (SES). A total of 860 high-resolution images (50 MP and 108 MP) of whole plants, shoots, and roots were captured during peak symptom expression (Days 12–14). In parallel, key growth and biomass parameters, including shoot length, root length, number of leaves, number of tillers, fresh weight, and dry weight were recorded to confirm the reliability of visual assessments. LBS were analysed using the Kruskal–Wallis test; growth traits were analysed using Two-way ANOVA and ART ANOVA. These analyses were performed prior to DL modelling to ensure that visual scoring and physiological traits consistently reflected variation in tolerance levels, thereby serving as biological validation for the classification framework. Dunn's test classified the varieties into four tolerance categories. AI Model development initialized with training four CNNs: VGG16, ResNet50, ResNet101, and DenseNet121, with DenseNet121 achieving the best accuracy (89%). To enhance performance, Vision Transformer (ViT), Swin Transformer, and DenseNet121 were fine-tuned using hyperparameter tuning. The Swin Transformer trained on whole plant images (without additional hidden layers, learning rate 0.0001) performed best, reaching 98% accuracy and a G-Mean of 0.9843. Cross-validation further confirmed the robustness of the model, yielding a mean accuracy of 99.42% and a G-Mean of 0.9944 across five folds. Grad-CAM visualizations confirmed symptom-based attention. These results highlight DL-based image classification as a promising phenotyping tool for iron toxicity tolerance. Future research should incorporate validation across broader genotypes and environments.

Keywords: Iron toxicity, rice, deep learning, image-based phenotyping, Swin Transformer

Morphological diversity and taxonomic resolution of Sri Lankan *Impatiens* (Family Balsaminaceae) with emphasis on evolution of floral characters

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The genus *Impatiens* (Family Balsaminaceae) exhibits high morphological and ecological diversity, with notable endemism in Sri Lanka's wet and montane forests. This study employed an integrative morphological framework to investigate interspecific variation and support the conservation of native *Impatiens* species, with particular emphasis on floral traits and their taxonomic significance. Field surveys across multiple ecological zones yielded specimens from 23 native and 2 introduced species. Vegetative and reproductive features were documented using standardized botanical protocols, and additional specimens were reviewed at the National Herbarium (PDA). A total of 46 morphological and morphometric characters were recorded from *Impatiens* species and the outgroup *Hydrocera triflora*. Factor Analysis of Mixed Data (FAMD) was used to reduce data dimensionality, identifying 19 key traits for further analysis. Principal Coordinate Analysis (PCoA) and Neighbor-Joining (NJ) tree construction, based on Gower distance matrices, revealed four well-supported clades three major and one minor distinguished by traits such as sepal spur length, leaf shape, and stem architecture. The first clade (Clade A) included species with long, filiform spurs and narrow leaves; the second (Clade B) grouped taxa with cuspidate leaves and bilobed lateral petals; the third (Clade C) consisted of robust perennials with semi-woody stems; and the minor clade (Clade a) showed unique morphological features. The alignment between PCoA and NJ trees affirms the evolutionary distinctiveness of these groupings. Ecological adaptations were evident: the first clade showed traits favoring low-light understory environments, while floral divergence in the second clade suggested pollinator specialization. Morphological convergence in the third major clade and evolutionary novelty in the minor clade highlight dynamic evolutionary processes. These results affirm the relevance of traditional morphological characters and underscore the value of morphometric integration for resolving species-level taxonomy. This framework strengthens the foundation for future phylogenetic and conservation efforts on *Impatiens* in tropical ecosystems.

Keywords: *Impatiens*, morphological diversity, taxonomy, conservation, clade differentiation

Morphological and fibre quality characterization of cotton populations in Sri Lanka

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Cotton, in the genus *Gossypium* (family Malvaceae) is important to the textile industry for its fibre quality. Among 55 globally accepted species, *G. arboreum*, *G. hirsutum* and *G. barbadense* were introduced to Sri Lanka. The limited success of cotton cultivation in Sri Lanka (1973–1984) due to economic and environmental constraints has highlighted the need to revisit and scientifically evaluate existing cotton germplasm. The present study is aimed to conduct detailed analyses of the morphology and fibre quality of cotton populations available in Sri Lanka. A total of 38 Vegetative and reproductive traits were recorded from sampling locations across four climatic zones, along with complete cotton specimens for taxonomic authentication. Morphological traits were analyzed using Factor Analysis for Mixed Data (FAMD) and Hierarchical Clustering on Principal Components (HCPC). Six clusters were primarily differentiated by vegetative traits (HCPC; $v > 3$, $p < 0.05$), including leaf and capsule characters. Based on standard botanical references and field observations, leaf, capsule and flower characters were used as key traits for the preliminary identification of *G. arboreum*, *G. hirsutum*, and *G. barbadense*. Clusters 02, 04, and 01 corresponded to *G. arboreum*, *G. barbadense*, and *G. hirsutum*, respectively. Clusters 03, 05, and 06 did not align with a single *Gossypium* species and exhibited combined morphological traits of the species mentioned above. Fibre quality assessment was conducted using standardized methods to evaluate staple length, bundle strength, water absorbency, and colour properties for the seven selected samples. The effect of NaOH treatment (mercerization) on fibre parameters was also evaluated. Statistical tests (Kruskal-Wallis and paired t-test) were performed at a 5% significance level. Staple length, bundle strength, and water absorbency varied significantly among the samples across selected localities. ($p = 0.01396$; 0.02174; 0.00883). However, mercerization caused no significant difference in bundle strength or water absorbency ($p = 0.896$, 0.0766), although colour properties, including whiteness, brightness, tint, and yellowness, varied significantly ($p = 0.00005$; 0.00737; 0.001269; 0.0001355). The study recommends further morphological and molecular analyses for species-level identification of *Gossypium* sp., and detailed climatic studies to aid its reintroduction in Sri Lanka.

Keywords: *Gossypium*, cotton, morphological traits, fibre quality

Do Plesispa beetles equally prefer and orient towards different coconut varieties?

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The olfactory system of insects plays a key role in locating suitable hosts for feeding and oviposition, often through kairomones released by plants. In Sri Lanka, *Plesispa reichei* (Plesispa beetle) is an invasive insect pest of *Cocos nucifera* (coconut), causing severe damage to seedlings in nurseries and to young palms shortly after transplanting. However, the susceptibility of different coconut varieties/forms to this pest remains unclear. This preliminary study assessed whether Plesispa beetles show differential attraction to various coconut forms. Two forms of coconut from the variety Typica, namely, Tall (T) and Ran Thambili (RT) and three forms of the variety Dwarf, namely, Red Dwarf (RD), Green Dwarf (GD), and Yellow Dwarf (YD) were tested. Leaf samples were collected from the second fully expanded leaf of 3-year-old plants, and volatiles were extracted using dichloromethane (DCM), then filtered, dehydrated and concentrated. The resulting extracts were used to assess the behavioural response of Plesispa using Y-tube olfactometer. Each treatment was replicated three times. For each replicate, twenty laboratory-reared beetles (2-3 months old; sexually mature; male: female ratio=1:1) were used. Insects were offered a choice between a coconut leaf volatile extract and DCM, or between extracts from two different coconut forms. A Chi-Square Goodness-of-Fit Test was used to determine the preference. Compared with DCM, Plesispa beetles were significantly attracted to T ($\chi 2 = 19.27$, $p<0.001$), YD ($\chi 2 = 26.67$, $p<0.001$), and RT ($\chi 2 = 5.4$, $p=0.02$) but not to RD or GD. When T, YD, and RT were tested in pairwise combinations, no significant preference for one over another was observed. These findings suggest that the beetles are equally attracted to the three most preferred forms (T, YD, RT) and that no single form is more susceptible based on volatile-mediated attraction alone. This information may assist in developing coconut varieties with reduced attractiveness to Plesispa beetles.

Keywords: *Plesispa reichei*, coconut, pest, behaviour, variety

Conservation-oriented *in vitro* propagation of *Munronia pinnata* and phytochemical comparison with *Andrographis paniculata*

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Munronia pinnata (commonly known as Bin Kohomba) is a medicinal plant native to Sri Lanka and classified as endangered due to overharvesting, habitat destruction, and low seed viability. Its traditional therapeutic uses and ecological significances highlight the urgency for conservation through alternative propagation methods. The present study aimed to establish an effective *in vitro* propagation system for *M. pinnata* and to compare its phytochemical properties with those of *Andrographis paniculata* (Heen Bin Kohomba), a widely used herbal substitute. Callus induction was initiated using leaf discs, with those containing the midrib from younger leaves yielding the highest amount of callus formation. For shoot initiation and regeneration, explants were cultured on Murashige and Skoog (MS) medium supplemented with 0.5, 1, and 1.5 mg/L BAP along with 1.5, 2 and 2.5 mg/L IBA. For the shoot elongation, *in vitro* generated *M. pinnata* shoots were cultured on MS medium supplemented with 0, 1.0, 2.0, and 3.0 mg/L GA_3 along with 1.0 mg/L BAP. The optimal combination of BAP and IBA for shoot initiation and regeneration was 1.0 mg/L BAP with 2.0 mg/L IBA, while the best shoot elongation was achieved using 2.0 mg/L GA_3 and 1.0 mg/L BAP. These results confirm the importance of specific growth regulator combinations for successful direct organogenesis. *In vitro* antioxidant activity, total phenolic content, total flavonoid content and alpha amylase inhibitory activity of *A. paniculata* and *M. pinnata* was determined using DPPH assay, Folin Ciocalteu method, Aluminium Chloride method and Alpha-Amylase inhibitory assay, respectively. A significantly higher antioxidant activity was recorded in the *A. paniculata* stem extract (IC_{50} = 466.76 µg/mL). Total phenolic content ranged from 65 to 86 µg GAE/mg with no significant differences between species. Significantly higher flavonoid content (54.25 ± 4.55 µg RE/mg) and α-amylase inhibitory activity (IC_{50} = 810 µg/mL) were observed in *A. paniculata* stem and root extracts, respectively. This comparative phytochemical analysis showed *A. paniculata* to possess higher antioxidant, flavonoid, and α-amylase inhibitory activities, reinforcing its role as a potential substitute for *M. pinnta*, though further validation is required.

Keywords: *Munronia pinnata*, *Andrographis paniculata*, *in vitro* propagation, plant growth regulators, phytochemical analysis

A comparative *in vitro* study of salt tolerance in cultivated chili (*Capsicum annuum*) varieties in Sri Lanka

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Salinity is a major abiotic stress limiting growth and yield in sensitive crops like *Capsicum annuum* L., an economically and nutritionally important species. With soil salinization rising due to poor irrigation and climate change, identifying salt-tolerant genotypes is vital to sustain productivity. This study evaluated six Sri Lankan *C. annuum* varieties (MI Waraniya 1, MI 2, KA 2, MICH HY 1, MIHP 1, and Ganga) under controlled *in vitro* conditions. Ten-day-old seedlings of each variety were exposed to four different NaCl concentrations (0, 50, 100, and 150 mM) in Murashige and Skoog (MS) medium for 4 weeks. The experiment was conducted in a completely randomized design (CRD) with three replicates per treatment, and data were analysed using one-way ANOVA followed by Tukey's HSD test at $p \leq 0.05$. Morphological traits such as germination percentage, shoot length, and root length were recorded alongside physiological and biochemical parameters, including total chlorophyll content, proline accumulation, total phenolic and flavonoid contents, and antioxidant activity assessed via the DPPH radical scavenging assay. Significant differences were observed among varieties in their responses to salt stress. Variety Ganga showed strong oxidative stress mitigation with antioxidant activity increasing from 24.76% ± 2.76 to 82.16% ± 1.90 and flavonoid content from 937.48 ± 109.58 to 1679.50 ± 125.02 µg RE g^{-1} DW at 150 mM NaCl ($p < 0.05$). Similarly, MIHP1 exhibited enhanced antioxidant responses (10.37% ± 6.59 to 84.92% ± 1.04) and higher phenolic content (0.91 ± 0.17 to 2.51 ± 0.33 µg GAE g^{-1} DW) under salt stress ($p < 0.05$). MI Waraniya 1 maintained the highest chlorophyll content (1.71 ± 0.47 mg/g FW vs. 0.54–1.30 in others) and showed greater proline accumulation (10.76 ± 2.64 to 41.73 ± 2.57 µmol g^{-1} FW), reflecting superior osmotic adjustment ($p < 0.05$). Although all varieties exhibited reduced germination and growth with increasing salinity, moderate stress (50–100 mM NaCl) highlighted tolerance traits in MIHP1 and MI Waraniya 1. These findings underscore the importance of genotype-dependent variability in salt stress tolerance and highlight the potential of MIHP 1, Ganga, and MI Waraniya 1 as promising candidates for breeding programs aimed at improving salt resilience in *C. annuum*.

Keywords: *Capsicum annuum*, salt tolerance, food security, abiotic stress, sustainable agriculture

Stomatal trait plasticity helps plant species to survive in environmental gradients in a forest restoration site

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In forest restoration sites, stomatal traits are key indicators of plant responses and adaptations to tolerate heterogeneous environments, making them vital for understanding species survival. This study investigated variation in stomatal traits among eleven tree species (7-year saplings; from each species, 3 saplings from each habitat treatment group) planted across three successional habitats: Marginal-Tea(MT), Scrubland(SC), and Woodland(WD), under two treatments: Weeding(T1) and Without-weeding(T2) in the Endane Biodiversity Corridor restoration site. Stomatal density(SD), epidermal density(ED), stomatal index(SI), guard cell length(GCL), and potential conductance index(PCI) were measured to assess trait plasticity, habitat-linked responses, and management interventions. For all stomatal traits, linear mixed-effects models (R software) revealed significant effects due to at least one of the following: habitat/treatment/their interaction. For SD, a significant difference ($p<0.05$) across habitats was seen in *Bhesa ceylanica* and *Doona trapezifolia* under T1. $SD_{SC}<SD_{WD}$ was seen in *Dipterocarpus zeylanicus, Litsea longifolia,* and *Mangifera zeylanica* under T2. *Syzygium nervosum* showed lower SD_{SC} due to habitat×treatment interaction effect. Many species reflect reduced SD_{SC} which may be due to surviving water stress in this sloped area in SC habitats. ED and SI varied significantly in three species each, driven by habitat/treatment/their interaction. *Bhesa ceylanica* and *Vateria copallifera* showed lower GCL_{MT} due to habitat×treatment interaction effect. $GCL_{MT}<GCL_{WD}$ may occur due to high light conditions in the MT habitat. This reflects plastic responses of smaller stomata, which can rapidly respond to minimize water loss. Higher GCL_{WD} suggests greater gas exchange efficiency under shaded, moist conditions. $PCI_{SC}<PCI_{WD}$ shown in *Doona trapezifolia* (under-T1) and *Litsea longifolia* (under-T2). Additionally, *Doona affinis and Syzygium amphoraecarpus* showed higher PCI_{WD} due to habitat×treatment interaction effect. These results highlight stomatal trait plasticity as a mechanism for resource regulation and stress tolerance under light and moisture variation, supporting species selection with high survival in similar restoration sites.

Keywords: Stomatal traits, plasticity, environmental variations, forest restoration

Uncovering regulatory modules and hub genes of somatic embryogenesis in *Coffea arabica* through gene co-expression network analysis

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Somatic embryogenesis (SE) is a complex molecular and biochemical process driven by cellular totipotency and serves as a valuable model for studying plant developmental biology. Gaining insights into the transcriptional regulation of this process is essential for enhancing its applications in plant biotechnology. This study aimed to (i) identify key gene modules associated with SE in *Coffea arabica*, (ii) determine key hub genes and transcription factors (TFs) involved in this process, and (iii) elucidate their potential roles in SE through *in silico* expression profiling and functional characterization. An RNA-sequencing dataset of *C. arabica*, retrieved from the NCBI Sequence Read Archive (PRJNA744419), encompassing twelve stages of SE. Following quality control, high-quality reads were aligned to the *C. arabica* genome using Bowtie2, and transcript abundance was estimated using Cufflinks. A scale-free GCN was constructed using Weighted Gene Correlation Network Analysis (WGCNA) with 21,598 genes exhibiting variance above the second quartile, including 13 SE-related marker genes, 320 EMBRYO DEFECTIVE genes, 99 epigenetic regulator genes, and 2,002 transcription factors. Using a dynamic tree cut algorithm, 23 gene modules (44–5,156 genes) were identified, functionally annotated using the Database for Annotation, Visualization, and Integrated Discovery (DAVID), and visualized in Cytoscape. Module–trait correlation analysis revealed two modules associated with stage L1 (leaf explants) and one module each associated with stages D1 (dedifferentiating explants), C1 (compact callus), R1 (pro-embryogenic masses, 1 week in redifferentiation medium), R4 (pro-embryogenic masses, 10 days in redifferentiation medium), and E1 (globular embryos). A total of 220 hub genes were identified based on intramodular connectivity. Further *in silico* expression analysis using publicly available datasets indicated that at least 70 of these genes are likely involved in embryogenesis, many of which remain functionally uncharacterized. These findings provide novel insights into the transcriptional regulation of SE in *C. arabica* and highlight the identified hub genes as promising candidates for future functional studies aimed at enhancing SE efficiency and reproducibility in coffee and other crops.

