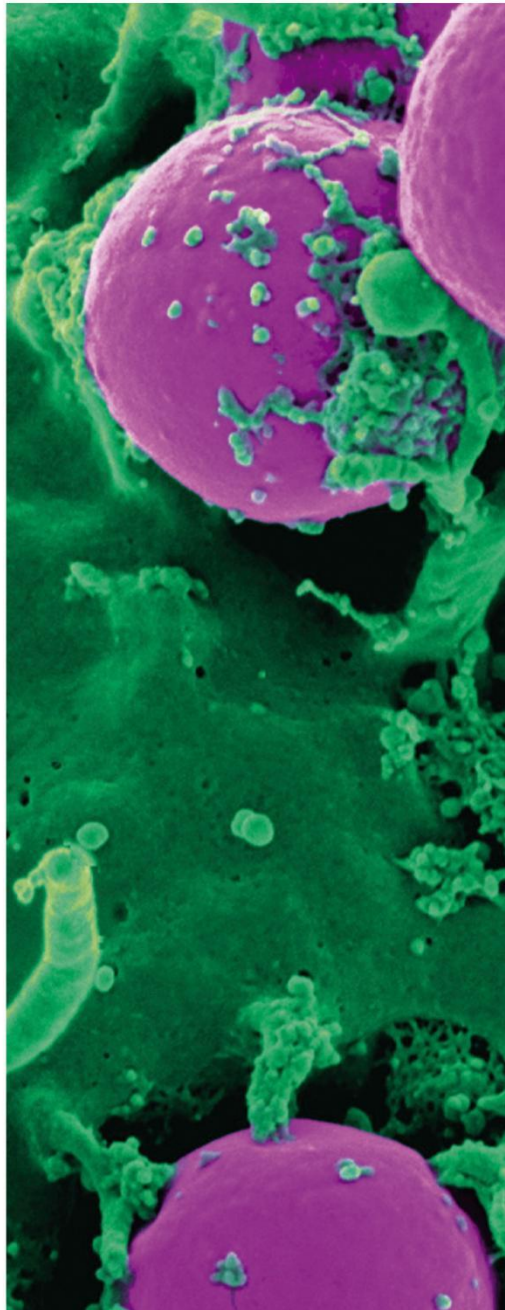
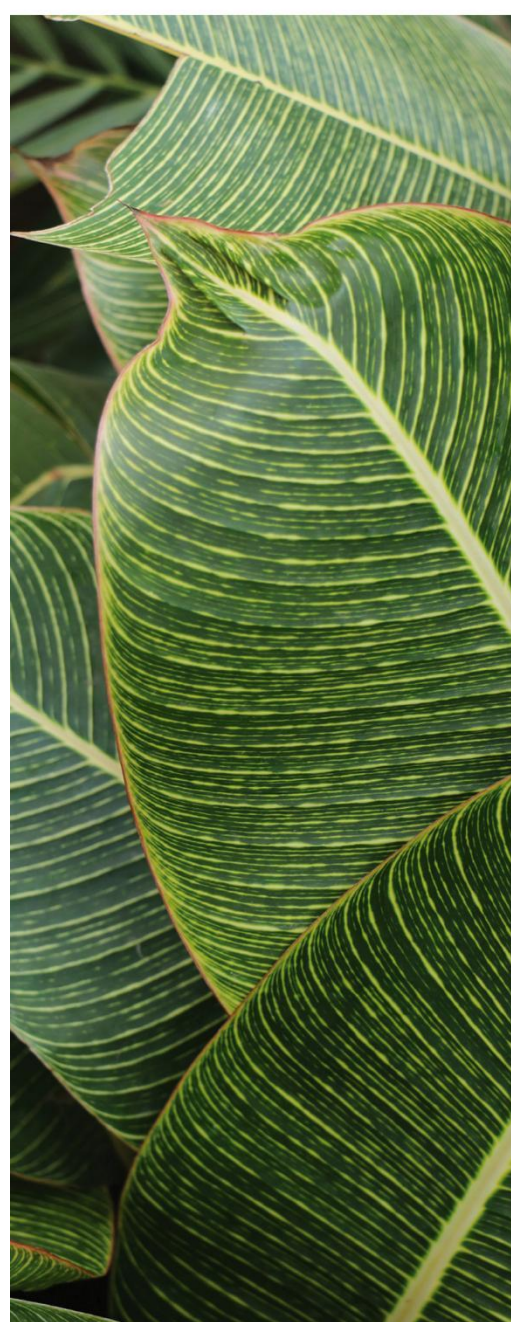


# PROCEEDINGS OF 43<sup>RD</sup> ANNUAL SESSIONS 2023



The Institute of Biology  
Sri Lanka



**BIOLOGICAL WEALTH FOR ECONOMIC PROSPERITY**



**Sitting (from left):** Prof. K.B. S. Gunawickrama, Dr. K.G.S.U. Ariyawansa, Prof. H. D. D. Bandupriya, Prof. S.A.C.N. Perera, Dr. R. Wimalasekara, Prof. B. D. R. Prasantha, Dr. I.A.J.K. Dissanayake.

**Standing (from left):** Mr. K. M.S. Ruvinda, Dr. D. Halwatura, Dr. Uthpala Jayawardena, Dr. A. M. Wickramasuriya, Prof. Hiran Amarasekera, Dr. I. U. Kariyawasam, Prof. G. Galhena, Dr. Vindhya K. Fernando, Dr. P. D. Dayananda.

**Absent:** Prof. Nissanka De Silva, Dr. C. D. Jayasinghe



**INSTITUTE OF BIOLOGY  
SRI LANKA**

PROCEEDINGS OF THE 43<sup>RD</sup> ANNUAL SESSIONS

Theme

***Biological Wealth for Economic Prosperity***

Institute of Biology, Sri Lanka

22<sup>nd</sup> September 2023

# Institute of Biology, Sri Lanka

Proceedings of the 43<sup>rd</sup> Annual Sessions

22<sup>nd</sup> September 2023

Colombo, Sri Lanka

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Dr. Devanmini Halwatura

Editor, IOB

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## **About the Institute of Biology, Sri Lanka**

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

### **The objectives of the institute are:**

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

### **Membership**

The institute has around 577 members, working in industry, research, education and healthcare. The institute also awards Fellowships and Charter of Biology status for members. There are seven categories of membership and members are encouraged to transfer to other grades in due course. Eligibility for each category depends upon a combination of professional experience and academic qualifications. Fellows are entitled to use the abbreviated designation F.I. Biol (Sri Lanka) while the Chartered Members are eligible to use C. Biol (Sri Lanka), Members M.I. Biol (Sri Lanka). The designation 'Chartered Biologist' endorses the high standards expected of biologists and is for international recognition as a hallmark of professional competence and ethical conduct.

### **Activities**

The Institute of Biology Sri Lanka (IOBSL) is a premier scientific body that plays a vital role in advancing education and professional development by organizing a wide array of courses, workshops, seminars and training programs for students at all levels and professionals in both academia and industry. The institute is also engaged in encouraging public interest in biology, by conducting fora on current topics in biology on a regular basis. The annual national Biology Olympiad competition is organized and administered exclusively by the IOBSL is a hallmark event in the country. Sri Lankan Biology Olympiad competition offers the students interested in the field of biology an opportunity to explore and challenge skills in biology. The IOBSL is dedicated to provide necessary training to the students selected to participate in the International Biology Olympiad; the world's largest biology competition for

secondary school students that takes place annually in a selected country. 'Inter-University Biology Quiz Competition' conducted by the IOBSL is an initiative taken to promote and popularize biology education among the undergraduates in the stream of biological sciences of the state and non-state universities and educational institutions in Sri Lanka. 'Inter-University Biology Challenge' is another competition organized by the IOBSL to promote awareness of undergraduates of universities in Sri Lanka in biology and interdisciplinary studies. The 'Young Scientist Award' is bestowed in the motive of recognizing outstanding contributions and achievements in research of the early career corporate members of the Institute. A national competition on biology photography initiated by the IOBSL offers an opportunity for the professional, amateur, and young photographers in Sri Lanka to communicate with the general public on wide arena of themes in biology.

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

The annual sessions of IOBSL provide a forum for both senior and junior biologists to communicate their research findings for a multifaceted audience. The annual sessions continue for the 43<sup>rd</sup> time this year.