Keywords: Somatic embryogenesis, *Coffea arabica*, gene co-expression network, WGCNA, hub genes

In vitro shoot regeneration from cultured leaf explants of *Passiflora edulis* f. *flavicarpa*

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'Horana Gold' is an improved cultivar of *Passiflora edulis* f. *flavicarpa,* which is commercially cultivated in Sri Lanka. Micropropagation offers a promising approach for the large-scale production of disease-free planting material. While previous studies have explored the *in vitro* propagation of 'Horana Gold' using shoot tip and nodal cultures, this study aimed to optimize callus induction and shoot regeneration from cultured leaf explants. Leaves from two-month-old seedlings were surface sterilized with 70% ethanol for one minute, followed by 25% liquid bleach for 25 minutes. Leaf explants (1 cm × 1 cm) were cultured on Murashige and Skoog (MS) medium supplemented with varying concentrations of BAP and 2,4-D. A total of nine treatment combinations (T1–T9) were tested in a factorial design using BAP and 2,4-D at 0.0, 1.0, and 2.0 mg/L. Each treatment consisted of 15 replicates with four explants per plate. Callus formation was observed in all treatments approximately two weeks after dark incubation at 25 °C. Upon transfer of explants to a 16/8 h light/dark cycle, shoot regeneration was recorded after four weeks in all treatments except in T1 (control, no growth regulators) and T3 (2.0 mg/L 2,4-D only). Median separation among treatments was analyzed using the Kruskal–Wallis test at the 0.05 significance level for Callus induction frequency (CIF), shoot regeneration frequency (SRF), and the number of callus clusters per explant (NCCE). All parameters tested varied significantly among treatments ($p > 0.05$). Post hoc pairwise comparisons were conducted using the Mann–Whitney U test. The highest CIF was observed in T9 (87.50%), with 2.0 mg/L of both BAP and 2,4-D, T5 (79.55%) with 1.0 mg/L of both BAP and 2,4-D and T3 (77.50%) with 2.0 mg/L 2,4-D. T9 produced the highest SRF (78.80%) and NCCE (11.03). Shoots regenerated in T9 were sub-cultured onto MS medium supplemented with 1.0 mg/L each of BAP and GA_3. After three subculture cycles each of four-week duration, the mean shoot regeneration potential (SRP), calculated as the average number of shoots per initial explant, was 11.33 ± 1.86. Histological analysis confirmed that regeneration occurred via both direct and indirect organogenesis.

Keywords: *Passiflora edulis*, leaf culture, callus induction, shoot regeneration, organogenesis

BlackPepKB: an interactive web platform for exploring black pepper (*Piper nigrum* L.) genomics

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Black pepper (*Piper nigrum* L.) is a globally important spice crop, valued not only for its culinary use but also for its medicinal and economic significance. Although genomic resources such as reference genomes and transcriptomic datasets are available, there remains a critical need for a centralized and user-friendly platform to facilitate the exploration and analysis of this data. To address this gap, we developed the Black Pepper Knowledgebase (BlackPepKB), an integrative genomic database designed to streamline access to black pepper genomic and transcriptomic resources. Constructed using MySQL 8.0 and built as a full-stack web application with Next.js, Node.js, and React, BlackPepKB provides a responsive interface, an intuitive user interface, along with a suite of specialized tools designed to facilitate genomic exploration. Key features include GeneViz, for visualizing exon-intron gene structures; the Pepper-eFP browser, for interactive gene expression visualization using electronic fluorescent pictographs; PepperExp and PepperClust tools for heatmap generation and hierarchical clustering of gene expression data; GO-Pep, for retrieving Gene Ontology (GO) annotations; JBrowse2, for dynamic visualization of genomic features; and a basic local alignment search tool (BLAST) for performing sequence similarity searches against curated black pepper datasets. In addition, the platform includes user-friendly modules for querying single nucleotide polymorphisms (SNPs) and exploring transcription factor (TF) families, further enhancing its utility for functional genomics research. Supplementary tools such as a gene summary viewer, an image gallery, and an integrated contact system facilitate user interaction and data accessibility. By centralizing diverse datasets and integrating interactive visualization tools, BlackPepKB serves as a comprehensive resource for investigating genomic features, gene functions, and expression profiles, ultimately supporting research and crop improvement efforts in black pepper. BlackPepKB is accessible at https://black-pepper-genomic-resource.vercel.app/.

Keywords: Black pepper, genomic database, eFP browser, JBrowse

Floral phenology and sex expression in *Piper nigrum* L. (black pepper)

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Piper nigrum L. (black pepper) is a perennial vine of the family Piperaceae and is the second most widely traded spice globally, after cinnamon. Despite its economic importance, studies on its reproductive biology remain limited. This study investigated floral development, sex expression, and floral phenology in *P. nigrum* var. Panniyur-1 using pot-grown plants maintained in Colombo, Sri Lanka. Observations included both spike-level (inflorescence) and single-flower level analyses, focusing on floral organ development, stigma receptivity, and timing of anthesis. *P. nigrum* flowers are minute and lack perianth parts. They are protected by a subtending bract. Flowers are borne in pendulous spikes. Among 50 inflorescences examined (10 inflorescences per plant x 5 plants), 38 (~75%) were completely bisexual, bearing both staminate (male) and pistillate (female) organs within each flower. Twelve (~24%) inflorescences displayed a mixed floral composition, with both bisexual and staminate (male-only) flowers on the same spike, suggesting potential sexual plasticity. Staminate flowers were rare, constituting only 0.1–2% of total flowers observed. Floral maturation followed an acropetal pattern, with basal flowers reaching anthesis before distal ones. It took approximately 15 days for all flowers on an inflorescence to complete anthesis. At the individual flower level, protogyny was typical, with anthesis lasting an average of six days. Anthers emerged 4–7 days after the onset of stigma opening. Five distinct anthesis stages were identified, based on stigma development and anther dehiscence. Stigma receptivity, assessed by peroxidase activity, peaked when the stigma lobes were fully open (stage 3). In vivo pollen germination indicated stigma receptivity at both stage 2 and stage 3. Peak anther dehiscence occurred between 7:00 and 9:00 AM. Pollen remained viable for up to 48 hours when stored at 4°C. These findings underscore the complexity of *P. nigrum* reproduction and highlight the need for broader varietal studies to better understand its reproductive biology.

Keywords: *P. nigrum*, Panniyur-1, floral phenology, sex expression, floral development

ABSTRACTS – ORAL PRESENTATIONS

Parallel Session 4: Zoology and Environment Sciences

The influence of protected area management practices on climate resilience

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Protected areas (PA) are primarily set aside for the conservation of biodiversity. The effectiveness of these habitats in safeguarding species would depend on their ability to provide congenial microhabitats. The present study assesses the microclimate buffering potential of two protected areas in Sri Lanka, the Kumana National Park (KNP) and the Panama-Kudumbigala Sanctuary (PKS) located adjacent. The two protected areas are under different management regimes –KNP, under stringent protection, whereas in PKS, traditional livelihood practices (paddy cultivation) are permitted. Temperature (T) and relative humidity (RH) were measured using sensors installed at randomly selected sites in the predominant habitats of each PA—scrubland in both KNP (n = 11) and PKS (n = 10), as well as the adjacent open habitat to each scrubland—grasslands in KNP (n = 11) and paddy fields in the non-cultivating dry season (n = 10) in PKS. Sensors were placed 2 m above the ground at 100 m from the edge of a habitat patch to record data for a minimum of 24 hours with 15-minute intervals. A 2 km distance was maintained between each sensor point. The vapour pressure deficit (VPD) was also calculated using T and RH values. Results indicated that scrublands and grasslands in the KNP differed significantly ($P<0.001$) in terms of Tmax, Tmax-min and RHmax-min. The microclimate variables did not differ between the scrubland and paddies in the PKS. Further, the scrublands in the KNP were significantly cooler and more stable (Tmax $P<0.01$, Trange $P<0.01$, RHrange $P<0.05$) than those in the PKS. Based on the VPD values, the KNP also exhibited a consistent negative buffering (4.87), indicating that scrublands within KNP can buffer against harsh conditions. PKS recorded negative buffering only after a threshold of 5 kPa, and its potential to maintain cooler temperatures was low (0.04). This study therefore demonstrates that management regimes influence the microclimate buffering capacity of protected areas such that those with more stringent regulations are better able to modulate extreme microclimatic conditions. Thus, Sanctuaries, which comprise lands where human activities are permitted to some extent, may fall short in their potential to provide suitable microclimates for many species.

Keywords: Microclimate, microclimate buffering effect, protected areas, Sri Lanka

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Incipient speciation through spatial divergence in Dark-fronted Babbler (*Dumetia atriceps*) of South Asia

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Incipient speciation through allopatry creates evolution in island populations of organisms. The resultant new species can have variations in morphometrics, plumage, vocalization and in genome because of natural selection, sexual selection or both. Dark–fronted Babbler (*Dumetia atriceps*) is a weak flying sedentary species common in Sri Lanka, Western Ghats and Southwest India. The Sri Lankan and Indian populations have been separated from Palk Strait in Indian ocean, while the Indian populations have been separated by the Palghat gap. In this study, we looked at the morphometric (n =33), plumage (n =50), acoustic (n =29), genetic (n=14) and spatial distribution of the three geographically isolated populations: Sri Lankan, above Palghat and below Palghat to check the potential of these populations to be elevated as separate species. Morphometrics, contrast variation of the extent of the dark front, percentage of black colour in beak and tarsus, analysis of temporal and frequency-based characters of short chirp and long chirp were used to check the differences of the populations. Results reveal that there are no distinct variations in morphometrics among three populations. Plumage wise, these populations are significantly different in extent of the dark front ($p = 1.27 \times 10^{-9}$), percentage of black colour area in the beak ($p = 3.97 \times 10^{-9}$) and tarsus ($p = 8.71 \times 10^{-8}$). There are no distinct variations in two vocal types: long chirp and short chirp, between these populations. The Bayesian phylogenetic tree that constructed for concatenated mitochondrial ND 2 and nuclear MUSK 13 shows a clear separation among Sri Lankan, above Palghat and below Palghat populations, while below Palghat population being basal to the other two populations. The maximum entropy species distribution model reveals that below Palghat population has greater ecological capacity than the other restricted populations which supports the argument that it is the basal population. This study shows that Sri Lankan *D. atriceps* has a great potential to be elevated to full species status while further research is needed to check the potential of the above and below Palghat populations to be separated as two species.

Keywords: Incipient speciation, Dark–fronted Babbler, allopatric speciation, spatial divergence, species distribution modeling

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

Detection and quantification of microplastics in pelagic seabirds from the Exclusive Economic Zone (EEZ) of Sri Lanka

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Marine plastic pollution, particularly microplastics, poses a significant threat to open-ocean (pelagic) seabirds, yet microplastic accumulation in South Asian species remains largely undocumented. The study presents the first investigation of microplastic ingestion in pelagic seabirds from the Exclusive Economic Zone (EEZ) of Sri Lanka, while developing an optimized protocol for the detection of microplastics specifically in seabirds. Nineteen seabird carcasses from four orders: Procellariiformes (5 carcasses), Charadriiformes (8 carcasses), Suliformes (3 carcasses), and Galliformes (3 carcasses), were examined, and the specimens were collected via systematic beach surveys and through seabirders. Dissected organs were digested with 4 M KOH (15 mL per gram of organ) at 50 °C and 150 rpm, followed by treatment with 30% H_2O_2 to remove remaining organic matter. The digested samples were filtered using Whatman GF/D filters, stained with Nile Red at a concentration of 0.1 g/L, then rinsed and air-dried. Visualization and quantification were performed using stereo microscopy, with image analysis via Proview software. Polymer composition was determined using Fourier Transform Infrared (FTIR) spectroscopy. The highest number of microplastics was observed in terns and shearwaters, while boobies and gulls exhibited relatively lower concentrations. Fragments were the most abundant microplastic type (77.62%), followed by fibres, foams, films, and pellets. Most microplastics were measured in the size range less than 100 µm, with brown, black, and white being the most predominant colours. Microplastics identified were comprised of polyamide, polyethylene, and polypropylene, as revealed by FTIR spectroscopy. The optimized Nile Red-based protocol proved effective for microplastic detection and revealed widespread contamination in pelagic seabirds from Sri Lankan waters. These findings indicate that both direct ingestion and bioaccumulation as the main exposure pathways for microplastics and highlight the urgent need for conservation strategies and stricter plastic pollution control measures in the region.

Keywords: Exclusive Economic Zone of Sri Lanka, FTIR spectroscopy, pelagic seabirds, microplastics

Acknowledgment: The authors gratefully acknowledge the Industrial Technology Institute (ITI) for providing the necessary funding and resources for microplastic quantification and the National Aquatic Resources Research and Development Agency (NARA) for facilitating the FTIR analysis.

Effects of microplastics on immunological properties of human peripheral blood mononuclear cells

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Microplastics (MP) are synthetic solid polymers (1 µm – 5 mm) which are non-biodegradable. Primary MP particles are small plastic particles that are artificially manufactured in industries as a byproduct. Secondary MPs arise from the degradation of large plastic items. Inhalation, oral intake and dermal contact are the main routes of human exposure to MPs. Recently MPs were detected in human peripheral blood ranging from 1.84 µg/ml to 4.65 µg/ml. PBMCs are continuously exposed to many xenobiotics. MPs exposed to the environment may enhance immune response. PEG (Polyethylene Glycol) is widely used in commercial products. PBMCs were isolated from twelve healthy donors using Ficoll-Paque density centrifugation method. Different concentrations (0.5 µg/ml, 5 µg/ml, 50 µg/ml, 500 µg/ml) of PEG and manually grinded natural MPs were exposed to PBMCs in RPMI 1640 (Roswell Park Memorial Institute medium) for 24 hours. Cell viability (%) assay, Neutral Red phagocytosis (%) assay, Griess colorimetric assay and Nitroblue Tetrazolium test were done to examine the cytotoxic effect of MPs on PBMCs. The One-way analysis of variance ANOVA) followed by Tukey's Post Hoc test was used for statistical analysis. Both natural MPs and PEG significantly reduced cell viability in concentration-dependent manner. The lowest significant concentration whereas natural MPs induce phagocytic activity is 5 µg/ml (23.28 ± 5.98, $p < 0.05$). These MPs may act as stimulants to increase phagocytic activity. The lowest significant concentration where natural MPs induce reactive oxygen species production (ROS) is 5 µg/ml (5.32 ± 0.75, $p < 0.05$), whereas PEG exposure didn't induce notable ROS production. Nitric oxide (NO) production levels remained unchanged in PBMCs after exposure to both PEG and natural MPs. Therefore, present study showed that MPs exposure to PBMCs can impair cell viability, induce phagocytosis and induce ROS production without altering the NO mediated inflammatory pathways.

Keywords: Absorption, cytotoxicity, microplastics, oxidative stress, phagocytosis

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

Variations in morphometry in populations of the common honeybee, *Apis cerana*, distributed across different bioclimatic zones in Sri Lanka

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The Asian honeybee, *Apis cerana*, demonstrates considerable phenotypic variation across environmental gradients, reflecting its ecological adaptability. This study aimed to quantify morphometric differences among *A. cerana* populations inhabiting Sri Lanka's three bioclimatic zones wet, dry, and montane using 56 morphological and morphometric parameters. Worker bees were sampled from three bioclimatic regions of Sri Lanka: wet (6 sites), dry (5 sites) and montane (6 sites). From each site, 30 worker bees were collected and morphometric traits related to head, thorax, abdomen, limbs, wings, and proboscis were measured using standardized imaging techniques. Out of the 56 variables that were analysed, 51 displayed statistically significant inter-zonal variation (Kruskal-Wallis, $p < 0.05$). Principal Component Analysis (PCA) revealed ten key morphometric variables contributing most to population differentiation, including total body length, thorax width, abdomen length and width, length of tergite 4, and forewing and cubital vein dimensions. This accounted for 52.8% of the observed variance. Montane zone bees exhibited the largest body sizes, with significantly higher body weights (0.07 ± 0.01 g), longer proboscises (4421.63 ± 143.90 µm), wider abdomens (3664.3 ± 174.59 µm), and greater forewing lengths (7914.3 ± 221.17 µm). Dry zone bees showed relatively longer abdomens (5903.20 ± 1480.71 µm) and the highest number of hamuli (18.5 ± 2.22), while wet zone bees had the smallest overall dimensions across nearly all measured parameters. These results suggest morphological adaptation to local environmental conditions: larger-bodied montane bees may be thermally adapted to cooler climates, whereas elongated abdomens in dry zone bees may reflect enhanced water retention or metabolic efficiency. Morphometric clustering closely paralleled bioclimatic zones, indicating environmentally driven, rather than random or purely geographical, variation. This comprehensive morphometric analysis underscores the phenotypic plasticity of *A. cerana* and establishes a valuable baseline for future ecological, taxonomic, and conservation-oriented studies in Sri Lanka.

Keywords: *Apis cerana*, Asian honeybee, phenotypic variation, phenotypic plasticity, morphometric clustering, ecogeographical adaptation

Morphological, plumage, and vocal characterization of the genus *Glaucidium* in Sri Lanka

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Ecological speciation happens when populations adapt to different environments, which leads to divergence and reproductive isolation. Yet these populations may appear phenotypically similar due to recent divergence, phylogenetic niche conservatism, or morphological convergence. This phenomenon is called crypsis. Island ecosystems, like those found in Sri Lanka, show significant bioclimatic and biogeographic zonation, making them hotspots for such speciation. In Sri Lanka, the endemic Chestnut-backed Owlet (CBO; *Glaucidium castanotum*) inhabits the wet zone, while the resident Jungle Owlet (JO; *G. radiatum*) occupies the dry zone. No detailed comparative studies have been conducted on this species pair. To characterize their morphology, vocalizations fieldwork was conducted in both wet and dry zones covering their ranges. From wet zone 7 owlets (CBO) and dry zone 8 owlets (JO) were captured using Mist nets, and morphological and plumage data were collected; vocalizations were recorded using a MARANTZ recording device. Morphological and plumage analysis showed that plumage colour patterns are the primary distinguishing feature. CBO displays a reddish mantle (77.34 ± 3.18%) while Jo lacks (10.52 ± 3.71%) reddish pigment ($p = 0.001$). And JO has heavily barred chest (15.50 ± 0.53) while CBO has fewer (9.29 ± 0.49) chest barring ($p = 0.001$). This red coloration in CBO reflects adaptation to humidity or low light intensity in wet zone as suggested in previous studies. Vocal analysis revealed only minor divergence that JO exhibited higher-frequency calls ($p < 0.05$), likely adapting to lower humidity in dry zones. These findings support phylogenetic niche conservatism, as CBO and JO, despite ecological divergence, retain notable morphological, plumage, and behavioural similarities, indicating phenotypic stasis. Both species are diurnal, insectivorous owlets, and occupy similar niches despite the differences in distribution and vocalization. Genetic characterization using mitochondrial molecular markers has initiated for further characterization of this cryptic species separated by the climate.

Keywords: Ecological speciation, crypsis, island biogeography, phylogenetic niche conservatism

Breeding ecology and feather molting pattern of recently described Hanuman plover (*Anarhynchus seebohmi*)

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The Hanuman Plover (*A. seebohmi*), recently split from the Kentish Plover *(A. alexandinus*) species complex. Here, we investigated the species' breeding ecology and molting patterns to characterise its variation of plumage across the year and breeding phenology to compare those with the broader Kentish Plover species cluster. Individuals(n=22) were captured using mist nets in Mannar Island, and after morphometric measurements and the status of the molt were recorded. Nest monitoring involved recording egg characteristics(n=28) and deploying thermal data loggers(n=8) to assess nest thermal homeostasis. Trap camera - Browning Dark Ops Pro XD – (BTC-6PXD)(n = 68 hours) were used to study breeding behaviour in the nests(n=3). Morphometric comparisons between available data on Hanuman Plover(n= 68), Kentish Plover(n=380) and White-faced Plover(n=155) indicate that the Hanuman plovern has shorter wing length, suggesting the non-migratory nature relative to the migratory Kentish plover. Hanuman plover molts into definitive basic plumage (Winter plumage) between August and September, often entering the breeding season in Definitive alternative plumage(summer plumage), possibly to reduce predation risk associated with conspicuous ornamentation. Its eggs were significantly smaller in breadth and width compared to those of the Kentish plover. Five distinct vocalization types were identified in the Hanuman plover vocal repertoire. Three types exhibited significant differences from homologous Kentish plover calls(P values<0.05). Hanuman plover nests in environments characterised by extreme heat during the daytime, up to 46 °C, and low temperatures at night, down to 26 °C; hence, breeding birds had to employ specific incubation behaviours, such as egg covering, light sitting, and tight sitting, to manage thermal homeostasis on the egg. During midday, incubating parents show panting and pteryloerection to reduce the thermal stress. Both sexes participate in incubation, although males contribute more frequently. Nest predation was common by feral cats, dogs, and crows. Human activity within nesting habitats was also observed to disturb breeding birds. This study provides the first detailed description of the breeding phenology, molting, natural predators and human threats for this newly described species.

Keywords: Breeding phenology, nesting thermal homeostasis, incubation, nest-predation, Hanuman plover

Comparative analysis of meteorological and soil moisture droughts in urban wetlands of Sri Lanka to validate the use of SPI as the primary measurement to assess drought

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Droughts are usually slow-onset disasters with long-lasting consequences, especially for vulnerable ecosystems like wetlands. The Standardized Precipitation Index (SPI) is widely used in drought studies due to its simplicity and the availability of precipitation data. However, it is primarily a meteorological indicator, it doesn't account for the soil water deficit which is critical to the health of plants and ecosystems. This study compares meteorological droughts (SPI-based) and soil moisture droughts in the Metro Colombo Wetlands, Sri Lanka aiming to assess the validity of using SPI alone in wetland drought management. HYDRUS-1D model was used to simulate soil moisture for a 50 cm soil profile using rainfall data from 1993–2021 and field-measured soil properties from the Colombo wetlands. Simulated soil moisture values were standardized (SSM) to allow comparison with SPI derived from the same rainfall dataset. Kolmogorov-Smirnov test revealed significantly different distributions between SPI and SSM, but they were strongly positively correlated (0.95). Kernel density estimation showed that SPI values had a sharp, narrow distribution centered around the mean, while SSM had a broader distribution with more extreme negative values. Time series plots also indicated that during wet years SPI index value were greater than SSM while during dry years SSM index value were greater than SPI. These results suggest that soil moisture droughts are more severe than meteorological droughts, which indicates the limitations of using the SPI indices alone to evaluate ecological drought. As wetland vegetation is highly sensitive to soil moisture, it is significant to evaluate soil moisture droughts separately. The integration of physically based models such as HYDRUS-1D enhances the accuracy of drought assessments and provides essential insights for more efficient wetland conservation, ecological forecasting, and climate change adaptation.

Keywords: Soil moisture droughts, meteorological droughts, SPI, HYDRUS-1D, drought modelling

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Metal-dominated nest architecture of the House Crow (*Corvus splendens*) in urban Colombo, Sri Lanka

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Urbanization modifies wildlife behavior with certain species, such as House Crows (*Corvus splendens)* exhibiting preferential use of urban habitats due to increased resource availability. Their extent of adaptation to urban life is evident through the utilization of anthropogenic materials in nest construction, yet quantitative data on nest composition in this region remain limited. Therefore, this study aimed to quantify the composition of anthropogenic and natural materials House Crows nests. Thirty abandoned House Crow nests were collected from seven densely urbanized areas in Colombo, Sri Lanka. Each nest was manually dismantled, and components were categorized and weighed by material type (metal, plastic, rubber, natural matter). The average weight of the nests measured was 1078.29 g ± 498.52 g. Results revealed a striking dominance of metallic materials, contributing 81.1% of total nest weight on average. Natural materials, such as twigs and leaves, accounted for only 12%. Metal items such as wires, nails, and metallic coat hangers were consistently used, highlighting a selective preference for strong, durable substrates. Plastic and rubber were used minimally, mainly confined to the nest lining while the metals composed the structural basket of the nest. A strong positive correlation was found between metal content and total nest weight (Pearson, $r = 0.95$, $df = 28$, $p < 0.001$). Contrary to the global trends of higher plastic incorporation in corvid nests, these findings demonstrate the extensive reliance on metallic materials by House Crows in Colombo, suggesting both behavioral adaptability and potential ecological risks associated with metal use such as entanglement, injury and altered microclimate due to higher thermal conductivity in the tropical urban environment of Colombo. Future research should investigate how metal-rich nests influence reproductive success, nest temperature profiles, and chick survival.

Keywords: Urbanization, anthropogenic materials, corvids, nest composition, altered microclimate

Morphometric and meristic analysis of endemic freshwater fish *Belontia signata* (Anabantiforms: Belontiinae) in six river basins in Sri Lanka

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Belontia signata, or the Ceylonese combtail, is an endemic freshwater fish found mainly in Sri Lanka's wet zone and the Mahaweli basin. This study examined the phenotypic variation among *Belontia signata* populations across six major river basins in Sri Lanka (Mahaweli, Kelani, Kalu, Gin, Nilwala and Walawe) using both morphometric and meristic approaches, based on samples collected from November to February. Forty-nine specimens (23 males, 26 females) were collected from nine sites. Each specimen was measured for 13 morphometric and 16 meristic characters. Initial PERMANOVA analyses demonstrated no significant differences between age or sex ($p > 0.05$), allowing for pooled comparisons across populations. Subsequent multivariate PERMANOVA confirmed significant inter-basin differences in morphometric traits ($p < 0.05$). Pairwise analysis revealed morphometric similarity only between Kelani–Kalu and Kelani–Nilwala populations ($p > 0.05$), while all other basin comparisons exhibited significant divergence. Principal Component Analysis (PCA) of morphometric data retained two principal components, PC1 and PC2, accounting for 69.4% of total variance (40.5% and 28.9%, respectively). Biplots demonstrated clear separation of Mahaweli and Walawe populations. Kruskal–Wallis tests identified ten morphometric characteristics as significantly variable ($p < 0.05$), which was further supported by Dunn's post hoc results. Meristic analyses also revealed significant inter-population differences ($p < 0.05$). Pairwise comparisons showed non-significant variation for Gin–Nilwala, Mahaweli–Walawe, Kelani–Kalu, Kelani–Nilwala, and Kalu–Nilwala, but significant differences among all other basin pairs. Principal Coordinates Analysis (PCoA) of meristic data explained limited variation (Axis 1 = 14%, Axis 2 = 13%), yet Kelani and Mahaweli clusters emerged distinctly, whereas other populations overlapped. Key meristic differentiators included dorsal fin length, dorsal and pectoral fin ray counts, anal fin spines, lateral-line scale counts, and scale numbers above and below the lateral line ($p < 0.05$), as highlighted via Dunn's comparisons and boxplots. These findings show significant morphological and meristic divergence in *B. signata* populations, likely due to river isolation or environmental factors.

Keywords: Ceylonese combtail, meristic approaches, inter-river basin differences, Morphometrics, population overlaps

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Phylogenetic characterization of Sri Lankan Hipposideridae and Rhinolophidae bats based on mitochondrial COI sequences

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Bats play a significant role in ecosystems as insect controllers, pollinators and seed dispersers. Sri Lanka, a small tropical island, harbors a rich bat diversity of 30 species, with nearly 23% belonging to the families Rhinolophidae and Hipposideridae. Sri Lanka's close proximity to India, together with the high mobility of bats, have resulted in close evolutionary affinities across the South Asian Range. This study aimed to investigate phylogenetic relationships of Sri Lankan hipposiderids and rhinolophids, using mitochondrial cytochrome oxidase subunit I (COI) gene sequences. Tissue samples were obtained through non-invasive toe clipping from four individuals per species, totaling 28 individuals, across multiple locations. Two individuals per species were selected for sequencing. Genomic DNA was extracted using the QIAGEN DNeasy Blood and Tissue Kit, followed by PCR amplification and Sanger sequencing. The newly generated sequences (n=14) were aligned with South Asian GenBank homologs using ClustalW program and analyzed using RAxML under the GTR+R model with 1000 bootstrap replicates. The resulting phylogenetic tree revealed two distinct clades, confirming the monophyly of the two families. Strong species-specific clustering supported by a high bootstrap value (>80) was observed for *H. speoris, H. fulvus, H. ater, R. beddomei* and *R. rouxii* with Indian relatives thus indicating low genetic divergence and recent common ancestry, *R. beddomei* appeared as a sister clade to *R. rouxii* supporting its taxonomic distinction. *H. lankadiva* and *H. srilankaensis* showed distinct clustering, highlighting Sri Lanka's unique evolutionary lineages. Importantly, this study presents the first molecular evidence for *H. ater* and *H. fulvus* in Sri Lanka. These findings reveal the close affinity between Sri Lankan and Indian bat populations, suggesting historical faunal exchange. They also highlight the need for regional collaboration in bat conservation and biodiversity assessments. Further, multi-locus approaches are recommended to clarify unresolved lineages and to enhance understanding of the evolutionary history of the Sri Lankan bats.

Keywords: Phylogenetics, cryptic diversity

Using ant diversity as bioindicators of soil health: the role of human influence and urbanization impact

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Urbanization significantly impacts soil quality through pollution and compaction, disrupting key ecosystem functions. Ants are valuable bio-indicators of soil health due to their sensitivity to environmental change and their ecological roles in nutrient cycling, soil aeration, and pest regulation. This study examined how urban soil alterations affect ant communities by comparing paired disturbed and undisturbed habitats (three sites each) at the University of Colombo. Sites were selected based on the frequency of anthropogenic activity: undisturbed areas like Butterfly gardens were seldom frequented by people, while disturbed sites included roads, walk-paths, and construction areas with regular human presence. Soil parameters were measured, including moisture, temperature, organic matter content, and pH. Ant populations were evaluated for abundance and diversity. Four ant species were identified: *Diacamma rugosum, Solenopsis geminata, Lasius niger, and Tapinoma melanocephalum*. Undisturbed areas showed the highest species abundance (Shannon-Wiener index: 0.497 ± 0.097), while areas with substantial human activity had the lowest (0.224 ± 0.389), with significantly lower diversity observed in disturbed sites (Mann–Whitney, $p = 0.002$). High temperatures (33.6 ± 2.6°C, Spearman's; $r = -0.715$) were associated with reduced ant populations, likely due to limited nesting and foraging opportunities. In contrast, higher organic matter content (0.63 ± 0.27% mg C, Spearman's; $r = 0.498$) supported greater abundance by improving soil structure and nutrient availability. These findings indicate that elevated temperatures, reduced organic matter, and increased human disturbance correspond with decreased ant diversity and abundance in urban areas. Conversely, undisturbed sites with higher organic content supported richer ant communities, highlighting the crucial role of organic matter in sustaining biodiversity. Preserving vegetation cover and minimizing soil disturbance may help sustain biodiversity in urban environments. Monitoring ant communities provides a practical, low-cost method to assess soil health and guide urban conservation efforts in tropical ecosystems.

Keywords: Urban soil quality, ant biodiversity, soil health indicators, urbanization and ecosystems, soil compaction effects

Effects of habitat complexity on growth and behavior in Neon Tetra Fish (*Paracheirodon innesi*)

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The ornamental fish trade often struggles to maintain healthy populations of Neon Tetra (*Paracheirodon innesi*) in captivity due to stress-induced conditions, such as fin rot, white spot disease, loss of coloration in aquariums. This study investigated how varying levels of habitat complexity influence behavior and growth in *P. innesi* to identify enrichment strategies that promote health and welfare in aquaria. Three experimental habitats were developed where each complexity level was represented by one tank: low complexity (aerator only), medium complexity (aerator, pebbles, one live plant), and high complexity (aerator, pebbles, and three plants. Each 20-liter tank housed randomly selected 15 fish of same age, maintained under natural lighting and normal water quality conditions. Over five weeks, standard length and weight were measured, using digital calipers (±0.01 mm) and an analytical balance (±0.01 g). Behavioral observations were also recorded weekly for 15 minutes in the morning before cleaning the tanks, considering feeding rate and line crossing frequencies to measure their activity level. A Kruskal-Wallis test revealed significant differences in length growth across groups ($H(2) = 14.82$, $p = 0.001$). Post-hoc analysis indicated that fish in low-complexity tanks exhibited significantly greater p value in length increases compared to those in mid and high-complexity tanks. Specifically, fish in the low-complexity tank showed a 26.13% increase in length, compared to 14.62% and 16.70% in the medium and high-complexity tanks, respectively. However, no significant differences in p value were observed in weight across the three treatment groups, although the low-complexity group showed a trend toward reduced weight gain. These findings suggest that structural enrichments can affect the somatic growth in *P. innesi*. While behavioral variation was limited, the physiological benefits underscore the importance of habitat design in ornamental aquaculture. The current study highlights the significance of habitat design in the management of ornamental fish.

Keywords: Aquarium enrichment, ornamental fish, growth rates, behavioral ecology, habitat design

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

Assessment of precipitation effects on atmospheric heavy metal concentrations using *Tillandsia usneoides* as a biomonitor

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Atmospheric heavy metal pollution causes significant environmental and health risks, particularly in urban areas like Kandy, Sri Lanka, which experiences high vehicular traffic, dense population, and due to its location between two mountain ranges. This study aimed to examine the relationship between precipitation and atmospheric concentrations of mercury (Hg), cadmium (Cd), lead (Pb), and arsenic (As) using *Tillandsia usneoides* (Spanish moss) as a biomonitor. Spanish moss, an epiphytic plant that absorbs nutrients directly from the atmosphere, was obtained from the Royal Botanical Garden, Peradeniya, and transplanted across selected urban locations. Samples were collected at 4-week intervals over a three-month period and analyzed using ICP-MS (NexION 2000B, PerkinElmer, USA) following microwave-assisted digestion. Precipitation data was obtained from the Meteorology Department of Sri Lanka. Pearson Correlation test was carried out in order to analyze correlation between the precipitation and each heavy metal. A positive but non significant correlation was observed ($r=0.9493$, $p=0.2037$) between Hg with precipitation. However, a spike in Hg levels during November coincided with the heavy rainfall caused by the Fengal cyclone (608.1 mm), suggesting atmospheric transport during convective storms. Cd shows a strong negative and non significant correlation with precipitation ($r=-0.5406$, $p=0.6364$). Pb levels showed relatively higher values, likely due to vehicular emissions and a cyclonic vortex event in December. Pb shows a very strong negative and statistically significant correlation with the precipitation ($r=-0.9974$, $p=0.04525$). As concentrations fluctuate with the precipitation yet it shows a strong positive correlation but statistically non-significant correlation. ($r=0.8719$, $p=0.3258$). The study demonstrates that precipitation influences atmospheric heavy metal accumulation in urban Kandy, highlighting the complex interplay between meteorological factors and pollution dynamics.