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## PRESIDENTIAL ADDRESS

### **Biological Wealth of Plants: From Domestication to Gene Revolution and Beyond**

S.A.C.N. Perera (PhD) (FI Biol)

Department of Agricultural Biology, Faculty of Agriculture, University of Peradeniya

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It is with great pleasure that I deliver the presidential address on this 22<sup>nd</sup> day of September, 2023, at the occasion where, the Institute of Biology, Sri Lanka, is hailing the 43<sup>rd</sup> annual sessions. In view of the worst economic crisis of the recent history of Sri Lanka, and recognizing the remarkable richness of the biological wealth of our motherland, we, the Institute of Biology declared the theme for the year 2022/2023 as 'Biological Wealth for Economic Prosperity' with the intention of identifying and promoting biological solutions for the economic crisis. In this presidential address I will be focusing on the historical aspects and the potential of genetic improvement of biological wealth of plants in relieving the pains of fellow citizens in Sri Lanka and driving towards a sustainable and a profitable agricultural economy in our country.

The era of crop cultivation started with the domestication of plants. Domestication is the process of adapting wild plants and animals for human use. Domestic species are raised for food, clothing, medicine, and many other uses. Domesticated species are not wild and thus whether they be plants or animals they must be raised and cared for by humans.

The initial plant domestication took place about 10,000 years ago, between the Tigris and Euphrates rivers in Mesopotamia (which includes the modern countries of Iran, Iraq, Turkey, and Syria). This simply happened with people collecting and planting the seeds of wild plants. However, these early cultivators ensured that their plants had as much water as they needed to grow, and planted them in areas with adequate sunlight. Weeks or months later, when the plants blossomed, people harvested the food crops for their consumption.

The plants that were first domesticated in Mesopotamia were wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), lentils (*Lens esculenta*), and different types of peas. People in other parts of the world, including eastern Asia, certain parts of Africa, and of North and South

America, also domesticated plants. Other plants that were cultivated by early civilizations included rice (*Oryza sativa* in Asia) and potatoes (*Solanum tuberosum* in South America). In addition to domestication of plants for food, there were some other species which were domesticated for other purposes such as; cotton plants for fiber, certain flowers such as tulips for ornamental, or decorative, reasons.

### **History of Plant Breeding**

Plant breeding is an ancient activity, estimated to date back to 9,000 to 11,000 years ago, along with the very beginnings of agriculture. Probably soon after the earliest domestications of cereal grains, humans began to recognize degrees of excellence among the plants in their fields and saved seeds from the best plants for planting new crops in the next season. Initially, early farmers simply selected food plants with particular desirable characteristics, and employed these as progenitors for subsequent generations, resulting in an accumulation of valuable traits over time.

Such tentative selective methods were the forerunners of early plant-breeding procedures and the results of such early procedures were quite conspicuous. Most present-day varieties are so modified from their wild progenitors that they are unable to survive in nature. Indeed, in some cases, the cultivated forms are so strikingly different from existing wild relatives that it is difficult even to identify their ancestors. These remarkable transformations were accomplished by early plant breeders in a very short period of time from an evolutionary point of view, and the rate of change was probably greater than for any other evolutionary event.

### **Malthus's Theory**

Thomas Malthus (1776-1834) in his published essay on the 'Principle of Population' predicted a massive shortage in global food supply which was attributed to the geometrical increase of the population and the arithmetical increase in the food supply. But this prediction did not become a reality mainly due to the efforts of the early plant breeders most of whom were farmers themselves.

## **Gregor Mendel and plant breeding**

Gregor Mendel (1822–84) is considered the "father of genetics". His experiments with plant hybridization led to establishing the laws of inheritance. The discipline of genetics stimulated research to improve crop production through plant breeding. Modern plant breeding is basically considered to be a practical application of genetics, but its scientific basis is broader, covering molecular biology, cytology, systematics, physiology, pathology, entomology, biochemistry, and statistics (biometrics).

## **Classical Plant Breeding**

Selection, which is one major technique of plant breeding is the process of selectively propagating plants with desirable characteristics and eliminating or "culling" those with less desirable characteristics. Yet another major technique in plant breeding is the deliberate interbreeding (crossing) of closely or distantly related individuals to produce new crop varieties or lines with desirable properties. In hybridization, plants are crossbred to introduce traits/genes from one variety or line into a new genetic background. Progeny from the cross would then be crossed with the high-yielding parent, which is referred to as backcrossing to ensure that the progeny were most like the high-yielding parent.

Classical breeding relies largely on homologous recombination between chromosomes to generate genetic diversity. The classical plant breeder may also make use of a number of in vitro techniques such as protoplast fusion, embryo rescue or mutagenesis to generate diversity and produce hybrid plants that would not exist in nature.

## **Green revolution**

The Green Revolution, was a period of technology transfer initiatives that led to greatly increased crop yields and agricultural production. In the middle of the 20<sup>th</sup> century, when the world was suffering from the worst effects of two world wars and limited food supply, a report in 1967 by the Scientific Advisory Committee to the President of the United States stated that the 'Scale, severity and duration of the world food problem are so great that a massive, long-range, innovative effort unprecedented in human history will be required to master it'. The said scientific innovation came in the form of 'Green Revolution' that had been introduced by the Father of Green Revolution, Dr. Norman Earnest Borlaug who won the



Nobel prize for peace in 1970. The green revolution in its simple form can be described as the application of science (genetics, physiology and agronomy) and technology to create high-yielding varieties of major food staples, mainly grains, to increase productivity.

The green revolution despite the criticism today, delivered a yield increase of 44% between 1965 and 2010. Cereal production, the yields of rice, corn, and wheat increased steadily and doubled the previous records during the period from 1961–1985 saving millions of lives from hunger and malnutrition especially in Asia and South America. Unfortunately, the merits of green revolution did not reach the African continent due to differences in their staple crops and other logistic issues and the benefits, basically, 'life' that was resulted by the green revolution and was enjoyed by many in other continents did not become a reality in Africa until much later. This would provide an indication as to what would have been the situation especially in the developing countries such as ours in Asia and South America had it not been for the merits of green revolution.

### **Molecular breeding and Gene revolution**

Molecular breeding in simple terms can be defined as the application of the tools of molecular biology in plant and animal breeding. In the broad sense, molecular breeding methods perform genetic manipulations at the level of DNA to improve traits of interest in plants and animals, and it may also include genetic engineering or gene manipulation, molecular marker-assisted selection, and genomic selection. More often, however, molecular breeding implies molecular marker-assisted breeding (MAB) and is defined as the application of molecular biotechnologies, specifically molecular markers, in combination with genomics and other omic sciences, to alter and improve plant traits on the basis of genotypic assays. The most used molecular breeding approaches include QTL mapping or gene discovery, marker assisted selection and genomic selection, genetic engineering and recombinant DNA technologies.

### **Need for more food and higher productivity**

Due to the ever-increasing population which is predicted to be 9 billion by the year 2040, the world must continue to steadily increase the food supply. The situation has become more alarming and the implementation has become more urgent due to the biotic and abiotic stress

factors anticipated to negatively affect the food supply especially owing to the predicted ill effects of global climate change. The solutions once again would lie in innovative methods in adding value to the biological wealth of plants, the plant genetic resources.

### **Crop Genetic resources**

Agriculture and genetic resources are critically interdependent. All agricultural commodities, even modern varieties, descend from an array of wild and improved genetic resources from around the world. Moreover, agricultural production depends on continuing infusions of genetic resources for yield stability and growth of plants. Genetic resources are the reservoirs of genes which hold the key for improving plant traits for increased productivity and delivering resistance or tolerance against stresses. Genetic resources can hardly be given a specific value. Approximately, estimating the benefits of the already utilized genetic resources may be possible but assigning values for their future uses would not be feasible. Accordingly, conservation of plant biological wealth is unconditionally important and crucial in achieving economic gains from plant biological resources.