Keywords: Kandy, precipitation, heavy metals, Spanish moss, air pollution

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ABSTRACTS – POSTER PRESENTATIONS

In silico analysis of virulence factors and secondary metabolite biosynthesis clusters in the genome of the plant pathogenic fungus *Rhizoctonia solani*

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Rhizoctonia solani is a devastating plant pathogen that causes a diverse range of diseases in numerous crop plants, including cereals, vegetables, and legumes, resulting in a significant economic impact on global agriculture. Therefore, understanding the molecular mechanisms underlying its pathogenicity is important for developing effective disease management strategies. This study aimed to conduct an in-depth in silico analysis of the *R. solani* AG-1 IA genome using bioinformatics tools and databases to comprehensively analyze the potential virulence factors and secondary metabolite biosynthetic gene clusters (BGCs) and to explore their possible roles in the pathogenesis of *R. solani*. A secretome and effectome prediction pipeline and antiSMASH-based genome mining were employed to identify candidate effector proteins and secondary metabolite BGCs. They were subjected to functional annotation, followed by expression and co-localization analyses. This study predicted 20 candidate effector proteins and 13 secondary metabolite BGCs, comprising 8 terpene synthases and 5 non-ribosomal peptide synthetase-like clusters. Functional domain analysis revealed that most of the annotated effectors contain domains associated with host cell wall degradation (3) or immune system suppression (3), such as those involved in carbohydrate hydrolysis and degradation of plant defense proteins. Notably, 11 of these effectors displayed no significant similarity to known proteins in fungi, suggesting species-specific virulence factors that may play critical roles in *R. solani* AG-1 IA pathogenicity. Functional annotation of BGCs indicated their involvement in the synthesis of bioactive compounds, such as toxins, which are potentially associated with virulence and host colonization. Expression analysis uncovered genes with strong expression as well as those that were dormant throughout the infection period. Co-localization analysis revealed that some virulence factor genes are in proximity to secondary metabolite BGCs. This study highlights key effectors and secondary metabolite BGCs in *R. solani* AG-1 IA, providing insights into its pathogenicity and aiding future disease control strategies.

Keywords: *Rhizoctonia solani*, effector proteins, secondary metabolite biosynthetic gene clusters, pathogenicity

Application of a newly isolated probiotic strain as a starter culture in curd production and determining the encapsulation efficiency

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Lactic acid bacteria are valuable bacteria in the food industry due to their fermentation ability and health and nutritional benefits. Therefore, bacteria belonging to the genus *Lacticaseibacillus* are used as starter cultures. Encapsulation involves enclosing active agents within a carrier material to enhance the delivery of bioactive compounds and living cells in food. This study aims to evaluate the newly isolated *Lactobacillus rhamnosus* strain as a starter culture in curd production and its encapsulation efficiency. Curd was prepared using pasteurised milk after the incorporation of newly isolated probiotic bacteria with four treatments: T1 *L. rhamnosus* (10^8 CFU/ml), new strain added curd, T2 combination (*L. rhamnosus* 10^2 CFU/ml & *L. bulgaricus* 10^2 CFU/ml), T3 *L. bulgaricus* (10^8 CFU/ml) and T4, control. The inoculum ratio was 100 ml milk: 1 ml inoculum. Treatments were incubated at 37°C for 12 hours. A Sensory and storage study was carried out to select the best treatment, and analysed for microbiological and physicochemical parameters for 3 days. T1 showed a significantly higher value for the overall acceptability, aroma, and taste compared to other treatments. The viable cell count of (T_1) showed 6.5±0.10 CFU/ml initially, which significantly increased to 7.55 ± 0.00 CFU/ml after 3 days. Surprisingly, T1 showed significantly higher viable cell counts compared to other treatments. In T1 and T2 the initial pH were 6.5±0.10, 6.4±0.15, respectively, which significantly decreased ($p<0.05$) to 4.22±0.01, 4.34±0.01 after three days, respectively. The acidity of T1 (0.84±0.01) and T2 (0.82 ±0.00) on the third day showed significantly higher values compared to T3 and T4. T1 containing *L. rhamnosus* new strain, had a pleasant aroma and produced probiotic curd with better stability over time, which makes it a good starter culture. The encapsulation efficiency is reported as 86.09%. The greater survival of *L. rhamnosus* new strain can be explained by its ability to tolerate an acidic environment (pH 4), with a minimum cell density of 6–7 log10 CFU/g maintained during the storage.

Keywords: Probiotics; microencapsulation; *L. rhamnosus* new strain; starter culture

Acknowledgement: Engineering Research Unit of the Faculty of Engineering Technology for financial support.

Mycoherbicidal potential of *Nigrospora sphaerica* against *Synedrella nodiflora*, a common weed in Sri Lanka

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Weeds greatly affect the yield and crop quality in agriculture. Mycoherbicides—bioherbicides utilizing fungal plant pathogens—offer a potentially more environmentally compatible approach to weed management compared to synthetic chemical herbicides. This study evaluated the mycoherbicidal potential of a fungal pathogen isolated from *Synedrella nodiflora*, a widespread broadleaf weed species. A putative fungal pathogen was isolated from symptomatic leaves exhibiting chlorotic and necrotic lesions. Pathogenicity was confirmed through Koch's postulates, and molecular identification based on ITS region sequencing revealed the pathogen as *Nigrospora sphaerica*. Preliminary tests were conducted by inoculating healthy plants of *S. nodiflora* with pathogen mycelial plugs (0.01g/mL) and spore suspensions (1×10^6 mL^{-1}). Five different inoculation methods and two different application protocols were used. The inoculation methods: Paint brush method, cutting and painting, pricking leaf with needle, local infiltration with syringe, and cutting and dipping. The experiment followed a protocol with one initial application and another involving a reapplication of inoculum on the 3rd day post-initial inoculation. The controls were a commercial glyphosate solution and sterile distilled water. Disease severity was measured as a percentage of leaf damage after 7 days. The Friedmans test revealed that different inoculation methods did not significantly affect the disease severity, while the Wilcoxon test indicated that re-application of inoculum enhanced the symptom severity for the paintbrush method and the cutting and painting method, concluding that both re-application and mechanical injury significantly increased the mean disease severity in 7.14 ± 3.77 percentage points and 7.158 ± 2.543 percentage points respectively. Importantly, pathogenicity tests carried out on *Capsicum annuum* (chilli) with the same inoculum concentrations showed no development of disease, suggesting potential host specificity of pathogen. Progressive chlorosis in the leaves, leading to plant death upon treatment with the crude extract, indicated the possible production of phytotoxic compounds by the pathogen. These findings highlight *N. sphaerica* as a promising candidate for the development of a mycoherbicide, offering an environmentally compatible alternative to chemical herbicides.

Keywords: Bioherbicide, host-specificity, pathogenicity, phytotoxins

Biorefinery potential of freshwater microalgae cultivated in synthetic wastewater: a sustainable approach for biomass valorization

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Microalgae are considered one of the most promising feedstocks for sustainable biorefinery applications due to their rapid growth rates, metabolic versatility, and ability to synthesize diverse high-value biomolecules. However, the high cost of conventional culture media limits large-scale applications. To address this gap, this study evaluated the biomass productivity and biorefinery potential of three locally obtained freshwater microalgae species—*Chlorella sorokiniana*, *Scenedesmus pectinatus*, and *Arthrospira* sp.—with a specific focus on their cultivation in 'synthetic' wastewater media that mimic the real wastewater as a cost-effective alternative to conventional growth substrates. Cultivation trials were conducted in synthetic wastewater under two mass-based nitrogen-to-phosphorus (N:P) ratios (8:1 and 16:1) for 12 days in triplicate 1 L batch cultures, and parameters including pH, dissolved oxygen (DO), biomass concentration, and nutrient removal efficiency were evaluated. Of the three isolates, *Arthrospira* sp. demonstrated better adaptability in synthetic wastewater, achieving enhanced biomass yield and stable pH regulation, particularly under the N:P 16:1 ratio. *Chlorella sorokiniana* exhibited the highest mean DO content (4.99 ± 0.12 mg/L), indicating greater oxygen evolution associated with photosynthesis. Biochemical profiling of *Arthrospira sp.* biomass revealed a protein content of 30.25% (w/w), moderate antioxidant activity (DPPH IC_{50} = 156.87 µg/mL), and notable pigment levels—chlorophyll-a (3.86 ± 0.33 µg/mg) and carotenoids (0.73 ± 0.10 µg/mg). Lipid extraction and subsequent transesterification yielded fatty acid methyl esters (FAMEs), with characteristic FTIR peaks confirming biodiesel formation; lipid content was recorded at 6.79% (w/w). This study demonstrates that cultivation of locally obtained freshwater microalgae in synthetic wastewater is a cost-effective method for low-cost biomass production, with *Arthrospira* sp. showing superior adaptability, biomass yield, and biochemical potential for protein, pigment, and biodiesel applications.

Keywords: Microalgae, biorefinery, synthetic wastewater, bioactives, biodiesel

First insights into HLA-C*06:02 (HLA-Cw6) prevalence and its association with disease onset and severity in pediatric and adult psoriatic patients in Sri Lanka

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Human Leukocyte Antigen C*06:02 (HLA-Cw6) is the most documented allele linked to psoriasis occurrence and severity in Type I psoriasis. This study investigated the prevalence of HLA-Cw6 among pediatric (n=53) and adult psoriasis (n=58) patient populations in Sri Lanka, a locally underexplored area. HLA-Cw6 positivity was examined using Polymerase Chain Reaction (PCR) – Sequence-Specific Primer (SSP) methods. A Restriction Fragment Length Polymorphism was followed by PCR to detect the homo/heterozygosity of HLA-Cw6. The disease reported an overall female predominance (61.2%). It was of interest to note that HLA-Cw6 allele positivity was significantly lower among pediatric patients (18.9%; homozygotes - 40%, heterozygotes - 60%) than the adults (43.1%, homozygotes - 38.9%; heterozygotes - 61.1%) (Pearson Chi-Square test, p=0.027). The discrepancy may be attributed to selection bias, low sample numbers, delayed disease manifestation, and the contribution of environmental and other genetic factors. No significant difference at the early onset nor disease severity was observed between HLA-Cw6 positive and negative patients in both pediatric and adult groups (Mann-Whitney U test, p=0.516, Pearson Chi-Square test, p=0.186). However, overweight and obese pediatric patients were reported to have more moderate and severe disease than underweight and healthy patients (Pearson Chi-Square test, p=0.003). Among patients below 40 years (Type I), early onset was predominantly observed in females (69.4%), while in patients above 40 years (Type II), a male predominance was noted (61.3%), with a significant difference in disease onset age between males and females (Pearson Chi-Square test, p=0.003). Only 17.2% of patients (Type I- 60%, Type II- 40%) had a positive family history. This study was the first to investigate and compare the prevalence of HLA-C*06:02 in adult and pediatric psoriatic patients in Sri Lanka. Future studies, including a larger representation of the general psoriasis population with longitudinal follow-ups, are crucial for understanding the observed discrepancy in HLA-Cw6 positivity across age groups.

Keywords: HLA-Cw6, adult psoriasis, pediatric psoriasis, Sri Lanka

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Preliminary validation of multiplex qPCR assay for the detection of 22q11.2 microdeletion in children showing neuropsychiatric phenotypes

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The 22q11.2 microdeletion is the most common microdeletion syndrome in humans and is associated with a broad spectrum of neuropsychiatric phenotypes. The high cost of standard diagnostic methods hinders its timely diagnosis and effective intervention. Accordingly, we have previously described the optimization of a low-cost TaqMan probe-based duplex assay to detect the copy number variation of 22q11.2 using *PI4KA* gene as the target and *SHANK3* gene as the reference (gene dosages: with microdeletion=0.5; without microdeletion=1.0).The current study aimed to validate this duplex qPCR assay in accordance with MIQE guidelines by assessing its diagnostic specificity, accuracy, efficiency, linearity, limit of quantification (LOQ), and precision for potential use in clinical settings. Accordingly, DNA samples collected from five patients positive for the microdeletion (by standard assays), five confirmed negative for microdeletion, and four unconfirmed healthy (negative control) were analysed using the optimised duplex qPCR assay based on a standard curve, and gene dosages were calculated using the $2^{-\Delta\Delta CT}$ method. The assay was able to determine the absence of microdeletion (gene dosage=0.85-1.15) in 88.9% (8/9) negative controls, indicating its diagnostic specificity and its presence (gene dosage=0.35-0.65) in 80% (4/5) of positive controls, producing an overall accuracy of 85.7%. The standard curves for both marker and reference gene reactions across seven runs demonstrated excellent performance with respect to efficiency (97.4-104.0%), linearity (correlation coefficient; R^2=0.983-0.999), and slope (-3.386 to -3.221). The LOQ assessed as the lowest concentration showing a coefficient of variation (CV) <35% was found to be 1 ng when tested with an extended standard curve. The precision of the assay was high with low intra-assay (6.7-12.3% across five replicates) and inter-assay (3.3-21.1% across five runs) variations (recommended range 20-25%). Preliminary validation suggests that the duplex qPCR assay holds strong potential as a robust, reliable, and cost-effective method for detecting 22q11.2 microdeletion in children showing neuropsychiatric phenotypes. Nevertheless, further validation using a larger cohort along with confirmation with standard assays is required prior to its adoption in clinical diagnostics.

Keywords: 22q11.2 microdeletion, duplex assay, copy number variation, gene dosage, MIQE guidelines
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Screening of antibiotic resistance in probiotic bacteria for tetracycline group antibiotics in aquaculture practices in Sri Lanka

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With the increasing reliance on probiotics in aquaculture to enhance animal health and productivity, their potential role as reservoirs of antibiotic resistance remains a critical concern. This study aimed to assess the antibiotic resistance of probiotic bacteria used in Sri Lankan aquaculture, focusing on tetracycline-class antibiotics. Seven commercial probiotic samples were collected from shrimp and ornamental fish farms. Bacterial isolates were obtained using the pour plate method, and antibiotic susceptibility was determined against tetracycline and oxytetracycline following Clinical and Laboratory Standards Institute (CLSI) guidelines. Genomic DNA was extracted from isolates using the freeze–thaw method, and PCR screening with primers from Integrated DNA Technologies was performed to detect resistance genes (*tetA* and *tetM*). A total of 63 resistant isolates were identified. The majority (66.7%) showed resistance to oxytetracycline, while 33.3% were resistant to tetracycline. Resistance was concentration-dependent, with higher prevalence at 5–15 ppm and reduced resistance at 25–50 ppm. Molecular analysis revealed that 24% of isolates carried the *tetA* gene, 38% carried *tetM*, and 10% harbored both, indicating the coexistence of efflux pump and ribosomal protection mechanisms. These findings demonstrate that probiotic bacteria in Sri Lankan aquaculture harbor significant tetracycline resistance genes, highlighting potential risks for horizontal gene transfer in aquatic environments. The results emphasize the urgent need for stringent probiotic screening, continuous resistance monitoring, and molecular-level characterization to safeguard aquaculture sustainability and public health.

Keywords: Antibiotic resistance in probiotics, aquaculture microbiome, tetracycline resistance genes, *tetA* & *tetM*, Sri Lankan aquaculture

Prevalence of clinically significant *PIK3CA* hotspot mutations: a comparative cohort study of HER2-positive and HER2-negative breast cancer subtypes in Sri Lanka

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Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha (*PIK3CA*) is one of the most frequently mutated oncogenes in breast cancer. Mutations such as E542K and E545K (exon 9) and H1047R (exon 20) have been associated with resistance to anti-HER2 therapies (e.g., trastuzumab) and endocrine therapies, particularly in HER2-positive, ER/PR-positive patients. However, region-specific data from Sri Lanka on the prevalence and clinical significance of these mutations are lacking. This limits their integration into treatment decision-making. This study profiled the *PIK3CA* mutations E542K, E545K, and H1047R in HER2-positive breast cancer patients from Sri Lanka for the first time. It also compared mutation frequencies with a previously studied HER2-negative cohort. Genomic DNA was extracted from 30 FFPE HER2-positive biopsy samples using the QIAGEN FFPE DNA extraction kit. Mutation detection was performed using the QClamp® *PIK3CA* Mutation Detection Test, which utilizes xenonucleic acid-mediated clamping to selectively suppress wild-type amplification. *PIK3CA* mutations were detected in 33.33% (95% CI: 17.3%–52.8%) of HER2-positive cases, which is higher than the global average of 20–25%. H1047R, which is widely known to be associated with high proliferative capacity, increased tumour aggressiveness, and poor clinical prognosis was the most frequent mutation (60.0%; 95% CI: 26.2%–87.8%). This was followed by E542K and E545K, each accounting for 20% (95% CI: 2.5%–55.6%). In contrast, the HER2-negative group showed a significantly lower mutation rate of 17.46% (95% CI: 9.0%–28.7%) ($p < 0.05$). However, the individual mutation distribution was similar, with H1047R being the most common. These findings reflect global trends, where exon 20 mutations contribute more to the overall mutation burden than exon 9. The significantly higher prevalence of *PIK3CA* mutations in the HER2-positive group underscores the potential clinical utility of incorporating genomic testing for *PIK3CA* mutations into routine diagnostics. The results also highlight the possible therapeutic benefit of PIK inhibitors in the treatment of *PIK3CA*-mutated breast cancers, particularly in HER2-positive patients.

Keywords: *PIK3CA* oncogene, HER 2-positive, HER 2-negative, genomic testing

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Evaluation of *in vitro* cytotoxicity and clonogenic activity of a clinically used traditional medicine formula

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Traditional medicine has shown great promise in both preventing and treating various diseases. It contains a wide variety of medicinal formulas, including Arishta. Arishta is recognized for its unique therapeutic features, which include higher pharmacological activity, improved extraction of bioactive components from herbal constituents, storage stability, and greater efficacy of dosage forms, all of which contribute to better health outcomes. However, there has been minimal scientific research to comprehensively evaluate its pharmacological activities. This study aimed to determine the cytotoxicity and clonogenicity of an Arishta formula against Rhabdomyosarcoma (RD) and breast cancer (MCF-7) cells. Cytotoxicity was screened using 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide assay (MTT) assay, followed by a clonogenic assay to determine the long-term proliferative potential of the treated cells. MTT assay, revealed a better half-maximal inhibitory concentration (IC_{50}) of 0.434 ± 0.085 mg/mL against RD cells, while the IC_{50} was >1 mg/mL against MCF-7 cells. To assess the long-term proliferative potential of RD cells post-treatment, a clonogenic assay was conducted at 1xIC_{50}, 2×IC_{50}, and 5×IC_{50} concentrations. The surviving fraction (SF) of RD cells decreased dose-dependently, with values of 10.10 at 1xIC_{50}, 4.602 at 2×IC_{50}, and 2.028 at 5×IC_{50}, indicating a strong inhibitory effect on colony formation. Afterwards, an Acridine Orange/Propidium Iodide (AO/PI) assay was performed on RD cells, revealing the presence of apoptotic bodies. The findings suggested that the Arishta formula exhibited significant cytotoxic and anti-clonogenic potential against RD cells, warranting further investigation into its mechanisms and therapeutic applicability in cancer treatment.