Conservation of genetic resources should be followed by their characterization and evaluation for their optimum utilization. The methods of characterization used by plant breeders of yester years were entirely phenotypic analyses using the principles of quantitative genetics. These methods have now been enriched with modern molecular methods; molecular markers, genome scans via GWAS and other omics approaches and using the bioinformatic tools in *insilico* analysis. Accordingly, crop genetic resources would be utilized optimally by combining quantitative genetics and modern molecular methods for identifying genes, their locations in the genome, genetic variability within species and among populations discovering gene function, and the relationship between gene structure, protein synthesis, and metabolic pathways, studying gene regulation, including gene activation and gene silencing, gene interactions and many more.

### **Opportunities**

Despite the multitude of challenges ahead of the humankind in relation to food supply and global climate change there are opportunities in overcoming them using rational and scientific approaches directed towards sustainability. The availability of plant biological

wealth is among the top in the list of opportunities followed by the high standards of scientific methods that are currently available. The approaches that we as the scientists would adopt should be critically evaluated prior to implementation for their sustainability for long term economic gains.

### **Plant Biological Wealth in Sri Lanka for economic gains**

The rich biological wealth is one of the most favourable factors that would contribute to the recovery of agricultural economy in Sri Lanka. The road towards sustainable and profitable crop productions lies through the vast array of our plant biological wealth which harbour genes of immense value to deliver high productivity traits and stress tolerance to our cultivated crops. Sri Lanka has recorded a remarkable success in doubling the yields of our staple crop, rice, in the second half of the 20<sup>th</sup> century by adopting the scientific techniques of green revolution, although this achievement was unnoticed and not appreciated by many with only the severe criticism prevailing till the agricultural crisis in the last year. However, it is doubtful whether we in Sri Lanka were successful in harnessing the scientific innovations of the molecular era. Lack of knowledge and skills, insufficient levels of infrastructure and the dilemma as to the level of adoption within the limited resources that are available would have hampered harnessing the potential benefits of molecular technologies in plant breeding in Sri Lanka. However, it is pleasing to note that some level of practical applications of molecular technologies are currently being adopted especially in the field of germplasm characterization and marker assisted breeding.

Currently, we in Sri Lanka should act wisely, rationally use our genetic resources, prudently select the scientific methods that we should adopt in increasing the value of our biological wealth to overcome the severe economic challenge that we are faced with for the betterment of the livelihoods of our people who are severely struggling even for the primary requirement, food. We as biologists of the nation do have a duty to perform and plant biologists and plant breeders should identify challenges, and by employing appropriate scientific approaches would add value to our plant genetic resources for the betterment of our people.

22<sup>nd</sup> September, 2023.

## **FELICITATION OF**

**Prof. D.P.S.T.G. Attanyaka**

Citation Presented by

**Dr. Wajira K. Balasooriya**

Senior Lecturer, Department of Biotechnology  
Faculty of Agriculture and Plantation Management  
Wayamba University of Sri Lanka.

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It is my great pleasure to have this opportunity of presenting to this distinguished membership of the Institute of Biology, Professor D.P.S.T.G Attanayaka, Fellow of the Institute of Biology, Sri Lanka, whom the Institute will be felicitating today in recognition of his invaluable services rendered to the fields of Genetics and Plant breeding, Molecular Biology and Biotechnology.

Professor Attanayaka graduated from the University of Peradeniya, with a Honours degree in Agriculture in 1982. After serving as a demonstrator in the Department of Agricultural Biology, University of Peradeniya, he joined the Quality seed Company (Pvt) Ltd, of the Hayles Group for a short stint. In 1984 he joined the Genetics and Plant Breeding Department of the Rubber Research Institute of Sri Lanka and served as an Assistant Geneticist and Plant breeder, Geneticist and Plant breeder and finally as the Head of the Department of Genetics and Plant Breeding until he joined the Wayamba University of Sri Lanka as an Associate professor in 2004. Prof Attanayaka obtained his PhD from the University of Birmingham, UK in Biological Sciences, in 1992 after following a qualifying M.Sc. course in Applied Genetics at

the Genetics Department of the same University, a pioneering Institute for the branch of Biometrical Genetics.

As one of the founder members of the newly established Department of Biotechnology of the Wayamba University of Sri Lanka, his time was fully devoted to the teaching and development work of this Department holding the position of the Head of the Department until he was appointed as the Dean of the Faculty of Agriculture for three consecutive terms. In the year 2018 he was appointed as a Professor, and in 2019 as the professor of Biotechnology of the Wayamba University of Sri Lanka. He has made an immense contribution to the development of the academic, research and infrastructure development of the department and the Faculty. He was instrumental in improving the course contents of many specialization courses of the biotechnology department. These included molecular biology, molecular genetics and genomes, Molecular markers and QTLs, Genetic Engineering and Biotechnology for Horticulture. He has supervised many research degrees at postgraduate level and authored over 80 scientific publications including 25 papers in peer reviewed journals. Further he made a noteworthy contribution in introducing the Bachelor of Biosystems Technology degree programme and the new Biosystems Engineering Department to the Faculty. He also contributed significantly to introduce the B.Sc. external degree programme in Plantation Management offered by the faculty.

Professor Attanayaka is a renowned geneticist and plant breeder. He worked mainly on the genetic improvement of the perennial tree crops. He was an active member of the rubber breeding team of the Rubber Research Institute of Sri Lanka and in 1997 he became the group leader of the breeding programme. The early work of his career on rubber reproductive biology solved a major problem of low fruit set success in artificial pollination programmes. The modified breeding pathway he introduced using participatory approach with estate and smallholder sector growers was able to cut short the long gestation period required for introduction of new rubber clones for planting. Many new rubber clones of RRISL 200, 2000, Centennial and 2100 series now recommended for planting are testimony to demonstrate the success of this clonal development procedure. In 1991 in his postgraduate research professor Attanayaka isolated, sequenced and characterized a gene involved in the biosynthesis of rubber from the natural rubber tree and developed methods for genetically engineer and express this gene in other plants and bacteria. This work on the rubber elongation factor gene have provided impetus to many research groups worldwide to explore on the rubber

biosynthesis and the allergenic properties of the REF protein, a problem in natural rubber-based products. After his return to Sri Lanka in 1993, he used this gene probe to introduce DNA technology for rubber breeding, under a grant received from the Council for Agricultural Research Policy, a pioneering work in introducing DNA technology for plant breeding in Sri Lanka. The copy number and the expression levels of the ref gene served as a molecular marker for selection of clones with high rubber yields. He also used several molecular marker systems to develop a key to identify the rubber clones and for genetic diversity studies. He shares a patent with three other researchers, for the invention of a Novel user Friendly and Effective Branch Induction Method for Young Rubber Plants. In recognition of his contribution to the rubber industry he was awarded the coveted global rubber industry accolade the GRC Wickham Award – 2014 in the technology innovative segment.

His expertise in Plant breeding, genetics and molecular biology was not limited only to the rubber sector. Professor Attanayaka contributed to crop improvement programmes in many other crops, predominantly, the plantation tree crop sector. While working at the Wayamba University of Sri Lanka, he made a praiseworthy national contribution to the cashew industry by serving as the chairman of the Cashew Research and Management Committee of the Cashew Corporation. The research work carried out under this committee, a long standing collaboration between the Cashew Corporation and Wayamba University, has made an immense contribution to the cashew industry by releasing 11 new cashew varieties for island-wide planting along with recommendations for other agronomic practices. In order to produce adequate amount of planting materials from these new varieties to accelerate the rate of adoption by the cashew farmers professor Attanayaka took a perseverance and consistent effort to introduce the patch budding technique for cashew propagation. Currently at the initial phase these new varieties have been planted in more than 2500 ha in the country and are popular among the farmers.

Prof Attanayaka has held many positions at the national level related to his chosen field, including Chairman of the National Committee on Plant breeding and Biotechnology of the Sri Lanka Council for Agricultural Research Policy, Member of the Rubber Research Board Consultative Committee on Research & Development, Member of the UGC Benchmark Panel in Agriculture, Member of Asian Biotechnology Association (FABA) Sub- Committee in 2015, Member of the working committee on Biotechnology and Bioethics of National Science Foundation Sri Lanka, Member of the committee on Professional Training and Development

in the Plantation Sector, Ministry of Plantation Industries Member of the National Sub-Committee on Technical and Technological aspects of the National Biosafety Framework of Sri Lanka, Member of the Board of Directors of the Coconut Research Board- 2009, member of the Boards of study in Agricultural Biology of the Postgraduate Institute of Agriculture and Biochemistry and Molecular Biology of the Postgraduate Institute of Science, University of Peradeniya, and Chairman of the expert cluster on perennial crops to achieve food security and nutrition of the steering committee appointed by the presidential secretariat in 2023. He has also contributed for reviewing articles, Selection committees for national awards, editorial boards of several local scientific journals and grade 10 and 11 text books in Agriculture and Food Technology of the education department. He served in evaluating and monitoring the progress of many research grants offered by National Research Council and National Science Foundation. Currently he is the Regional Secretary, Sri Lanka of the Society for Advance Breeding Research in Asia and Oceania (SABRAO), and an Associate editor of the SABRAO journal of Breeding and Genetics.