Keywords: *In-vitro* cell culture assays, cytotoxicity, clonogenic, polyherbal formulation, RD cells

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TLC-based phytochemical screening and quantitative determination of total phenolic content in tuberous roots of *Mirabilis jalapa* L. under different extraction conditions

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The medicinal value of *Mirabilis jalapa* L. (Sinhala name: Hendirikka), also known as the 'four o'clock plant', is attributed to its bioactive phytochemicals, which are employed in folk medicine. This study aimed to investigate the aqueous, methanol, dichloromethane (DCM), and hexane extracts from different extraction methods, namely maceration, sonication, and Soxhlet extraction of *Mirabilis jalapa* tubers for their bioactive compounds using thin-layer chromatography coupled with spray reagents to identify specific phytochemicals and to analyze the total phenolic content assay. Tuberous roots (1 kg) of *Mirabilis jalapa* was collected from Kandy, Sri Lanka, and authenticated. The shade-dried roots were ground into coarse powder and extracted using maceration, sonication, and Soxhlet methods with aqueous, methanol, dichloromethane, and hexane solvents (1:5 ratio). Extracts were concentrated via rotary vacuum evaporation, separated by TLC with spray reagents such as Dragendorff reagent, 1% ferric chloride, 5% alcoholic potassium hydroxide, anisaldehyde-sulphuric acid, 10% ethanolic sulphuric acid, iodine, and 0.02% ethanolic DPPH for phytochemical screening, and analyzed for total phenolic content using the Folin-Ciocalteu method, expressed as gallic acid equivalents. Through thin-layer chromatography, polar phytochemicals, including phenolics and tannins, were detected in extracts prepared with polar solvents, such as methanol and aqueous solutions. On the other hand, terpenoids, saponins, and cardiac glycosides were seen in hexane and dichloromethane extracts. Phenolics were higher in methanol, aqueous macerates, and aqueous Soxhlet extract, with total phenolic content (TPC) of 320.12, 232.31, and 167.30 mg GAE/g TPC, respectively. Alkaloids, anthrones, and anthraquinones were seen less frequently throughout the solvents. TLC analysis for tuberous roots of *M. jalapa* extracts for mentioned solvents using different extraction methods revealed that maceration and Soxhlet extraction separated most compounds, particularly in methanol, dichloromethane, and hexane extracts, demonstrating various potentially bioactive compounds separated and may have high antioxidant activity.

Keywords: Thin layer chromatography, phytochemical screening, total phenolic content, *M. jalapa* L., Hendirikka

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A helical motif as perfect foil: Nudix Box residues and folate biosynthesis

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Folate biosynthesis in plants is governed by a committed step that catalyzes the hydrolysis of dihydroneopterin triphosphate (DHNTP) by a Nudix hydrolase [An enzyme with the Nudix Box Loop-Helix-Loop motif], known as FolQ in bacteria and by association, in plants. FolQ is predominantly found in eudicots and only 22 monocot FolQ proteins are listed when the NCBI protein database is queried with the *Arabidopsis* DHNTPase [UniProtKB/Swiss-Prot: Q9CA40.1] as a BLASTp search query specified to monocots. To decipher the landscape of what makes these 22 monocots evolve a FolQ enzyme, when most monocots are not expected to harbour FolQ proteins, a bioinformatics exploration was performed using molecular phylogeny based on Maximum Likelihood in MEGA-12 software and structural clues from the AlphaFold protein structure database. The monocot FolQ enzymes are largely distributed in orchids, in the family Dioscoreaceae, in basal monocots such as Acorus, and in Asparagus, which has a high folate content that earmarks it as a high folate food ideal for human consumption. When phylogeny was assessed, a monophyletic clade was observed between DHNTPases of Asparagus and the genus Dioscorea, both high folate foods. One Asparagus Nudix hydrolase [XP_020269481.1 - Asp-FolQ/Asp-DHNTPase] has unique features such as a serine N-terminal to the RExxEE motif, a residue that is predicted to be phosphorylated, while there are three unique glutamines downstream of the Nudix Box. Glutamines are known as key residues in the hydrolysis of GTP by GTPases such as Ras GTPases. The presence of three unique glutamines downstream of the Nudix Box in Asp-FolQ, coinciding with the wider catalytic domain of Nudix hydrolases, may be significant in substrate recognition and catalysis. In summary, the author has used bioinformatics tools to establish the phylogeny of rare monocot FolQ enzymes and demonstrated macromolecular traits that may feature in roles beneficial to catalysis for a counterpart from Asparagus.

Keywords: Folate, FolQ, dihydroneopterin triphosphate, Nudix Box, Asparagus

Investigating selected tissue extracts of *Artocarpus* spp. and *Nymphaea* spp. for potential antimicrobial activity

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The growing threat of antibiotic-resistant microorganisms has driven the search for alternative antimicrobial agents from natural sources, particularly plant-derived compounds. This study aimed to evaluate the antimicrobial efficacy of crude extracts obtained from ethanol-extracted and evaporated plant materials, which were subsequently dissolved in dimethyl sulfoxide (DMSO), against four bacterial strains *Staphylococcus aureus*, *Bacillus subtilis*, *Escherichia coli* and *Pseudomonas aeruginosa* and the fungus *Candida albicans*. The study evaluated seven crude extracts including bark extracts from *Artocarpus nobilis*, *Artocarpus altilis* and *Artocarpus heterophyllus*, as well as petal and stamen extracts from *Nymphaea nouchali* and *Nymphaea pubescens*. The agar disk diffusion method was employed using extract concentrations of 1, 2.5 and 5 mg/mL. Ciprofloxacin and fluconazole served as positive controls for antibacterial and antifungal assessments, respectively, while DMSO was used as the negative control. Among the tested extracts, only *Artocarpus altilis* bark extract demonstrated antibacterial activity at 5 mg/mL, producing mean inhibition zones of 1.1 ± 0.1 cm against *Staphylococcus aureus* and 1.0 ± 0.1 cm against *Bacillus subtilis*. Statistical analysis was carried out using SPSS software (version 26). An independent samples t-test confirmed significant activity against *S. aureus* ($p = 0.000$) compared to the negative control, while a Mann–Whitney U test indicated that inhibition of *B. subtilis* was not statistically significant ($p = 0.100$). No extract showed activity against gram-negative bacteria or *C. albicans*. Disk diffusion was selected due to its simplicity, speed, reproducibility and low extract requirement. However, poor diffusion of crude viscous or non-polar compounds may explain the lack of activity, as previous studies using agar well diffusion or broth dilution showed stronger effects, emphasizing the role of assay choice in assessing antimicrobial potential. These findings suggest that *A. altilis* bark contains active compounds effective against *S. aureus* and highlight the importance of method optimization in evaluating plant-based antimicrobials.

Keywords: Antimicrobial activity, plant extracts, *Artocarpus altilis*, disk diffusion method, Gram-positive bacteria

Influence of glyphosate on leaf phenolics, flavonoids, and antioxidant potential of *Camellia sinensis* var. *assamica* TRI 4042

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Camellia sinensis var. *assamica* TRI 4042 is a hybrid tea cultivar widely cultivated in Sri Lanka, valued for its superior quality and rich phytochemical profile. Tea remains as a vital agricultural export for the country; however, the widespread use of herbicides such as glyphosate raises concerns regarding their impact on plant metabolism and tea quality. This study investigated the influence of glyphosate on the total phenolic content (TPC), total flavonoid content (TFC) and total antioxidant capacity (TAC) in *Camellia sinensis* var. *assamica* TRI 4042. Leaves from 30 plants (n = 30) were treated with glyphosate at final concentrations of 0% v/v (control), 0.5% v/v (low), 1% v/v (medium), 1.5% v/v (high), and 2.2% v/v (highest), based on Tea Research Institute (TRI) recommended doses. After 30 days, biochemical assays were performed on the harvested leaves: TPC was determined using the Folin-Ciocalteu method, TFC was measured using the aluminum chloride colorimetric assay, and TAC was evaluated using the phosphomolybdenum assay. One-way ANOVA was employed to determine statistical differences among treatment groups. A dose-dependent decline in TAC, TPC, and TFC relative to the control was observed. Subsequent post-hoc analysis using Dunnett's test confirmed that only the highest glyphosate concentration (2.2% v/v) induced a statistically significant ($p < 0.05$) reduction in these parameters compared to the control. These findings suggest that glyphosate exposure may interfere with the shikimate pathway, which is consistent with the observed reductions in phenolic, flavonoid levels and the associated decline in antioxidant potential. Consequently, the phytochemical composition and antioxidant potential of *Camellia sinensis* var. *assamica* TRI 4042 leaves may be altered, potentially compromising both tea quality and its associated health benefits.

Keywords: *Camellia sinensis*, glyphosate, TPC, TFC, TAC

Comparative analysis of protein-protein interaction network modules responsible for Kranz and non-Kranz leaf development: a systems biology approach

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In the race to secure food production in the face of climate change, improving photosynthetic efficiency in crops has become more urgent than ever. C4 plants such as maize outperform their C3 counterparts in high light and heat, yet the complexity of engineering these traits into C3 crops remains a major challenge. A key bottleneck is our limited understanding of the Kranz anatomy, the structural hallmark of C4 photosynthesis. Kranz anatomy is the spatial and functional separation of cells that enables carbon concentration, which in turn improves the efficiency of photosynthesis. This study tackles that gap through a systems biology lens, comparing co-expression and protein-protein interaction (PPI) networks from Kranz (foliar) and non-Kranz (husk) tissues in maize. By integrating transcriptomic data with PPI networks, we identified developmental modules and key regulatory hubs linked to Kranz and non-Kranz leaf differentiation. Louvain clustering and GO enrichment analyses revealed tissue- and stage-specific patterns. Module detection using WGCNA, PPI network construction, Louvain clustering to identify submodules, and functional enrichment revealed significant regulatory shifts between tissue types. Hub proteins were identified based on intra- and inter-modular connectivity to detect key molecular switches relevant to Kranz development. Our findings suggest that Kranz anatomy emerges from delayed but tightly regulated translational and plastid-related processes, contrasting with the stress-adaptive responses seen in C3 husk tissues. Proteins such as Zeamatin and specific heat shock factors emerged as potential regulatory hubs in Kranz (C4) development. These insights highlight stage-specific translation-related differences as possible drivers of C4-specific anatomical traits. By bridging transcriptomics with protein interaction networks, this work brings us closer to decoding Kranz anatomy- an essential step toward designing climate-resilient C3 crops.

Keywords: Kranz anatomy, systems biology, protein-protein interaction networks, co-expression network, hub proteins

Investigation of genotoxic effects of common food preservative, calcium propionate, on root tips of *Allium cepa*

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Calcium propionate (CP; E282) is a widely used food preservative that prolongs the shelf life of various food products. However, studies indicate that such preservatives may pose health risks, including carcinogenicity and heritable genetic disorders, due to their genotoxic effects. In the present study, the genotoxic effects of CP were evaluated using *Allium cepa* root tip assay. Roots of *A. cepa* were exposed to CP at concentrations of 1000 ppm, 2000 ppm, and 3000 ppm, for 24, 48, and 72 h periods. Distilled water was used as the negative control. Following staining with 2% acetocarmine, Mitotic Index (MI) and percentage chromosomal aberrations of root meristematic cells were examined microscopically. For each treatment group, 30 roots were treated, and 30,000 cells were examined to calculate the MI. Data were analyzed using the General Linear Model (GLM) and Tukey's post hoc test at a 95% confidence level ($P \leq 0.05$). Microscopic analysis revealed a significant decrease in the MI ($P = 0.001$) and an increase in chromosomal aberrations with increasing CP concentration and exposure duration, compared to the negative control. After 72 h, the MI in the negative control group was 53.09%, whereas treatment with 1000 ppm and 3000 ppm CP resulted in reduced MIs of 34.38% and 31.37%, respectively. Chromosomal abnormalities, including c-mitosis, metaphase distortion, and chromosomal stickiness, were observed across all CP-treatments. Additionally, anaphase distortions and telophase bridges were observed at all concentrations following 48 h and 72 h exposure. The highest percentage of chromosomal aberrations (4.91%) was observed at 3000 ppm after 72 h, which was statistically significant ($p = 0.001$) compared to the other treatment groups. The decline in MI and presence of aberrations indicate that CP may disrupt normal chromosome segregation and contribute to genomic instability. These findings demonstrate that CP exerts significant genotoxic effects on the chromosomes of *A. cepa*.

Keywords: Genotoxicity, Calcium propionate, Mitotic Index, chromosomal aberrations, *Allium cepa*

Investigating the thermal capacity, total phenolic and flavonoid contents of selected herbal extracts

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Topical application of certain plants provides a cooling effect that can comfort the skin. Arguably, this cooling effect can be due to the production of plant secondary metabolites. Direct measurement of the thermal capacity will enable understanding of heat exchange and cooling effects, an approach limitedly applied in direct studies specifically on plant extracts. Accordingly, this study aimed to assess the thermal capacities of plant extracts. The specific objectives were: (i) to determine their cooling properties in relation to thermal capacity, and (ii) to analyze their chemical constituents. *Aloe vera*, *Azadirachta indica*, *Chrysopogon zizanioides*, *Mentha piperita*, and *Santalum album* were selected based on their traditional use. Soxhlet extraction was used for all plants except for *Aloe vera*, which was processed fresh using a shaker method. Extracts were prepared at a concentration of 10 mg/mL in triplicate per plant extract. The thermal capacities of the herbal extracts were calculated using Newton's Law of Cooling, based on heat loss over time. Triplicate measurements were analyzed using one-way ANOVA, followed by Fisher's LSD. Chemical composition was studied by quantifying total phenolic and total flavonoid contents using the Folin-Ciocalteu and the Aluminium chloride methods, respectively. Statistical tests were performed using SPSS (version 26). In thermal capacity results, *A. vera* (37.77 J/K) has recorded significantly higher thermal capacity than *C. zizanioides* (32.20 J/K) and *A. indica* (31.75 J/K). *M. piperita* (36.90 J/K) was significantly higher in thermal capacity than that of *A. indica* (p <0.05 at 95 % CI). High thermal capacity indicates that the plant extract resists rapid temperature changes when exposed to heat. Kruskal-Wallis and Dunn tests confirmed that *A. vera* is also significantly higher in total phenolic content (30.96 ± 1.91 µg/mL), whilst One-Way ANOVA and Tukey HSD tests indicated a significantly higher total flavonoid content in *M. piperita* (86.41 ± 6.66 µg/mL). The Spearman correlation test between total phenolic content and the thermal capacity declares a significantly positive correlation ($r = 0.775$, $p < 0.05$). In conclusion, the thermal capacity of *A. vera* is superior among the plant extracts and can be influenced by metabolites such as phenols.

Keywords: Thermal capacity, cooling effect

Exploring natural pigments from selected true salt marsh species in Kalpitiya, Sri Lanka

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Growing environmental concerns about the negative effects of synthetic dyes have led to a significant increase in interest in the extraction and use of natural dyes in recent years. Saltmarsh species which display showy colors under different salinity levels have not been exploited for studying the possibility of extracting their natural pigments. The potential of three underutilized true salt marsh halophytic species from Kalpitiya, Sri Lanka, *Suaeda maritima*, *Salicornia brachiata*, and *Sesuvium portulacastrum,* as sustainable, eco-friendly, natural dyes was investigated by employing modern colorimetric analysis to provide their individual dye profiles. The objective of this study was to extract natural dyes from selected halophytes using different solvents, qualitatively analyze their phytochemical properties, determine the most suitable solvent for liquid–liquid extraction, identify the pigments present in the extracts, and establish the best mordant for dyeing fabric. Three plants from each species were randomly harvested, and the study employed alcoholic, acidic, and aqueous extraction methods to separate pigments from the chosen species in three replicates per method. The extracted dyes from selected plant species exhibited distinct color profiles, qualitatively analyzed using a six-digit alphanumeric representation of color (HEX codes), Red, Green, Blue (RGB) values, and Hue, Saturation, and Lightness (HSL) parameters, with alcoholic and acidic extractions yielding the most vibrant hues. While acidic extraction showed improved pigment stability and solubility, especially for anthocyanins, aqueous extraction was the most effective extraction method. Alcoholic extraction demonstrated its versatility by successfully targeting both polar and nonpolar dye compounds with methanol. The presence of important bioactive substances such as phenols, tannins, flavonoids, and cellulose in each extract was verified by using standard methods of phytochemical analysis, underscoring the plant species' potential for both medicine and industry. The solubility of pigments in hexane, toluene, chloroform, dichloromethane, diethyl ether, ethanol, and ethyl acetate were assessed through liquid-liquid extraction experiments. The best solvent was found to be ethanol, since both *S. maritima* and *S. portulacastrum* extracts were insoluble in nonpolar solvents. The pigments were further examined using Thin Layer Chromatography, which revealed the presence of carotenoids, flavonoids, anthocyanins, and chlorophyll. Experiments with mordanting were carried out to improve fabric coloration and dye fixation. Three replicates of each extracted dye sample were used to test the three mordants: Aluminum Sulphate (alum), vinegar, and Sodium Chloride. These mordants significantly influenced the final colour intensity and shade, with alum particularly suitable for applications requiring long-lasting and versatile coloration. As future recommendations, extraction parameters can be improved by testing various sample-to-solvent ratios and mordanting time beyond those used in this study.