Professor Attanyaka has received President's Award for Scientific Publication in 2007, Presidential Awards 2018 – Merit recognition on Invention in the field of Agriculture, National Award for Excellence in Agricultural Research – 2017, 3rd Prize, and several Faculty and University level awards for his research and publications. He has authored two book chapters and three books. After his retirement from the University in 2023, he joined the Horizon Campus, Malabe to the staff of the Biotechnology Degree Programme, Faculty of Science. I am honoured to present to you, Prof. D.P.S.T.G. Attanayaka for felicitations by the Institute of Biology at its 43rd Annual Sessions, and wish him good health and fortune to continue his work for many more years to come.



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# ABSTRACTS

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## **Evaluation of anti-inflammatory and antioxidant activity of *Fromia indica* (a common starfish) crude extract**

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Starfish are a rich source of bioactive secondary metabolites, including antibacterial, cytotoxic, antitumor, anti-inflammatory and many more. *Fromia indica* star fish species reported from Sri Lankan coast since 1905, is a commonly available ornamental Echinodermata species. The present study aims to investigate the anti-inflammatory and antioxidant activity of *Fromia indica* crude extract. The specimens were obtained from a local aquarium and confirmed the identity by external morphology. The crude extract was prepared by incubating diced samples in methanol and dichloromethane (1:1 v/v) and the resulting extract was filtered and vacuumed to obtain dry crude extract which yielded 4.09 % w/w. A concentration series of the crude extract was prepared by dissolving in 5% ethanol. Determination of anti-inflammatory activity of the extract was performed by egg- albumin denaturation assay using Diclofenac sodium as the standard drug. To evaluate antioxidant activity of the crude extract, 2,2-diphenyl-1-picrylhydrazyl (DPPH) free radical scavenging assay and hydrogen peroxide radical scavenging assay were performed using Ascorbic acid as the reference drug. The crude extract demonstrated a dose dependent negative linear correlation with *in vitro* anti-inflammatory activity with respect to protein denaturation with a  $IC_{50}$  value of 6.22  $\mu\text{g/ml}$ .  $IC_{50}$  values for DPPH and  $H_2O_2$  radical scavenging assays were 5.67  $\mu\text{g/ml}$  and 3.81  $\mu\text{g/ml}$  respectively, where both are lower than that of standard drug Ascorbic acid ( $IC_{50}$ - 21.66  $\mu\text{g/ml}$  and 9.54  $\mu\text{g/ml}$  respectively). However, anti-inflammatory activity with respect to egg albumin denaturation assay was not reported, suggesting different *in vitro* and *in vivo* models to evaluate anti-inflammatory activity. The present study confirms strong antioxidant properties of the crude extract with possible applications in treating several diseases. Further studies need to be conducted in order to identify its full extent and this is the first report of anti-inflammatory and antioxidant activity of *F. indica* crude extract from Sri Lanka.

**Keywords:** Anti-inflammatory, Antioxidant activity, *Fromia indica*, Radical scavenging activity, Starfish

**Acknowledgement:** Undergraduate research funding from University of Sri Jayewardenepura is acknowledged.



## Heavy metal loads in the dung of wild Asian Elephants (*Elephas maximus*) in Sri Lanka

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Fecal matter has frequently been used as acceptable bio-indicators of heavy metal pollution. In the case of wild elephants (*Elephas maximus*) in Sri Lanka who range widely in search of food, feeding on garbage has been noted as a serious concern as it might induce health impacts. In the current study, we assessed loads of five heavy metals (Pb, Cr, Cd, Ni and Cu) in dung samples of wild elephants collected from anthropogenic habitats in five locations (Madawachchiya, Waddagala, Sigiriya, Randenigala and Katharagama) across Sri Lanka and compare the pollution levels. Sites were selected which are far from each other and three fresh boluses from widely separated piles were collected from each site, on the same day and samples for heavy metal analysis taken from the center of each bolus. Samples were all completely digested using acid digestion by aqua regia (12 M HCl and 6 M HNO<sub>3</sub>) method. Metals were analyzed using Flame Atomic Absorption Spectrometer. The results showed that the heavy metal levels recorded in the dung differed significantly between locations ( $P < 0.05$ ). The highest mean levels of Pb ( $354.38 \pm 15.77 \mu\text{g/g}$ ), Ni ( $231.88 \pm 15.17 \mu\text{g/g}$ ) and Cr ( $140.23 \pm 12.49 \mu\text{g/g}$ ) were detected from Madawachchiya, and Cd ( $199.38 \pm 7.81 \mu\text{g/g}$ ) and Cu ( $97.71 \pm 5.46 \mu\text{g/g}$ ) from Kataragama and Weddagala, respectively. The multiple correlation analysis showed a strong and significant positive correlation between Pb and Cd ( $r = 0.88$ ;  $P < 0.05$ ), and between Ni and Cr ( $r = 0.91$ ;  $P < 0.05$ ), suggesting common sources of contamination. Considering that these levels are relatively high, this information is nonetheless important given that it divulges potential threats to wild animals, through exposure to toxic heavy metals in anthropogenic landscapes. The study also reinforces the usefulness of dung as a tool for assessing heavy metal contamination in the environment.

**Keywords:** Pollution, Bio- indicators, Heavy metals, Dung samples, Wild Asian elephants

**Acknowledgement:** Undergraduate research funding from Institute of Chemistry Ceylon in acknowledged.



## Herbivory of mangrove crabs (*Sesarmidae*) in regenerating mangrove ecosystems - A study from Southern Sri Lanka

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Herbivory of sesarmid crabs plays an important role in the regeneration of mangrove ecosystems. They significantly affect the structure and functions of the mangrove ecosystems through the process of leaf degradation, propagule predation and thus in turnover of organic matter. Accordingly, to assess the food preference of herbivorous mangrove crabs, the field experiments were designed in a fringe mangrove patch in Unawatuna of Southern Sri Lanka. The main habitat types were chosen representing roadside and forest vegetations. In both vegetation types, the feeding preference of crabs on different species of mangroves and factors related to the propagule and leaf consumption were assessed once a month from May to August 2022. Three dominant sesarmid crab species (*Neosarmatium smithi*, *Perisesarma cf. guttatum*, *Episesarma versicolor*) were identified using their morphological characters. The rate of leaf and propagule consumption between roadside and forest vegetation was compared using Mann-Whitney U test. Further, to test whether the number of consumed leaves and propagules in roadside and forest vegetation depends on the mangrove species and two vegetation types, Permutational Multivariate Analysis of Variance (PERMANOVA) test was used. The propagules were consumed at a higher rate than the leaves. However, propagule consumption was not significantly different among mangrove species and the vegetation type. Contrarily, the leaf consumption among different mangrove species and vegetation types was significantly different. Both propagule and leaf consumption positively correlated with the crab abundance, which also had a positive relationship with the canopy openness. *N. smithi* showed the highest overall amount of leaf and propagule consumption while *P. cf. guttatum* showed the lowest. Our results indicated that the sesarmid crabs preferred propagules more than leaves. The propagules of different mangrove species were equally preferred by crabs and equally consumed among the two vegetation types, but leaf consumption was species-specific and was considerably higher in roadside vegetation. *N. smithi* was observed as highly competitive and mainly contributed to the propagule and leaf predation. The canopy openness was the primary factor that influences on crab abundance and propagule predation. Consequently, the mutual relationships between vegetation and crab populations could be important for mangrove restoration success and management.

**Keywords:** herbivory, propagule predation, regenerating mangroves, sesarmid crabs

**Acknowledgement:** We express our sincere thanks to Mr. Michael Wijeadasa from Unawatuna, Sri Lanka, for his assistance during the field visits.



## Molecular characterization and the record of host range of Rugose Spiraling Whitefly (*Aleurodicus rugioperculatus* Martin): A newly emerging pest of coconut in Sri Lanka

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Over the past years, coconut plantations in Sri Lanka have faced numerous pest and disease incidences. One of the recent challenges encountered is the whitefly infestation. The current study was conducted to identify the Rugose Spiraling Whitefly (*Aleurodicus rugioperculatus*) (RSW) at the molecular level and to report its potential host plants. The adults of *A. rugioperculatus* were collected from morphologically identified puparium for total DNA extraction using the CTAB method. The PCR amplification of mitochondrial COI gene 249 bp was performed using 1852 forward and 2100 reverse primers. The resulting sequences obtained from bi-directional Sanger sequencing were subjected to BLASTn similarity search with GenBank depositions through NCBI. Subsequently, surveys were randomly conducted in forty-five locations in three districts to identify potential hosts of RSW. The results (Accession no. OR239053) showed 100% similarity with *A. rugioperculatus* sequences deposited in the GenBank. A total of 17 potential plant species from 13 families were identified as hosts. All the instars of the life cycle were observed in Coconut (*C. nucifera*: Arecaceae), Arecanut (*Areca catechu*: Arecaceae), Oil palm (*Elaeis guineensis*: Arecaceae), Banana (*Musa* spp.: Musaceae), Mango (*Mangifera indica*: Anacardiaceae), Jackfruit (*Artocarpus heterophyllus*: Moraceae), Cassava (*Manihot esculenta*: Euphorbiaceae), Guava (*Psidium guajava*: Myrtaceae), Indian almond (*Terminalia catappa*: Combretaceae) indicating, these plants serve as true hosts. However, only eggs of RSW were observed in Sugarcane (*Saccharum officinarum*: Poaceae), Betel (*Piper betle*: Piperaceae), Ceylon ebony (*Diospyros ebenum*: Ebenaceae), Boob plant (*Ficus religiosa*: Moraceae), Hummingbird tree (*Sesbania grandiflora*: Fabaceae), Shoe-flower (*Hibiscus* sp.: Malvaceae), Black pepper (*Piper nigrum*: Piperaceae) and Papaya (*Carica papaya*: Caricaceae). Accurate identification of *Aleurodicus rugioperculatus* can be done using the mitochondrial COI gene and the pest can be categorized as a generalist as it is found in host plants belonging to many families. Thus, when planning for control interventions, the multi-host nature of the pest should be considered.

**Keywords:** *Aleurodicus rugioperculatus*, coconut, host plants, invasive pest, molecular confirmation.

**Acknowledgement:** Authors wish to extend their heartfelt appreciation to all the staff members in the Crop Protection Division, Coconut Research Institute, Sri Lanka for their support.



## A preliminary study of rs4913269 in IFNG-AS1 gene as a genetic risk factor for susceptibility to cutaneous leishmaniasis in a selected endemic cohort in Sri Lanka

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Leishmaniasis is a neglected tropical disease and is a vector-borne parasitic infection of which Sri Lanka is the latest focus in the Asian subcontinent. The main form of the disease in Sri Lanka is cutaneous leishmaniasis (CL) which is caused by *Leishmania donovani* zymodeme MON-37. The differences in the responses to infection by the exposed individuals, ranging from self-healing wounds to full-blown disease raise the involvement of inherited factors in modulating the disease outcome. A recent genome-wide association study has identified rs4913269 in the IFNG-AS1 gene to be one of the lead polymorphisms that affect CL susceptibility in Brazil, where *Leishmania braziliensis* is the causative agent. Accordingly, the present study was designed to investigate an association between CL and rs4913269 in a CL endemic area in Sri Lanka by conducting a case-control study. Finger prick blood was collected from 30 CL patients and 29 controls from Hambantota and genotyped for the polymorphism using an in-house developed polymerase chain reaction-based restriction fragment length polymorphism (PCR-RFLP) assay, i.e. 471 bp region flanking the polymorphism was PCR amplified and digested using Tsp45I and resolved in agarose gels. According to the results, rs4913269 genotypes showed a similar distribution between the cases (CC:0.567, CG:0.367 GG:0.067) and controls (CC:0.483, CG:0.414, GG:0.103). When analyzed using binary logistic regression with SPSS 21, none of the genotypes or alleles (p values >>0.05), showed an association with CL. The minor allele (G) frequency of the population (0.28) was observed to be much higher than the value reported for South Asians (0.05), suggesting a lack of evolutionary pressure on the allele in the studied cohort. Our results indicate that the rs4913269 in the IFNG-AS1 gene is unlikely to exert a modulatory effect on CL susceptibility in the Hambantota population, despite it being identified as a lead polymorphism for CL elsewhere. However, considering the limited sample size, more exhaustive studies are required to confirm the observed null association.

**Keywords:** SNP polymorphism, PCR-RFLP, genotyping, case-control study, candidate-gene association



## **Parasitic profiles of edible fish catch from selected inland water bodies and culture systems in Sri Lanka**

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Inland fish is a rich protein source while inland fisheries and aquaculture is a developing industry in Sri Lanka. The presence of parasites in edible inland fish poses significant risks to human health, food safety, and the economic viability of the aquaculture sector. The lack of broader parasitological research to understand the diversity, host preference, and the relationship between edible host fish and parasites is an overlooked concern in Sri Lanka. Therefore, this preliminary study aimed to investigate the parasitic profiles of edible fish catch from inland water bodies; wild catch from Sri Jayawardenepura area, Beira and Bolgoda lakes, and a culture system, in Sri Lanka. A total of 55 inland edible fish, consisting of 12 species, were dissected afresh, and examined for ecto and endo parasites. Parasite abundance and richness were recorded, and prevalence was calculated. Out of 55 fish, 26 were infected with parasites, exhibiting an overall prevalence of 47%. A total of 21 parasite species ranging from protozoans, trematodes, cestodes to crustaceans including *Trichodina* sp., *Enterogyrus* sp., *Parvitaenia macropeos*, *Ergasilus* sp. and a possible parasitic mite were detected. Nile Tilapia exhibited the highest parasite prevalence (83%), followed by Grey Mullet (80%) among wild catch while Mrigal carp (33%), and Genetically Improved Farmed Tilapia (GIFT) (20%) harboured the highest among cultured fish. The highest parasite species prevalence and mean abundance were of *P. macropeos* in Nile Tilapia (100%, 53) and Mozambique Tilapia (67%, 25) harvested from Beira. Piscivorous birds are their definitive hosts, and the presence of many Pelicans and Cormorants can be the underlying reason. It is of concern that *Amirthalingamia* sp. recorded in Nile Tilapia (20% prevalence) from Beira has a zoonotic potential. Parasite prevalence was notably higher in wild-catch male Tilapia (89%) than in females (50%). The study indicates a higher susceptibility of wild caught edible fish to parasitic infections in urban areas than in remote culture facilities; especially, the high parasite prevalence in the commonly consumed wild caught Tilapia species, raising potential health risk concerns. Further studies in Sri Lanka are warranted to better understand the associated health risks to humans.

**Keywords:** Edible fish, inland water, parasites, prevalence, Tilapia

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



## **New record of *Knemodynerus coriaceus* (Giordani Soika, 1970) (Hymenoptera, Vespidae, Eumeninae), a vespid wasp from Sri Lanka**

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Family Vespidae of the order Hymenoptera consists of potter wasps, pollen wasps, paper wasps, hover wasps, yellow jackets and hornets which are collectively known as Vespid wasps. However, similar to many other insect groups in Sri Lanka, the family has been largely understudied. Thus, the present study was conducted to investigate their current diversity and distribution within the country. The field sampling was conducted from July 2022 to March 2023, in 27 locations representing 20 districts and all the provinces of the country. The sampling locations included different habitat types such as plantations, forests, aquatic habitats, and human settlements. Each sampling habitat was thoroughly surveyed using the visual encounter sampling method. The specimens were morphologically identified using taxonomic keys and descriptions for the Vespidae of the Indian subcontinent, Vietnam, and China, by Pannure et al., 2016 and Kumar et al., 2019. As a result of the study, 26 species of vespid wasps were identified which belonged to 17 genera of 3 subfamilies, Eumeninae, Polistinae and Vespinae. A single male specimen of *Knemodynerus coriaceus* (Giordani Soika, 1970) of subfamily Eumeninae was recorded from Araviyal Nagar in Kilinochchi district, Northern province, for the first time in Sri Lanka. Until now, this species has been only recorded from South India. The ferruginous coloured body with yellow bands, and first metasomal tergum having large, less dense punctures with interspaces often equal to punctures are key features that separate the species from the other species of genus *Knemodynerus*. At present, the distribution of this species within the island is not clear and further investigations are required to establish their distribution and morphological characters. This record points to a range expansion of the species and contributes largely to the knowledge of the distribution of the genus *Knemodynerus* in the Indian subcontinent. Further, this discovery elaborates the urgency for further explorations and conservation efforts of the understudied arthropod groups in Sri Lanka.