Keywords: Natural dye, halophytic species, fabric dyeing, mordants

Factors influencing adoption decision of integrated rice-fish farming among agriculture instructors in Hambantota district, Sri Lanka

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Integrated rice-fish farming (IRFF) is a promising agronomic strategy that enhances crop and fish productivity in a sustainable manner. This study investigates the factors influencing the adoption decision of IRFF among agriculture instructors (AIs) in Hambantota district, Sri Lanka. Data were collected from 36 AIs across nine randomly selected Agrarian Service Divisions. A structured questionnaire was used for data collection. Demographic and attitudinal data (knowledge, perception, mythical believes, constraints and perceived potentials regards to IRFF) were collected. A set of statements for each with 5-point Likert scale were provided. Mean score of these variables were calculated for each case. Descriptive statistics were used to summarize demographic characteristics while Pearson correlation and chi-square tests were applied to examine relationships. A Binary Logistic Regression Model was applied to identify potential predictors of the IRFF adoption decision. Results showed that most AIs were male (69.4%), aged 35–44 years (50.0%), held diploma-level qualifications (66.7%), and had 6–10 years of professional experience (47.2%). The 88.9% of officers perceived IRFF as a sustainable practice and 86.1% expressed willingness to adopt it. However, none had implemented the practice. Age, gender and working experience of AIs were significantly associated with adoption decisions ($p < 0.05$). AIs had high mean knowledge (3.86), perception (3.93), perceived potentials (3.63) and low level of mythical believes (2.20) regarding IRFF. Correlation results were indicated that significant positive relationships between AI's adoption decisions and knowledge ($r = 0.398$, $p = 0.016$), perception ($r = 0.371$, $p = 0.026$), while myths ($r = -0.377$, $p = 0.024$) were negatively associated. Knowledge and myths were identified as potential influences but they were not statistically significant ($p>0.05$ level). In conclusion, institutional and policy support from government with targeted mobilization strategies should be directed to encourage to adopt IRFF.

Keywords: Adoption, constraints, knowledge, perception, Sri Lanka

Comparative analysis of the vocal repertoires of *Centropus* Coucals of Sri Lanka

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Bird vocalization is influenced by several factors, including body size, sex, and habitat. Coucals provide a useful model for studying these effects, as they show sexual dimorphism. Morphological studies indicate that females of both the Southern Greater Coucal (*Centropus sinensis*) and Green-billed Coucal (*Centropus chlororhynchos*) are larger than males, though this difference has not been clearly reflected in their duet vocalizations. This study recorded the solo calls, alarm calls and duets of both species using a Marantz Professional PMD661 recorder, equipped with a Sennheiser Shotgun mic and analyzed the Begin Time (s), End Time (s), Low Freq (Hz), High Freq (Hz), Avg Entropy (bits), BW90 (Hz), Delta Freq (Hz), Delta Time (s), Energy (dBFS), Dur 50 % (s), Dur 90% (s) of both species using RavenPro. Principal Component Analysis (PCA) was applied, followed by one-way ANOVA for solo and alarm calls and two-way ANOVA for duet calls. Results show that the Green-billed Coucal produces solo calls with narrower frequency ranges, alarm calls with lower energy and longer intervals, and duets that are temporally compressed and limited in frequency range. In contrast, the Southern Greater Coucal exhibits broader frequency ranges, higher amplitudes in solo calls, faster alarm calls, and more temporally spread duets. These differences appear to be shaped by habitat and its possible effect on the auditory filters of the birds as the Green-billed Coucal lives in denser forests, where narrow frequency ranges reduce sound distortion from vegetation. In contrast, the Greater Coucal lives in more open habitats and has fewer barriers for acoustic communication. Spectrograms showed that in both species, the female sings at a lower pitch. The pitch gap was more pronounced in the Greater Coucal, suggesting a more pronounced sexual size dimorphism in the Southern Greater Coucal than the Green-billed Coucal.

Keywords: Cuculiformes, Green-billed Coucal, Southern Greater Coucal, vocal divergence, sexual dimorphism

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Sensitivity of *Poecilia reticulata* and *Danio rerio* to polyethylene terephthalate microplastic fibers: implications for freshwater ecotoxicology

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The increasing prevalence of microplastics in freshwater ecosystems poses a significant threat to freshwater biodiversity. This study aimed to investigate the impacts of polyethylene terephthalate (PET) microplastic fibers on two freshwater fish species: *Poecilia reticulata* (guppies) and *Danio rerio* (zebrafish). The larval stages were obtained from two aquaria and acclimatized to laboratory conditions until the fish reached the required size range (I.e., 1–2 cm). PET fibers (520 ± 325 µm) were prepared from a locally sourced material, after its polymer type confirmed by Fourier Transformed Infrared (FTIR) spectroscopy. Acute toxicity tests were conducted separately with the two species under static-renewal exposure conditions following standard protocols. For each test, a series of PET fiber concentrations (i.e., 0, 0.05, 0.1, 0.5, 1, and 5 mgL^{-1}) was used with three replicates consisted of 10 juveniles per replicate. After an exposure period of 96 h, endpoints including the survival rate, total length, standard length, and body weight were recorded. The probit analysis was used to estimate LC50 values, and one-way ANOVA followed by the Tukey's post hoc test was used to compare the other endpoints using Minitab 22. The 96-h LC50 value for *P. reticulata* was estimated as 0.95 (0.67–1.42) mgL^{-1} with significant reductions in survival rates, total length, standard length, and body weight at concentrations ≥0.1 mgL^{-1} (p<0.05). In *D. rerio*, the 96-h LC50 value was higher, at 3.02 (2.18–4.58) mgL^{-1}, and the survival rate, total length, and standard length was significantly affected at concentrations ≥0.5 mgL^{-1}, while weight was significantly affected at concentrations ≥0.1mgL^{-1} (p<0.05). *P. reticulata* showing greater sensitivity compared to *D. rerio*, indicated its suitability as an early warning indicator species in freshwater ecotoxicological assessments. Adverse effects observed even at high PET concentrations emphasize that urgent regulations are needed to control microplastic fiber pollution in freshwater.

Keywords: *Danio rerio*, ecotoxicology, microfiber toxicity, microplastic fibers, *Poecilia reticulata*

Wing morphometry of Sri Lankan honeybee (*Apis cerana*) across different agro ecological zones in Sri Lanka

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Apis cerana Fabricius (1793) has been utilized for honey production in Sri Lanka. The diversity of *A. cerana* is poorly understood in Sri Lanka, creating a research gap. This study aimed to assess regional variation in wing morphometry of *A. cerana* across agro-ecological zones in Sri Lanka. In this study, 720 pollen carrying foraging worker bees were collected from 72 maintained beehives, covering all seven agro climatic regions and 24 agro-ecological regions in Sri Lanka. These regions included WU1, WU2b, WU3, WM1a, WM2b, WM3b, WL1a, WL2b, WL3, IU1, IU2, IU3b, IM1a, IM2a, IM3b, IL1b, IL2, IL3, DL1b, DL2a, DL2b, DL3, DL4 and DL5. A total of 16 wing morphometric traits were measured on both left and right sides, including forewing and hindwing length and width, cubital vein a and b lengths, cubital index and hamuli count. Data was analyzed using ANOVA, Tukey's test and Kruskal Walli's test. Multivariate cluster analysis in PAST, using a Bray-Curtis similarity index and 1,000 bootstraps, was performed to construct a dendrogram. Significant differences ($p < 0.05$) were observed in all wing traits across agro-ecological zones. Forewing length × width ranged from 7.30–8.17 × 2.43–2.75 mm (left) and 7.29–8.17 × 2.43–2.76 mm (right), cubital index, 0.35–0.44 (left) and 0.33–0.43 (right). Hind wing length × width ranged from 5.08–5.88 × 1.40–1.69 mm (left) and 5.12–5.88 × 1.47–1.66 mm (right); hamuli, 16–20 (left) and 16–19.5 (right). Cluster analysis identified three clusters as, IU1–DL5(Rangala and Hambantota), DL3–DL4 (Jaffna and Kareinagar) and a third with remaining zones. These findings provide the first evidence of wing morphometric variation in *A. cerana* across Sri Lanka and reveals regional differentiation. Also, highlights the importance of recognizing local diversity in *A. cerana* populations, forming a foundation for future breeding.

Keywords: *Apis cerana*, wing characters, morphology, cubital index, hamuli numbers

Utilizing Duckweed (*Lemna minor*) for sustainable Lead removal: a phytomining approach to water treatment and resource recovery

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Biotechnology plays a vital role in environmental sustainability and pollution control. Among phytoremediation technologies, phytomining has gained attention as a sustainable method for the recovery of valuable or toxic elements from contaminated environments. This study evaluates the freshwater species, Duckweed (*Lemna minor*), as a phytoremediation agent for the sustainable removal and recovery of lead (Pb) from industrial wastewater, utilizing the natural accumulation capacity of plants to extract valuable or toxic elements from contaminated environments. Even though direct electrolysis of industrial wastewater is technically possible, it is often inefficient due to the presence of bulk water and interfering impurities. By using Duckweed as a biological pre-treatment method, the Lead is concentrated in the biomass, significantly enhancing the efficiency of the electrochemical recovery process. Pre-cultivated lead-free duckweed was cultivated in Lead-contaminated water for 14 days at the Faculty of Technology, University of Colombo Sri Lanka, under ambient light and temperature conditions, within a pH range of 7–8 pH, and exposed to a Pb concentration series of 0–6 ppm. Then the plants were allowed to absorb and accumulate lead from the contaminated water, after which the biomass was harvested and processed using acid digestion followed by electrolysis to recover the metal. Results revealed that Duckweed could accumulate nearly up to 1.886 (±0.086) g of Lead per square meter of wetland area over the 14-day period, which is approximately 15 times more effective than direct electrolysis of raw wastewater under similar conditions. This indicates that the phytomining approach not only improves metal recovery efficiency but also contributes to wastewater treatment in an environmentally friendly and sustainable manner. The use of *Lemna minor* as a pre-treatment phytomining agent offers a dual benefit: efficient lead removal from wastewater and sustainable resource recovery. This approach provides a cost-effective, sustainable biotechnology for coupling pollution control with resource recovery. It may be extended by evaluating diverse aquatic plants in Sri Lanka across various wastewater types to determine their phytomining potential.

Keywords: Phytomining, industrial wastewater, Lead, Lemna minor, circular resource management

Nesting ecology and hatching success of marine turtles in the eastern coast of Sri Lanka

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Marine turtles, acting as herbivores, predators and nutrient transporters, play a crucial role in sustaining healthy marine ecosystems. Currently, sea turtles are globally threatened and hence warrant attention in terms of more stringent conservation efforts. In Sri Lanka, sea turtle hatcheries serve as vital ex-situ conservation platforms. This study aimed to investigate the nesting ecology of marine turtles in the Kumana beach and to assess the conservation effectiveness of the Turtle Conservation Centre through monitoring of hatching success. The study was conducted from 2022 to 2025, spanning three nesting seasons (early December to late March). A 10 km-beach stretch was monitored daily through night patrolling for the purpose of locating nests for relocation. For each relocated nest, clutch size and distance from the nest to the shoreline was recorded and thereafter the hatching success. A total of 294 nests of four species Olive Ridley (*Lepidochelys olivacea*), Green turtle (*Chelonia mydas*), Hawksbill (*Eretmochelys imbricata*), and Loggerhead (*Caretta caretta*) were relocated. Leatherback turtles (*Dermochelys coriacea*) were not observed. A total of 32,134 eggs were relocated to the hatchery from which 18,445 hatchlings were released successfully, yielding an overall hatching success of 57.0%. Olive Ridley turtles were the most dominant nesters (74.1 % of relocated nests), followed by the Green turtle (13.8 %), Hawksbill (8.08 %), and Loggerhead (3.81 %). Mean clutch sizes differed significantly across species (Olive Ridley 107.7 ± 26.2, Green turtle 111.8 ± 32.3, Loggerhead 122.4 ± 20.9, Hawksbill 125.2 ± 18.2; $p<0.01$), while hatching success (Olive Ridley 73.6 ± 26.9 %, Green turtle 74.8 ± 25.4 %, Hawksbill 81.8 ± 21.7 %, Loggerhead 74.7 ± 25.8 %) and distance from nest to shoreline (Olive Ridley 19.0 ± 7.5 m, Green turtle 21.8 ± 6.1 m, Hawksbill 24.1 ± 17.9 m, and Loggerhead 25.3 ± 15.0 m) also varied, but not statistically ($P > 0.05$). This study represents the first documentation of sea turtle nesting along Sri Lanka's eastern coast. This information is important for assessing the suitability of the beach for sea turtles, the effectiveness of the ex-situ conservation facility, and for planning for logistics in terms of adequate ex-situ space and personnel.

Keywords: Marine turtle conservation, hatching success, ex-situ management, nesting site selection

Acknowledgement: Financial support of Haycarb PLC and Puritas (Pvt) Ltd is acknowledged.

The impact of health condition, sex, life stage, environmental variables, and human influence on the feeding behavior of Elephants in selected areas of Udawalawa National Park

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Elephants are keystone species whose feeding behaviour is influenced by various biological, ecological, and anthropogenic factors. Understanding these interactions is crucial for mitigating conflicts and promoting coexistence. This study aims to investigate the impact of body condition (weak/moderate/good), age (juvenile/adult), sex (male/female), anthropogenic influences, and environmental parameters on the feeding patterns of elephants in Udawalawa National Park, Sri Lanka. The study was conducted from June 2024 to January 2025, and observations were conducted from 0600 h to 1800 h. A standard ethogram was prepared, and behaviour was recorded for 20 minutes per elephant. Environmental variables, viz., ambient temperature (°C), humidity (%), light intensity (Lux), and rainfall (mm) were measured using standard methods. The anthropogenic influence was measured as the distance of the feeding ground to the main road, safari tracks, and park edge. The behaviour data of 41 elephants (24 males, 17 females) were collected, and the mean feeding time for males and females was 11.83±1.57 and 9.69±1.76 minutes, respectively. Feeding time followed the decreasing order based on health conditions: weak (12.91±1.91)> healthy (10.55±2.31)> moderate (9.50±1.95). Statistical analysis revealed no significant feeding behaviour differences between body conditions, life stages, or sexes ($p > 0.05$). However, elephants feeding inside the park spent significantly more time on feeding (17.67±2.09) than those near the park's edge (7.00±7.88) ($p < 0.05$). Principal Component Analysis indicated that temperature and humidity were the most influential environmental factors governing variations in feeding. A weak negative correlation was observed between feeding duration and temperature ($p = 0.136$), while a weak positive correlation was found between feeding duration and humidity ($p = 0.223$). These findings highlight the complex interplay between biological, ecological, and anthropogenic factors affecting elephant feeding behavior. The study suggests that the changing environmental conditions influence the feeding behavior of larger herbivores rather than their intrinsic biological factors.

Keywords: Asian Elephants, ethogram, park edge, anthropogenic factors, feeding behaviour

A morphometric assessment of Indian Palm Squirrel (*Funambulus palmarum*) across Sri Lanka

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The Indian palm squirrel (*Funambulus palmarum*) is a widely distributed small mammal in Sri Lanka, predominating the human-modified landscapes, and historically classified into four subspecies based on geography and external morphology. However, this classification remains unvalidated through quantitative and genetic analyses. Morphometric traits, shaped by both ecological and evolutionary forces, are conventionally used in phylogenetic studies. This study aimed to assess morphological and pelage variation among *F. palmarum* populations and investigate whether geographic and ecological variations across the described ranges correspond with measurable traits. Sampling was conducted from November 2024 to March 2025 in 15 locations across Sri Lanka covering all climatic zones and the historical ranges of the four subspecies described by Phillips. Forty-two body and pelage measurements were taken from 66 individuals, focusing on consistent right-side parameters. Data was standardized by total body length (TBL) and normalized prior to statistical analysis. Contrary to expectations, statistical analysis conducted using R statistical software revealed no significant differentiation among the subspecies (MANOVA and PERMANOVA $p > 0.05$). Principal component analysis also confirmed substantial overlaps. However, PERMANOVA conducted for the 27 pelage measurements alone revealed a significant variation ($p < 0.05$). This variation was most significant between the subspecies *F. p. olympius* (Highland Ceylon palm squirrel) and *F. p. kelaarti* (Southern Ceylon palm squirrel), likely reflecting adaptation to contrasting habitats and climatic conditions rather than genetic divergence. The most prominent differences were in stripe lengths, widths and spacing. Morphological traits did not vary with sex, reflecting the absence of sexual dimorphism. The morphometric uniformity, despite ecological variation of the four historical subspecies, may reflect a degree of phenotypic plasticity and stabilizing selection. This study highlights the need for an integrative approach, combining morphometry with genetics and other aspects of ecological relevance such as vocalization to resolve the subspecies level differentiation of this species.

Keywords: Small mammal, pelage variation, genetic variation, phenotypic plasticity

Enhancing toxicological predictions through Machine Learning on Zebrafish model data

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Zebrafish are commonly used in scientific research for toxicity testing and genetic conditions. Most of the time many researchers conduct studies on the same toxins or environmental conditions, often without knowing that similar research has already been done, due to the publications being scattered across different platforms. This leads to unnecessary harm to zebrafish and fish embryos, causing ethical concerns and wasting time and other resources. This study aimed at building a database on zebrafish and its embryo-related research in Sri Lanka for a wider audience and as a data repository. The study involves the design and implementation of a centralized web-based platform developed using the MERN stack, MongoDB for flexible, schema-less data storage, Express.js and Node.js for backend API handling, validation, and file uploads, and React.js for an interactive, responsive frontend interface. This platform collects user information, keywords, and toxic conditions, and asks users to upload research papers. The system then understands the uploaded paper and automatically extracts relevant content, including concise summaries along with figures, tables, and final result descriptions, enabling researchers to quickly grasp the outcomes of toxicity tests. Furthermore, it contains features of flexible keyword-based searches, allowing users to find relevant studies based on toxin names, research titles, etc. To enhance searchability and exploration, the system integrates machine learning techniques, including Bidirectional Encoder Representations from Transformers (BERT) for semantic search, enabling users to query using natural language beyond exact keyword matching. An automatic summarization module processes uploaded research papers into concise summaries. Validation and reliability will be ensured in the next phase of the project through standard techniques such as k-fold cross-validation for the models and benchmarking the semantic search module against traditional keyword-based retrieval. These steps will confirm the robustness, reliability, and scientific integrity of the platform once sufficient data has been collected. By bridging machine learning, toxicity assay and drug screening using zebrafish and its embryo as alternative animal models, this platform aims to support the 3Rs principle (Replace, Reduce, Refine) in animal research. This platform not only addresses the ethical imperative of reducing redundant testing but also empowers researchers, particularly in Sri Lanka, with accessible, intelligent tools for evidence-based toxicological assessment.

Keywords: Zebrafish, embryo toxicity, MERN stack, web-based platform, bioassay

Ulva fasciata pigments: extraction, chemical characterization, and evaluation of antioxidant and anti-inflammatory activities

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Despite extensive ecological and biotechnological studies on *Ulva* species, research on their pigments remains limited. The present study aims to extract and characterize pigments and evaluate the antioxidant and anti-inflammatory activities of pigments extracted from *Ulva fasciata* collected from Sri Lankan coast. *Ulva fasciata* was collected from Koggala, Sri Lanka, by handpicking (DWL permission no: WL/3/2/29/21). Pigments were extracted from dried seaweeds by grinding them with acetone, then centrifuging and filtering to collect the supernatant. The acetone was evaporated to obtain the crude pigment extract. The extracted pigments were characterized using Ultraviolet-Visible (UV-Vis) Spectroscopy and Fourier Transform Infrared (FTIR) Spectroscopy. Doses of crude pigment extract (25 - 800 µg/ml) was evaluated for antioxidant activity through 2, 2-diphenyl 1-picrylhydrazy (DPPH) and nitric oxide (NO) radicals scavenging assays, while *in-vitro* anti inflammatory activity was assessed using the egg albumin denaturation assay. Ascorbic acid and diclofenac sodium were used as standard drugs for anti-oxidant and anti-inflammatory assays, respectively. Each assay was triplicated, and the inhibition concentration of 50 (IC_{50}) was calculated. The results were compared by Pearson correlation using Excel (2013), and the coefficient of determination (R^2) indicated the goodness of fit for each linear regression model. The Yield of crude pigment extract from *U. fasciata* was 19.69%. The UV and FTIR spectra confirmed the presence of carotenoids and chlorophylls pigments in *U. fasciata*. The IC_{50} for DPPH was reported as 19.44 µg/ml for ascorbic acid 443.80µg/ml for pigments while it was 32.96 µg/ml for ascorbic acid and 2626.86 µg/ml for pigments for NO radical scavenging activity. IC_{50} values for the egg albumin denaturation assay were reported as 85.1 µg/ml for diclofenac sodium and 748.39 µg/ml for pigments. In conclusion, the present study, for the first time, provides chemical confirmation of pigments from *U. fasciata* and their bioactivities; anti-oxidant and anti-inflammatory activities in varying degrees.

Keywords: *Ulva fasciata,* UV-Vis, FTIR, antioxidant, anti-inflammatory

Acknowledgement: The authors acknowledge the Department of Zoology, Faculty of Applied Sciences, University of Sri Jayewardenepura, for providing funding and facilities throughout the research project.

Spatial and temporal variation of phytoplankton diversity and abundance in Chilaw lagoon, Sri Lanka

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Despite the ecological significance of the Chilaw Lagoon, research on its plankton dynamics is limited, leaving a critical gap in understanding how nutrient inputs influence community structure and potential eutrophication. Plankton samples were collected monthly from eleven sampling locations (CH1 to CH11) in the Chilaw Lagoon over a six-month period from May 2024 to October 2024. Phytoplankton samples were collected using a 55 µm mesh net, preserved with Lugol's solution, and transported to the lab in a cool box. A total number of 32,054 individuals were examined and identified to genus level under a microscope using standard identification guides. Five major taxonomic groups of phytoplankton were recorded: Bacillariophyta (diatoms), Chlorophyta (green algae), Cyanophyta (cyanobacteria/blue-green algae), Dinophyta (dinoflagellates), and Ochrophyta. Bacillariophyta dominated all locations (92.8%), indicating stable primary productivity under nutrient-enriched conditions, particularly favoring *Chaetoceros* sp. and *Coscinodiscus* sp. Cyanophyta (6.1%), the second most abundant group, suggests moderate nutrient enrichment. The presence of Cyanophyta (6.1%), mainly *Oscillatoria* sp. and *Lyngbya* sp., indicates localized eutrophication that may trigger blooms under low flushing. The relatively low percentage of Dinophyta (0.1%) and Chlorophyta (0.6%) was observed. Sampling locations, CHL4 and CHL5 exhibited high abundances (2,712 and 4,722 individuals), likely due to nutrient inputs from shrimp farms and fish cages. The nutrient-driven proliferation of *Chaetoceros* sp. and *Coscinodiscus* sp. at CHL4 and CHL5 demonstrates the influence of aquaculture inputs on estuarine phytoplankton structure. However, the abundance of Ochrophyta, Dinophyta, and Chlorophyta was significantly highest at CHL1 ($p<0.05$). Temporally, phytoplankton abundance peaked in July and was lowest in October, with the abundance of Bacillariophyta and Chlorophyta showing significant monthly variation ($p<0.05$). Phytoplankton abundance peaked in July (22,262) and was lowest in October (872). Bacillariophyta dominated May–July (>90%), with peak abundance in July, while from August–October cyanobacteria (*Oscillatoria* sp., *Lyngbya* sp.) increased, reflecting nutrient shifts and eutrophication. In conclusion, Chilaw Lagoon exhibits nutrient enrichment characterized by dominant diatom communities. The rising cyanobacterial presence in the later month signals emerging eutrophic conditions, likely driven by aquaculture activities and reduced water exchange.

Keywords: Chilaw Lagoon, diatom, dinoflagellates, eutrophic, phytoplankton
Acknowledgement: The authors gratefully thank and acknowledge the research grant provided by the National Aquatic Resource Research and Development Agency (NARA), Sri Lanka.

Assessing the effects of Devil's trumpet (*Datura metel*) on muscle strength, muscle 1 coordination, and hematological parameters using the Wistar rat model

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Datura metel (Devil's trumpet, Thorn–apple, Aththana) is a widely used folk medicinal herb in temperate and tropical regions. Traditional medicine in Sri Lanka claims its seeds may enhance muscle strength and relieve pain, in addition to their hallucinogenic, sedative, and antiasthmatic effects. Seeds contain abundant alkaloids such as scopolamine, hyoscyamine, and atropine, which are responsible for multiple pharmacological activities. This study aimed to evaluate the effects of *D. metel* seed extract on muscle strength, coordination, and hematological parameters in Wistar rats. Eighteen male rats were randomly assigned into three groups (n=6): a negative control (distilled water, 2 ml/day/animal), a positive control (Tramadol, 0.57 mg/day/animal), and the treatment group (*D. metel* seed extract, 0.127 mg/day/animal) for five consecutive days. Muscle strength and coordination were assessed using the bar test, bridge test, and memory board test (crossings, rearing, head dipping). Total white blood cell counts were determined from tail blood samples. Data were analyzed using one-way ANOVA ($p<0.05$). The results indicated no significant differences among treatment, positive, and negative control groups in muscle strength (bar test), coordination (bridge and memory board test parameters), or WBC counts. Datura, distilled water, and Tramadol showed distinct bar time patterns, with Tramadol peaking highest on day 3, though variance tests ($p = 0.613$) showed no significant differences across treatments. The Bridge test revealed a significant treatment effect ($F = 3.84$, $p = 0.027$) with distilled water decreasing times, while WBC counts showed no significant differences ($p = 0.382$). Mean values for the *D. metel* group were comparable to controls, with no observable enhancement in muscle strength or coordination. This study provides the first *in vivo* evaluation of crude *D. metel* seed extract for muscle-related effects. Findings suggest that, despite traditional claims, the crude seed extract does not improve muscle performance in rats under tested conditions. Further in vivo and in vitro advanced studies are warranted to investigate its hypnotic effect.

Keywords: Wistar rat model, Devil's trumpet (*Datura metel*), haemotology, muscle coordination, pharmacological evaluation

Assessment of regional variations in vocalization structures of the Oriental Magpie Robin (*Copsychus saularis*) in Sri Lanka

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The Oriental Magpie Robin (*Copsychus saularis*) is a small passerine native to Sri Lanka, renowned for its intricate vocalizations produced via a specialized syrinx which facilitates mate attraction, territory defence, and communication, reflecting individual characteristics and environmental influences. This study investigates the regional variations in the vocalization structures of the Oriental Magpie Robin across two contrasting ecological zones in Sri Lanka: Divulapitiya (rural, agriculture-dominated; n = 13 recordings), and Hokandara (rapidly urbanizing wet zone town near Colombo; n = 13). Recordings were captured using smartphone recording applications and converted to WAV files and analyzed in Raven Pro 1.6. Four key acoustic parameters were considered for the analysis: Minimum frequency, maximum frequency, frequency bandwidth, and the rate of vocal elements per minute, testing differences with Wilcoxon test for minimum frequency, and t-tests for others ($\alpha = 0.05$). Mean minimum frequency was 1.65 ± 1.35 kHz at Divulapitiya versus 2.35 ± 0.89 kHz in Hokandara ($p = 0.065$; $d = 0.56$), and vocal-element rate was 9.2 ± 1.8 versus 6.8 ± 2.4 elements/min ($p = 0.093$; $d = 0.57$). Maximum frequency and bandwidth differences were smaller and non-significant (all $p > 0.5$; $d = 0.25$). While no comparison reached conventional significance, marginal trends in minimum frequency and element rate suggest ecological modulation of vocal traits: rural birds may lower pitch to optimize open-area transmission, whereas urban birds increase frequency and repetition to counter low-frequency noise. These preliminary results emphasize potential for environment-driven vocal plasticity in *C. saularis*, supporting the acoustic adaptation hypothesis, and they underscore the need for further research with larger sample sizes and recommend urban planning and conservation strategies that preserve the natural acoustic environment.

Keywords: Oriental Magpie Robin**,** urban ecology, bird song, acoustic adaptation, bioacoustics

45th Annual Sessions of the Institute of Biology, Sri Lanka

Schedule of the Scientific Sessions

25th September 2025

Center for Banking Studies, Sri Jayewardenepura Mawatha, Kotte

ORAL PRESENTATIONS

Parallel Session 1: Microbiology and Chemical Biology

Time	Abstract Number	Title and Author(s)
1.30 – 1.40 pm	**MC_001**	***In vitro* evaluation of synergistic antibacterial effects of three Sri Lankan medicinal plants against selected skin-infecting bacteria** J.R. Geeganage, R.D.S. Isara, S.D.U. Senarathna, L.A.L. Saundarya, G.T.C. Neththrika, A.L.A.P. Randika, N. Ullah and B. Deepachandi
1.40 – 1.50 pm	**MC_002**	**Enhancing the biodegradation of nylon-based textile waste using microbial consortia** I.G.N.B. Wijewardhana, T.A. Perera, R.U. Halwatura and A. Sathsarasinghe
1.50 – 2.00 pm	**MC_003**	**Bioactivities of termite nest-derived actinomycetes** K.H. Kaumadi, C.M. Nanayakkara, E.D. De Silva and P.A.N. Punyasiri
2.00 – 2.10 pm	**MC_004**	**Preliminary assessment of the enzyme activity of wild mushrooms collected from Baduraliya, Sri Lanka** E.A.D.S. Madhubashana and S.S. Ediriweera
2.10 – 2.20 pm	**MC_005**	**Preliminary investigation of plant-growth promotion and bioremediation of diesel by fungal endophytes associated with salt marsh plants in Kalpitiya, Sri Lanka** G.K. Perera, S.S. Ediriweera and I.A.J.K. Dissanayake

Time	Abstract Number	Title and Author(s)
2.20 – 2.30 pm	**MC_006**	***In vitro* antimicrobial and antioxidant activity of some mangrove-derived fungi isolated from Kalpitiya, Sri Lanka** W.D.S.N. Sewmini, C.M. Nanayakkara, K.G.S.U. Ariyawansa, S.S. Ediriweera, E.D. De Silva and P.A.N. Punyasiri
2.30 – 2.40 pm	**MC_008**	**Understanding the influence of environmental factors on cyanobacterial dynamics in Nuwara Wewa, Sri Lanka** D.A.D. Weththasinghe, H.M. Herath and R.P. Wanigatunge
2.40 – 2.50 pm	**MC_009**	**Isolation of algicidal bacteria from Beira Lake to control bloom-forming *Microcystis aeruginosa*** P.G.S. Ishadani, M.A.P.C. Piyathilaka, G.Y. Liyanage, A.R. Pilapitiya and P.M. Manage

Parallel Session 2: Molecular Biology and Biotechnology

Time	Abstract Number	Title and Author(s)
1.30 – 1.40 pm	**MB_001**	**Do life history traits and ecological features shape up MHC diversity? The patterns of selection and polymorphism in exon 3 of the avian MHC** N.V.P.G. Chathuranga, P.C. Fernando, E.S.C. Scordato and S.S. Seneviratne
1.40 – 1.50 pm	**MB_004**	**Dual regulatory role of the Mycobacterium xylanase Regulator (MxyR): a promising drug target in drug-resistant tuberculosis** R.G.V.R.B. Rathnayake, S.P.N.N. Senadeera, S. Mauran, N.P. Senanayake and I.C. Perera
1.50 – 2.00 pm	**MB_007**	**Feasibility of designing a CADMA-based real-time PCR assay for the detection of the R248Q & R273C TP53 mutations** C.D.G. Prabodhya, M. Kajan, I. Kumarasinghe, R. Perera, J. Balawardana, N. Perera and G.H. Galhena
2.00 – 2.10 pm	**MB_008**	**Association of *TERT* rs2736100 gene polymorphism with interstitial lung disease and its prognostic significance in a Sri Lankan cohort** Y.B. Dias, B. Hamza, R.D.S. Karunathilake, D.K. Weerakoon, G.N. Malavige and G.H. Galhena
2.10 – 2.20 pm	**MB_009**	**Comparative evaluation of the anti-gastric activity of *Eclipta prostrata*, *Tinospora cordifolia*, *Acrostichum aureum*, and their polyherbal formulation using *in vitro* antacid assays** M.S.A. Cooray, I.U. Kariyawasam and C.D. Jayasinghe
2.20 – 2.30 pm	**MB_011**	**Molecular insights into the regulation of copper detoxification in pathogenic *Leptospira*** R.B.A.R. Wijerathna, S.P.N.N. Senadeera, J.M.D.D. Jayasundara, S. Mauran and I.C. Perera

Time	Abstract Number	Title and Author(s)
2.30 – 2.40 pm	**MB_012**	**Evolutionary analysis and host state reconstruction of rust fungi (Pucciniales; Basidiomycota), with emphasis on the morpho-molecular characterization of coffee rust (*Hemileia vastatrix*) in Sri Lanka** U.S.R. Isanka, D.A.D.A. Daranagama and M.C. Samarakoon
2.40 – 2.50 pm	**MB_013**	**Characterization of Xylariales diversity in the Kanneliya forest reserve** K.A.D.H. Jayasekera and D.A.D.A. Daranagama
2.50 – 3.00 pm	**MB_014**	**Uncovering the transcriptional factors of *Cocos nucifera*: a genome-wide study** N.U. Ranaweera and H.D.D. Bandupriya
3.00 – 3.10 pm	**MB_015**	**Evaluating the dietary impact of cooking – induced changes in Essential Trace Elements in Sri Lankan rice (*Oryza sativa* L.)** J.W. Gunawardana, S.A. Gunawardena, C. Witharana, N.D.A. Wageesha and I.C. Perera
3.10 – 3.20 pm	**MB_018**	**Full genome annotation of polythene-degrading fungus *Phlebiopsis flavidoalba*** H.M.B.Y. Chandrasena and R.N. Attanayake
3.20 – 3.30 pm	**MB_019**	**Characterization of *Sclerotinia sclerotiorum* isolates collected from cabbage fields in Sri Lanka, with insights into mycovirus-associated hypovirulence** D.G.D.R. Gunawardhana, Sudeep Bag and R.N. Attanayake
3.30 – 3.40 pm	**MB_020**	**Integrating morphological characterization and DNA barcoding for the identification of *Aporosa* species in Sri Lanka** W.M.D.K. Wickramasingha, A.G.K.S. De Silva, Y.K.D.D. Thathsarani, D.V.S. Kaluthanthri and R.A.S.P. Senanayake