**Keywords:** Vespidae, Eumeninae, new species, India, Sri Lanka

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



## Potential of the aqueous extract of *Terminalia chebula* ('Aralu') powdered dry fruit in reducing serum triglyceride levels – A pilot study in albino Wistar rats

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Fruits of *Terminalia chebula* ('aralu') have been used by traditional medical practitioners in the treatment of hyperlipidemia. However, limited research has been conducted to test the effects of these fruits against hyperlipidemia. The present pilot study was conducted to assess the anti-lipidemic potential of *T. chebula* dry fruit crude extract in albino Wistar rats. Five groups of Wistar rats (151.7 – 218.0g) each with 03 females and 03 males were maintained as Group 1 (Control): normal feed; Group 2: normal feed + 500mg/kg *T. chebula* (orally), and Groups 3-5: normal feed + 3ml/kg high-fat diet (ghee 3: coconut oil 2 to induce lipid levels). While maintaining the same feeding regimes for all groups, Group 4 and Group 5 were given *T. chebula* extract (500mg/kg daily oral dose) and anti-hyperlipidemic drug Atorvastatin (20mg/kg daily oral dose) respectively, from the fourth week onwards. At the end of seven weeks, blood was drawn, and serum triglyceride levels were assessed. No significant difference ( $P > 0.05$ ) was observed in the final mean body weight of rats and liver somatic index (ANOVA) among the groups. There was a significantly lower level of triglycerides in Group 2 ( $90.019 \pm 7.802$  mg/dl) compared to all other groups (Group 1:  $162.465 \pm 8.391$ , Group 3:  $148.918 \pm 14.391$ , Group 4:  $159.756 \pm 12.052$ , Group 5:  $159.009 \pm 12.969$  (mg/dl)) ( $P < 0.05$ , ANOVA, Tukey test). *T. chebula* extract significantly reduced the triglyceride levels in Group 2 indicating that *T. chebula* has a potential to lower the serum triglycerides in albino Wistar rats. The triglyceride levels in groups 4 and 5 remained not significantly different from that of the control indicating the anti-lipidemic effect. Any lipid induction due to a high-fat diet in those groups may have been lowered by *T. chebula* extract and Atorvastatin. Further research is needed to verify the results further and to see the antihyperlipidemic effect of *T. chebula* fruits.

**Keywords:** Anti-lipidemic activity, hyperlipidemia, *Terminalia chebula*, serum triglycerides





## **Influence of land use and land cover attributes on population dynamics of Indian Peafowl (*Pavo cristatus*) in a selected expanse of peafowl accident susceptible zone of the Southern Expressway**

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Construction of the Southern Expressway can be considered to be one of Sri Lanka's largest initiatives for development. After the opening of the expressway, roadkill including peafowl was a common sight. The objective was to investigate how changes in land use and land cover (LULC) due to Expressway construction impacted the population dynamics and dispersion of Peafowl. ArcGIS 10.3 was employed to construct four maps (before and after the Expressway construction) to assess the change in LULC. The influence of LULC on population size, age structure, and sex composition of Indian Peafowl was investigated from November 2022 to April 2023. The study area was delineated by using the Southern Expressway as the reference. Thus, six zones of the extent of 5 km (length) and 0.3 km (width to both sides) were selected from Imaduwa to Aparekka (total 30 km) including five interchanges namely Imaduwa, Kokmaduwa, Godagama, Kapuduwa and Aparekka. All zones consisted of six land use types namely paddy fields, Expressway interface, forest patches, barren lands, agricultural land, and home gardens. Line transects (n=210) laid on a stratified random method were employed to collect data based on direct observations. The total population size of the peafowl of the study area (six zones) was  $69.22 \pm 8.12$  (Mean  $\pm$  SD). Age structure was depicted by 64:4:1 (Adult: Juvenile: Chick). The quaternary sex ratio was 2:3.2 with a skewness towards females while a polygynous mating system was revealed. Out of the six land use types, the highest abundance of peafowl was recorded in the Expressway interface ( $5.39 \pm 5.69$ ) while barren lands recorded the lowest ( $0.09 \pm 0.40$ ). A significantly higher abundance of peafowl was recorded in the Aparekka zone (132km-136km) (One-way ANOVA  $P < 0.05$ ), a zone rich with wetlands (paddy fields). The study revealed that the peafowl population is mostly confined to roadsides represented by the Expressway interface than interior habitats (t-test  $P < 0.05$ ). The finding indicated that the construction of the Southern Expressway has resulted in creating habitats that benefit the peafowl population.

**Keywords:** Population dynamics, Indian peafowl, Southern expressway, Land use & land cover



## Patterns of distribution in endemic birds along a one-kilometer elevational gradient in the submontane zone of Sri Lanka

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### Abstract

Endemic species mostly are habitat specialists. Therefore, the survival of endemic species is limited by the availability of their preferred habitat. Along an elevational gradient, the distribution of endemics may vary depending on the geology, availability of resources, energy, and space. This study was carried out in order to investigate the distribution of endemic birds along an elevational gradient and understand the drivers behind any emerging patterns. The Issengard Biosphere Reserve, a submontane forest in Belihuloya, within the Ratnapura district, Sabaragamuwa province (6°42'50.93"N, 80°45'6.39"E) was used as the main study area. Encompassing nearly 1 km elevational gradient from 480 m (MSL) to 1420 m (MSL), ten horizontal line transects were established along the elevation. Bird counts, camera trapping, and mist netting were done for the data collection from August 2022 to April 2023 along the complete elevational gradient. The primary analysis was based only on bird counts reported; 752 total bird observations representing 21 endemic species, which encompasses 60% of the 34 endemic species found in Sri Lanka. Species richness, abundance, and diversity of endemics showed a hump-shape variation with their inter-quartile range spanning between 700 m -1100 m, along the elevational gradient due to the mid-domain effect, where species from both extremes were represented in mid-elevations. However, the montane forests at 1420 m showed higher values for the measured diversity and density parameters of endemics due to the local availability of a forest-bird favourable habitat. 29% of the recorded endemics were found along the complete gradient, while 71% were found above 1000 m elevations. The accumulation of endemics at higher elevations reflects topography-driven ecosystem isolation of endemics in the montane zone of Sri Lanka.

**Keywords:** Altitudinal variation, Belihuloya, Endemic birds, Endemicity, Sri Lanka

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## The study investigating the population dynamics of a critically endangered hog deer (*Axis porcinus*) population in Honduwa island sanctuary in the wet zone of Sri Lanka

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Hog deer (*Axis porcinus*) is considered as a critically endangered species in Sri Lanka. Thus, ex-situ conservation measures are important to maintain viable populations. Although, an ex-situ conservation measure was implemented in 2013 in the Honduwa island sanctuary to conserve this critically endangered species in Sri Lanka, this population could face inbreeding and the founder effect in the future as the population was by few founders (2013 – 2 animals, 2016- 8 animals). Population size, age structure, sex composition, and productivity (Reproductive efficiency) of this isolated population were determined using direct observations, photographic and video methods during the ten-month study period (July 2022 to April 2023). Block count method and line transects revealed that the population size of hog deer at Honduwa island depicted by a single herd is composed of 30 individuals. The herd's age structure comprises 19 adults, 6 sub adults and 5 fawns. A slightly skewed quaternary sex ratio that favours females (8:11) was evident and it is compatible with the possible mating system of deer where one male pair bonded with multiple females depicting polygamous mating system. Behavioural observations confirmed that the mating system is polygyny. During the study, 3 female hog deer gave birth to 3 fawns. According to the past recorded data, the rate of natural growth of the population during the last 7 years was found to be 10.4 percent. However, no signs of inbreeding were observed such as deformities, poor offspring, or sterile animals. To ensure the long term viability of the population, it is crucial to conduct genetic analyses to assess the genetic diversity and the potential risk of inbreeding.