Time	Abstract Number	Title and Author(s)
3.40 – 3.50 pm	**MB_024**	***In silico* analysis of non-synonymous single nucleotide polymorphisms in the human *HNF1A* gene** P.A.R.R. Wijerathne and A.M. Wickramasuriya
3.50 – 4.00 pm	**MB_025**	**Antioxidant properties of the methanolic crude extract, beta-carotene, and carrageenan from *Hypnea* sp. (Rhodophyta)** W.V. Seneviratne, H.M. Weerasinghe, W.M.K.M. Ratnayake and K.V.K. Gunathilake
4.00 – 4.10 pm	**MB_026**	**Molecular characterization of *Citrus* species in Sri Lanka using *matK* and *rbcL* DNA barcode markers** W.A.N.R. Wickramaarachchi, W.W.P. Rodrigo and S.R. Weerakoon

Parallel Session 3: Plant Sciences and Agriculture

Time	Abstract Number	Title and Author(s)
1.30 – 1.40 pm	**PS_002**	***Brontispa longissima* (Gestro): an emerging pest of coconut in Sri Lanka** D.H. Dilrukshika, P.H.P.R. De Silva, D.P.M. Silva, N.S. Aratchige and K.S. Hemachandra
1.40 – 1.50 pm	**PS_003**	**First identification of *Nigrospora* sp. causing blister blight on tea in Sri Lanka** P.D.P.M.D. Silva and T.R. Glare
1.50 – 2.00 pm	**PS_004**	**Artificial intelligence in crop development: using protein sequences, structures, and protein-protein interaction networks in deep learning to predict root development proteins** S.A. Weththasinghe, S. Ganeshiny, D.L. Abeywardhana and P.C. Fernando
2.00 – 2.10 pm	**PS_005**	**Genome-wide identification and comprehensive *in silico* analysis of aspartate aminotransferases in Poaceae crops** W.M.M. Upeka and P.C. Fernando
2.10 – 2.20 pm	**PS_006**	**Developing an AI model for classifying the level of tolerance for iron toxicity in new improved rice lines/varieties** S.L.S. Jayamini, D.L. Abeywardhana, P.C. Fernando, D.M.R.G. Mayakaduwa, W.R.K.D.W.K.V. Wickramasinghe and G.D.A. Priyantha

Time	Abstract Number	Title and Author(s)
2.20 – 2.30 pm	**PS_007**	**Morphological diversity and taxonomic resolution of Sri Lankan *Impatiens* (Family Balsaminaceae) with emphasis on evolution of floral characters** Kosala Abeykoon, H.D. Jayasinghe and H.S. Kathriarachchi
2.30 – 2.40 pm	**PS_008**	**Morphological and fibre quality characterization of cotton populations in Sri Lanka** A.S. Rathmalgoda, H.S. Kathriarachchi, D.M.R.G. Mayakaduwa and C.N. Hearth
2.40 – 2.50 pm	**PS_011**	**Do Plesispa beetles equally prefer and orient towards different coconut varieties?** D.P.M. Silva, D.H. Dilrukshika, P.H.P.R. De Silva, N.S. Aratchige, H.D.M.A.C. Dissanayaka and K.P. Waidyarathne
2.50 – 3.00 pm	**PS_012**	**Conservation-oriented *in vitro* propagation of *Munronia pinnata* and phytochemical comparison with *Andrographis paniculata*** R.M.D.P. Rathnayake and H.D.D. Bandupriya
3.00 – 3.10 pm	**PS_014**	**A comparative *in vitro* study of salt tolerance in cultivated chili (*Capsicum annuum*) varieties in Sri Lanka** P.A.H. Hansima and H.D.D. Bandupriya
3.10 – 3.20 pm	**PS_015**	**Stomatal trait plasticity helps plant species to survive in environmental gradients in a forest restoration site** C.S. Jayasinghe, H.I.U. Caldera, A. Perera and N. Geekiyanage
3.20 – 3.30 pm	**PS_017**	**Uncovering regulatory modules and hub genes of somatic embryogenesis in *Coffea arabica* through gene co-expression network analysis** T.H.N. Malinda and A.M. Wickramasuriya

Time	Abstract Number	Title and Author(s)
3.30 – 3.40 pm	**PS_018**	***In vitro* shoot regeneration from cultured leaf explants of *Passiflora edulis* f. *flavicarpa*** A.S. Dassanayake and T.D. Silva
3.40 – 3.50 pm	**PS_019**	**BlackPepKB: an interactive web platform for exploring black pepper (*Piper nigrum* L.) genomics** L.M.D. Bawanga, S. Viswakula and A.M. Wickramasuriya
3.50 – 4.00 pm	**PS_021**	**Floral phenology and sex expression in *Piper nigrum* L. (black pepper)** E.A.D.D.S.C. Edirisinghe and T.D. Silva

Parallel Session 4: Zoology and Environment Sciences

Time	Abstract Number	Title and Author(s)
1.30 – 1.40 pm	**ZE_001**	**The influence of protected area management practices on climate resilience** M.D. Dulashi Chathunika, Mayuri R. Wijesinghe and Hiran H.E. Jayaweera
1.40 – 1.50 pm	**ZE_002**	**Incipient speciation through spatial divergence in Dark-fronted Babbler (*Dumetia atriceps*) of South Asia** A.V.P.P.Y.V. Gunewardene, C.K. Wijekulathilake, C.K. Vishnudas, P.N. Chalke, V.V. Robin, P. Koparde, D. Halwatura and S.S. Seneviratne
1.50 – 2.00 pm	**ZE_003**	**Detection and quantification of microplastics in pelagic seabirds from the Exclusive Economic Zone (EEZ) of Sri Lanka** P.V.S. Iresha, K.D.S. Meecle, L. Walpita, S.R.C.N.K. Narangoda, L. Jayawickrama, K. Mahatantila and S.S. Seneviratne
2.00 – 2.10 pm	**ZE_006**	**Effects of microplastics on immunological properties of human peripheral blood mononuclear cells** H. Sivarathan, M.G.Y.L. Mahagamage, A.D. De Silva and M. Mapalagamge
2.10 – 2.20 pm	**ZE_011**	**Variations in morphometry in populations of the common honeybee, *Apis cerana*, distributed across different bioclimatic zones in Sri Lanka** S.S. Kannangara, M.R. Wijesinghe, W.A.I.P. Karunarathne and D.K. Weerakoon
2.20 – 2.30 pm	**ZE_012**	**Morphological, plumage, and vocal characterization of the genus *Glaucidium* in Sri Lanka** T.H. Edirisinghe, D. Halwathura and S.S. Seneviratne

Time	Abstract Number	Title and Author(s)
2.30 – 2.40 pm	**ZE_013**	**Breeding ecology and feather molting pattern of recently described Hanuman plover (*Anarhynchus seebohmi*)** M.I. Bilal, Jude Janith Niroshan, Yang liu and Sampath S. Seneviratne
2.40 – 2.50 pm	**ZE_014**	**Comparative analysis of meteorological and soil moisture droughts in urban wetlands of Sri Lanka to validate the use of SPI as the primary measurement to assess drought** I.A. Seneviratne and D. Halwathura
2.50 – 3.00 pm	**ZE_015**	**Metal-dominated nest architecture of the House Crow (*Corvus splendens*) in urban Colombo, Sri Lanka** S.M. Samarajeewa, G.P.N. Poojani, M.P.O.T.B. Jayarathna, D.M.Y. Ravisara, B.M.K.S. Jeewamali, U.L.P. Induwari, K.A.D.S. Meecle and P.N. Dayawansa
3.00 – 3.10 pm	**ZE_017**	**Morphometric and meristic analysis of endemic freshwater fish *Belontia signata* (Anabantiforms: Belontiinae) in six river basins in Sri Lanka** N.S. Malage, T.S.P. Fernando, V.R. Gunasekara, N. A. Liyanarachchi and D.K. Weerakoon
3.10 – 3.20 pm	**ZE_018**	**Phylogenetic characterization of Sri Lankan Hipposideridae and Rhinolophidae bats based on mitochondrial COI sequences** S.M.P.S. Samarakoon, A.M.P.E.K. Atapattu, T. Kusuminda, T.S.P. Fernando and M.R. Wijesinghe
3.20 – 3.30 pm	**ZE_019**	**Using ant diversity as bioindicators of soil health: the role of human influence and urbanization impact** B.A.P.R. Perera, D.R.I.L. Silva, M.G.J.T. Guruge, A. Niroshan, G.P.S.K. Perera, E.H.I.C.E. Hewage and P.N. Dayawansa

Time	Abstract Number	Title and Author(s)
3.30 – 3.40 pm	**ZE_021**	**Effects of habitat complexity on growth and behavior in Neon Tetra Fish (*Paracheirodon innesi*)** S.H.N.I. Siriwardhana, C.V. Vithana, V.T. Kaluthota Arachchige, D.V. Wijesooriya, W.P.S.R. Weerawardana, K.S. Lokubalasuriyage, T. Tharmarasa, H.U.O.C. Uluwaduge, K.A.D.S. Meecle and P.N. Dayawansa
3.40 – 3.50 pm	**ZE_024**	**Assessment of precipitation effects on atmospheric heavy metal concentrations using Tillandsia usneoides as a biomonitor** W.M.N.A. Wijekoon and R.L. Jayaratne

E-POSTER SESSIONS

Time	Abstract Number	Title and Author(s)
3.00 – 4.30 pm	MC_007	***In silico* analysis of virulence factors and secondary metabolite biosynthesis clusters in the genome of the plant pathogenic fungus *Rhizoctonia solani*** S.A. Matharage and K.G.S.U. Ariyawansa
	MC_011	**Application of a newly isolated probiotic strain as a starter culture in curd production and determining the encapsulation efficiency** W.M.N.H. Wijesingha and N.S. Weerakkody
	MC_012	**Mycoherbicidal potential of *Nigrospora sphaerica* against *Synedrella nodiflora*, a common weed in Sri Lanka** D.L. Gunasena and K.G.S.U. Ariyawansa
	MB_002	**Biorefinery potential of freshwater microalgae cultivated in synthetic wastewater: a sustainable approach for biomass valorization** U.D. Samaranayake and P.S. Saputhanthri
	MB_003	**First insights into HLA-C*06:02 (HLA-Cw6) prevalence and its association with disease onset and severity in pediatric and adult psoriatic patients in Sri Lanka** N.D. Wanniarachchi, N.N. Samarakoon, N. Ranaweera, Sriyani Samaraweera, Jayamini Seneviratne, J. Akarawita, H.A.S.G. Dharmaratne and A.D.D.S. Amarasekara
	MB_005	**Preliminary validation of multiplex qPCR assay for the detection of 22q11.2 microdeletion in children showing neuropsychiatric phenotypes** W.A.D.M. Subawickrama, T.M.O.D. Tennakoon, N. Warsapperuma, D.M. Ranaweera, D.C. de Silva, N. Perera and G.H. Galhena

Time	Abstract Number	Title and Author(s)
3.00 – 4.30 pm	MB_006	**Screening of antibiotic resistance in probiotic bacteria for tetracycline group antibiotics in aquaculture practices in Sri Lanka** T.H.H.E. Jayathma, M.A.P.C. Piyathilaka, A.R. Pilapitiya, J.A.G.V. Sewmi, G.Y. Liyanage and M.M. Pathmalal
	MB_022	**Prevalence of clinically significant *PIK3CA* hotspot mutations: a comparative cohort study of HER2-positive and HER2-negative breast cancer subtypes in Sri Lanka** C.B. Ganegoda, I. Kumarasinghe, J. Balawardena, N.R.P. Perera, S. Viswakula and G.H. Galhena
	MB_023	**Evaluation of *in vitro* cytotoxicity and clonogenic activity of a clinically used traditional medicine formula** A.G.N. Nirmali, K.W. Gunawardana, N. Kumarasinghe, N. Salim, and A.I. Kuruppu
	PS_001	**TLC-based phytochemical screening and quantitative determination of total phenolic content in tuberous roots of *Mirabilis jalapa* L. under different extraction conditions** M. Luvedika, N. Ladhurshika, A. Manoraj, S.P.N. N. Senadeera and C.B. Ranaweera
	PS_009	**A helical motif as perfect foil: Nudix Box residues and folate biosynthesis** D. Gunawardana
	PS_010	**Investigating selected tissue extracts of *Artocarpus* spp. and *Nymphaea* spp. for potential antimicrobial activity** K.D.N.S. Kalubowila and P.S. Saputhanthri
	PS_013	**Influence of glyphosate on leaf phenolics, flavonoids, and antioxidant potential of *Camellia sinensis* var. *assamica* TRI 4042** U. Adshaja, J. Minal and H.D.S. Kavishka

Time	Abstract Number	Title and Author(s)
3.00 – 4.30 pm	PS_016	**Comparative analysis of protein-protein interaction network modules responsible for Kranz and non-Kranz leaf development: a systems biology approach** K.A.B.K. Wijeratne, P.C. Fernando and T.L.S. Tirimanne
	PS_020	**Investigation of genotoxic effects of common food preservative, calcium propionate, on root tips of *Allium cepa*** V.T. Koggalage and R. Wimalasekara
	PS_022	**Investigating the thermal capacity, total phenolic and flavonoid contents of selected herbal extracts** O.C. Wijekoon, I.A.J.K. Dissanayake, N.P.O.V. Pathirana, M.N. Kaumal and S. Gopura
	PS_023	**Exploring natural pigments from selected true salt marsh species in Kalpitiya, Sri Lanka** B.M.N.S. Balasooriya, B.G.C.I. Bopitiya, R.P.T. Chamuditha, D.M.H.S. Dissanayake, N.S.G. Punchihewa, R.V. Ranasinghe, P.G.T.N. Ranruwini and I.A.J.K. Dissanayake
	PS_024	**Factors influencing adoption decision of integrated rice-fish farming among agriculture instructors in Hambantota district, Sri Lanka** H.K.R.S. Kumara, M.M.K.I. Marasinghe, K.S.S. Atapaththu, S.S. Herath and N.P. Vidanapathirana
	ZE_004	**Comparative analysis of the vocal repertoires of *Centropus Coucals* of Sri Lanka** M.D. Farook and S.S. Seneviratne
	ZE_005	**Sensitivity of *Poecilia reticulata* and *Danio rerio* to polyethylene terephthalate microplastic fibers: implications for freshwater ecotoxicology** V.S. Jayasinghe, H.M.T.R. Samarakoon and C.K. Hemachandra

Time	Abstract Number	Title and Author(s)
3.00 – 4.30 pm	ZE_007	**Wing morphometry of Sri Lankan honeybee (*Apis cerana*) across different agro ecological zones in Sri Lanka** R.L.P.M. Somarathna and W.H. Jayasinghe
	ZE_008	**Utilizing Duckweed (*Lemna minor*) for sustainable Lead removal: a phytomining approach to water treatment and resource recovery** K.G.S.S. Maduwantha, M.A.P.C. Piyathilaka, K.G.N. Nanayakkara, E.M.M.S. Ekanayake and A.R. Pilapitiya
	ZE_009	**Nesting ecology and hatching success of marine turtles in the eastern coast of Sri Lanka** B.M.G. Chinthaka Bandara, M. Akila S.W. Peiris, D.M. Wasantha Dissanayaka, R.A.D.D.D. Samaranayake and Mayuri R. Wijesinghe
	ZE_010	**The impact of health condition, sex, life stage, environmental variables, and human influence on the feeding behavior of Elephants in selected areas of Udawalawa National Park** W.M.V.K. Kumarihami and K.M.S. Ruvinda
	ZE_016	**A morphometric assessment of Indian Palm Squirrel (*Funambulus palmarum*) across Sri Lanka** A.G.R.H. Amarasooriya, T.S.P. Fernando, V.R. Gunasekara, N.A. Liyanarachchi and D.K. Weerakoon
	ZE_022	**Enhancing toxicological predictions through Machine Learning on Zebrafish model data** P.H.D.G.N. De Silva, L.N.C. De Silva, D.P.N. De Silva and Kasun De Zoysa
	ZE_023	***Ulva fasciata* pigments: extraction, chemical characterization, and evaluation of antioxidant and anti-inflammatory activities** H.W.G.P. Sewwanthi and K.V.K. Gunathilake

Time	Abstract Number	Title and Author(s)
3.00 – 4.30 pm	ZE_025	**Spatial and temporal variation of phytoplankton diversity and abundance in Chilaw lagoon, Sri Lanka** N.D. Hettige, T.L. Gamage, S.R.C.N.K. Narangoda, H.V.A.B. Nuwanthi, S.P.Y.B. Pathirana, K.A.W.S. Weerasekara and Sansfica M. Young
	ZE_026	**Assessing the effects of Devil's trumpet (*Datura metel*) on muscle strength, muscle 1 coordination, and hematological parameters using the Wistar rat model** P.V. Gunawardena, P.H.R. Sushmika, R. Amarasooriya, I. Bilal, T. Edirisinghe, D. Farook, S. Kannangara, P. Samarakoon, N.S. Malage, T. Wickramasinghe, J.R.A.C. Jayakodi, V.K. Fernando, D. Weerakoon and M. Mapalagamage
	ZE_028	**Assessment of regional variations in vocalization structures of the Oriental Magpie Robin (*Copsychus saularis*) in Sri Lanka** D.S. Sudusinghe, D.W.R. Shashimal, P.K. Abeynayake, Y.M.S. Yapa, G.M.S.N. Ariyarathna, M.I.S. Fernando, W.A.T.S. Samanthilake, K.A.D.S. Meecle and P.N. Dayawansa

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