**Keywords:** Hog deer, Critically endangered, Ex-situ conservation, Isolated, Inbreeding

**Acknowledgement:** Financial assistance by the Department of Zoology and Environment Sciences, University of Colombo.



## Vitamins, minerals, and fatty acids composition of Mackerel scad (*Decapterus macarellus*): a common edible fish from Sri Lanka

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Fish serve as the most feasible and healthiest nutritional source for human consumption, as they contain high-quality proteins, essential vitamins, minerals, and omega-3 fatty acids. Fish consumption is highly recommended for normal growth and development in children and to avoid nutritional deficiencies in adults. Present study was aimed at exploring the vitamins, minerals, and fatty acids composition of the muscle of mackerel scad (*Decapterus macarellus*), a commonly available, commercially low-valued fish in the Sri Lankan local market. Fish samples (N=10) were collected from fish markets in the Western Province, Sri Lanka and morphological measurements were recorded. The mineral composition in terms of calcium (Ca), magnesium (Mg), potassium (K), sodium (Na), zinc (Zn), selenium (Se), copper (Cu), iron (Fe), phosphorous (P) and manganese (Mn) was analysed with Inductively Coupled Plasma Mass Spectroscopy (ICP-MS). The lipid profile was analysed with Gas Chromatography-Mass Spectrometry (GC-MS) and the availability of vitamins A, D and E was determined with High-Performance Liquid Chromatography (HPLC). The morphological measurements were reported with an average standard length of 27.3±1.95cm, total length of 32.03±2.45cm and weight of 334.15±78g. *D. macarellus* contained Ca (15.5mg/100g), Mg (35.3mg/100g), K (264.5mg/100g), Na (66.2mg/100g), Zn (1.2mg/100g), Fe (1.5mg/100g), Cu (2.3mg/100g), and P (242.5mg/100g) while Se and Mn were not detected. The Fatty acid profile resulted in saturated fat (0.4g/100g), monosaturated fatty acid (0.2g/100g), polyunsaturated fatty acid (0.4g/100g), Omega-3 eicosapentaenoic acid (0.05g/100g), Omega-3 docosahexaenoic acid (0.3g/100g) and cholesterol (2.1mg/100g). The vitamin D level was 21.72µg/kg while Vitamin A, and E were not recorded. Thus, the present study for the first time provides a detailed vitamin, mineral and fatty acid profile of mackerel scad. In conclusion it is recommended to serve as a potential source of minerals, vitamin D and essential fatty acids among local communities in Sri Lanka.

**Keywords:** nutritional profile, micronutrients, food composition, minerals, fatty acids

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## Investigation of haemoparasites in avian communities along an altitudinal gradient

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Altitudinal gradients offer an ideal research setting to investigate the patterns of distribution of parasites, vectors, hosts, and host immune responses across different environmental conditions. However, very few studies had been done on the parasite profile in birds along the altitudinal gradient in Asia. The study was conducted at the Issengard Biosphere Reserve in Belihuloya, Sri Lanka, which has a 1 km steep elevational gradient ranging from 480 m at Samanalawewa Reservoir to 1420 m at Haagala Peak. A total of 49 bird individuals representing 18 species from 13 families, were captured using mist nets and their blood was collected via brachial vein puncture to assess the presence of blood parasites, parasite intensity, and parasite prevalence. Blood parasites were present in 26.53% (13/49) of the birds from 6 different species. A total of 12.24% (6/49) of the birds, representing 3 species, had microfilaria larvae, while a total of 14.28% (7/49) of the birds, representing 4 species, had *Haemoproteus* sp. The presence of intracellular parasites and their intensity are increased with elevation while the presence of microfilaria parasites and microfilaria intensity are decreased with elevation. The highest prevalence of *Haemoproteus* sp infection was found in the bird group of White-eye (55.55%). Sri Lanka white-eye (*Zosterops ceylonensis*) (n=2) and Oriental white-eye (*Zosterops palpebrosus*) (n=3) were both parasitized with *Haemoproteus* sp. Six birds were observed to have microfilaria as parasitic worms. Even though the prevalence of microfilaria in the Flycatcher group is higher, the greatest number of infections were recorded in the brown-capped babblers (*Pellorneum fuscicapillus*). This research revealed a high occurrence (4/7) of microfilaria in Brown-capped Babblers (*Pellorneum fuscicapillus*), which could be the first record of microfilaria in the *Pellorneum* genus in Sri Lanka.

**Keywords:** Altitudinal gradient, Blood parasites, *Haemoproteus*, Microfilaria

**Acknowledgement:** Avian Sciences and Conservation, Department of Zoology & Environment Sciences, Faculty of Science, University of Colombo and Department of Zoology & Environment Sciences, Faculty of Science, University of Colombo.



## **Investigating the potential of *Scenedesmus* sp. isolated from Beira Lake, cultivated under non-axenic, ambient conditions in open bioreactor systems, for biodiesel production in Sri Lanka.**

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Third generation biodiesel is functionally similar to conventional diesel and is produced by transesterification of microalgal lipids. This is potentially highly suited for production in Sri Lanka due to the abundance of diverse microalgae species, ample freshwater, and sunlight. This research was aimed to investigate the potential of local freshwater microalgae, cultivated under ambient conditions, for biodiesel production. This was carried out by (1) microalgae isolation from natural habitats and morphological identification (2) cultivation of the isolated microalgae (3) harvesting the biomass, lipid extraction, gravimetric measurement of extracted lipids and (4) acid-catalysed transesterification, followed by GCMS analysis of the biodiesel product. *Scenedesmus* sp. was isolated from water samples of Beira Lake using spread and streak plate techniques in solid standard BG 11 media. It was then cultivated in liquid standard BG 11 media for 20 days in open bioreactor (test) and closed bioreactor (control) systems in duplicates. The microalgae biomass was then harvested using alum, dried to reach a constant weight and the Bligh and Dyer lipid extraction was done in triplicate. The extracted lipids were transesterified with methanol, using sulfuric acid catalyst at 90° C for 60 minutes. The separated product was confirmed as biodiesel by quantitative analysis of fatty acyl methyl esters using GCMS. *Scenedesmus* sp. cultivated under natural ambient light (12:12, light: dark cycle) at room temperature, in 4L closed bioreactor systems and in 4L open bioreactor systems gave average lipid yields of 11.7 ± 1.05 % and 14.93 ± 1.55 % respectively. Average lipid yield of the open cultivation system was significantly higher than that in the closed system at 95% confidence level (Two-sample T test on SPSS Version 21). This non-axenic culture of *Scenedesmus* sp. that can be cultivated with best utilization of ambient conditions, has a significant potential for biodiesel production in Sri Lanka.

**Keywords:** Microalgae, Biodiesel, *Scenedesmus*, Bioreactor, Lipid extraction and transesterification

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## **Conventional and modern methods of measuring N, P and K levels in the soils around the world and their adaptability in Sri Lanka**

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Maintaining optimal levels of primary nutrients, Nitrogen (N) Phosphorus (P) and potassium (K) [NPK] in soil holds significant importance for optimum crop growth and development. Major objective of this study was to examine conventional and modern soil NPK detection methods around the world and evaluate the farmer knowledge and adaptability of these methods to Sri Lanka. A thorough literature survey was conducted to find out methods available to analyze NPK levels in soil. Thereafter, a randomly selected sample of 100 individuals involved in Agriculture (farmers, Agricultural inspectors and research and production assistants) from Galle and Mathara district were interviewed to find out their knowledge about NPK detection methods. A structured questionnaire used to systematically gather information. Literature revealed that observing nutrient deficiency symptoms of plants is the most common conventional method used by farmers around the world and is followed by soil testing for NPK. Utilization of NPK sensors (electrochemical, optical, mechanical, electromagnetic and fiber optics) coupled with Internet of Things (IoT) are the latest technologies used. Our findings indicate that farmers and agricultural officers in Sri Lanka rely on soil testing as the sole method of assessing soil nutrient levels. Based on the results of farmers, it was found that only 5% of farmers are aware of soil testing while only 10% of them have actually conducted it. The survey revealed that only 3% of farmers are familiar with sensor based NPK detection methods. These findings indicate a significant lack of knowledge among farmers and technical officers in Sri Lanka regarding new technologies. The participants have highlighted the need for more accurate, user-friendly, and cost-effective modern techniques to address the limitations of conventional methods. In conclusion, the results of the survey highlight the need for improved awareness and adoption of new technologies in the agricultural sector in Sri Lanka.

**Keywords** – Soil, Nutrients, Detection methods, Sensors, Adaptability,



## **Carbon footprint calculation for scope-2 indirect emissions of a knowledge-based institution and its impacts under the post covid-19 conditions**

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Climate change is one of the devastating challenges, which the entire world faces. Global warming is a reality and Green House Gas (GHG) emissions are known to be the main cause of the Global Warming. Carbon Footprint is a tool, which is used to assess the GHG emissions emitted by organizations. This study was carried out to assess the indirect energy emissions (purchased electricity) of a knowledge-based institution: University of Sri Jayewardenepura under pre-covid-19 and post-covid-19 conditions (during 2019 and 2020 period). Primary data related to electricity usage were collected from the University of Sri Jayewardenepura. Carbon Footprint calculation under scope-2 was done by using DEFRA UK electricity conversion factors for 2019 and 2020. Highest energy consumption was observed in 2019 when compared to 2020. The main reason for this could be the closing of universities under the government-imposed rules and regulations with respect to the health guidelines which enables the social isolation. Consequently, two surveys were conducted for academic staff and students of the University via Google forms to assess impact of online teaching system during the post COVID-19 conditions. According to the results, 3.72 tCO<sub>2e</sub> were emitted by the academic staff while the 45.17 tCO<sub>2e</sub> were emitted by the students domestically due to the online teaching and learning system. Therefore, these emissions also should be taken into consideration when assessing the carbon footprint during the post Covid-19 conditions. Moreover, university population is more interested towards a blended learning system. Since university had the first –ever experience in distant learning, the ratings of the experiences and challenges faced which have been discussed in this study can be taken to strengthen the future crisis scenarios.

**Keywords:** Green House Gas, Carbon footprint, pre-covid-19, post-covid-19, Knowledge based institution





## **The impacts of the lockdown and economic crisis on energy-related greenhouse gas emissions from selected apparel industry factories in Sri Lanka**

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The global apparel industry holds a prominent position within the industry sector and significantly contributes to the emission of greenhouse gases contributing to climate change. Considering the close connection between the apparel industry and economic conditions, it is vital to examine how economic fluctuations can impact emissions. This study focuses on analyzing monthly CO<sub>2</sub> emissions during the COVID-19 lockdown and the subsequent economic crisis periods compared to the pre-COVID-19 period. Secondary data collected from six apparel manufacturing factories in Sri Lanka, spanning January 2019 to December 2022 were utilized for this study. Direct [i.e., Scope-1 ( $\bar{x}$ =167.19 t CO<sub>2</sub>) including onsite fuel combustions] and indirect [i.e., Scope-2 ( $\bar{x}$ =559.03 t CO<sub>2</sub>) related to purchased electricity and Scope-3 ( $\bar{x}$ =3.16 t CO<sub>2</sub>) associated with water consumption] emissions were analyzed. The study, employing ANOVA (Scope-1 emissions) and Kruskal-Wallis (Scope-3 emissions) tests, reveals significant differences in CO<sub>2</sub> emissions during the economic crisis period compared to pre-COVID-19 and COVID-19 periods while no significant difference between pre-COVID-19 and COVID-19 periods. Scope-2 emissions exhibited no significant difference across periods, with a marginal distinction between pre-COVID-19 and COVID-19 periods per the Kruskal-Wallis test. The linear regression results revealed a robust positive correlation ( $r = 0.72$ ) between Scope-1 emissions and monthly average exchange rates, a weak negative correlation ( $r = -0.11$ ) between Scope-2 emissions and monthly average exchange rates, and a weak yet positive correlation ( $r = 0.32$ ) between total emissions and monthly average exchange rates. In conclusion, study findings verify that global crises, including the COVID-19 pandemic, have a tendency to reduce emissions in situations where internal or localized crises, such as those resulting from sovereign debt crises lead to an increase in emissions. Overall, the above findings highlight the importance of taking steps to reduce emissions to mitigate the environmental impact of any future crises and achieve climate goals.

**Keywords** – Apparel industry, CO<sub>2</sub> emissions, Economic periods, Exchange rates, Carbon footprint



## **A Socio-economic investigation of landslide disasters in the Kegalle district**

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Landslide disasters pose great threats to the community due to their impacts on different socio-economic aspects. Moreover, they result in serious impacts on the environment too. With a growing population, unsustainable development and changing climate, landslides are becoming increasingly evident locally and globally. This study was conducted to analyse socio-economic impacts of landslides and land subsidence in Kegalle District, which is highly vulnerable to landslides. The investigation was conducted using data (from year 2016 to year 2021) available (landslides, cutting failure, rock falls and land subsidence data) at the Disaster Management Centre and District Secretariat office, Kegalle. A weighing method was used in analysis and the highest marks received DSDs (District Secretariat Divisions) were identified as landslide hot spots in the study area. A scale was developed and used to weight each individual incident reported from 2016 to 2021 with in eleven DSD. Using recorded data of number of reported deaths, missing cases, injured cases, destroyed houses, damaged houses weighing scale was developed and all the DSDs were scaled using it. The Dehiowita DSD was recognized as the highest impacted DSD with highest marks received for reported deaths, missing cases, injuries, destroyed houses, damaged houses and affected individuals. Aranayaka, Ruwanwella, Yatiyanthota and Bulathkohupitiya DSDs were the other top five with the highest impacts. The results showed a general increase in landslides in some DSDs over the years. A linear regression test showed a significant increase in incidents from 2016 to 2021 in Warakapola and Rambukkana DSDs ( $p < 0.05$ ). The results highlight the need of immediate attention on adopting disaster risk reduction strategies, including vulnerability analysis, early warning, and preparedness. Raising community awareness on landslide safety is also suggested as an essential requirement.

**Keywords:** Landslides, Disasters, Socio-Economic Impact, Kegalle District

**Acknowledgement:** The authors are grateful for the support provided by the Department of Zoology and Environment Sciences., University of Colombo.



## **Water quality analysis based on physical-chemical parameters in selected urban wetlands in the Colombo district, Sri Lanka**

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Tropical freshwater urban wetlands serve as crucial ecosystems, offering a range of ecosystem services through their hydrological, biochemical, ecological, and socioeconomic functions. Urban wetlands in the Colombo district play a key role in flood control, water retention, water purification, and habitat provision. In order to successfully provide these services, water quality is of vital importance. The objective of the current study was to examine and compare the water quality in two wetland areas within the Colombo district, one of which had been successfully restored, while the other is currently undergoing restoration. The study was conducted at the Green Isle urban wetland (part of the Bellanwila – Attidiya sanctuary, which is undergoing restoration) and the Beddagana urban wetland, (a successfully restored wetland of the Colombo Ramsar wetland complex) using eighteen sampling plots over a period of three months (December 2022 to February 2023). A two-way ANOVA test on the water quality parameters, demonstrated a significant distinction between the two research locations over the three-month period. Notably, water temperature, conductivity, total dissolved solids (TDS), dissolved oxygen (DO), biochemical oxygen demand (BOD), phosphorous, and potassium content differed significantly between the sites. Additionally, under flooded conditions, water conductivity, pH value, nitrate content, and potassium content exhibited noteworthy variation compared to normal conditions. The study found that the water quality parameters in the Beddagana urban wetland complied better with the irrigation water quality standards, though both wetlands under study did not meet the optimum levels of water quality. In conclusion, based on the assessment using the simple water quality index (ISQA), it is evident that the water quality of the restored urban wetland surpasses that of the wetland currently undergoing restoration. The study highlights the importance of conserving existing urban wetlands while working towards the restoration of degraded ones.

**Keywords:** Urban wetlands, Restored wetlands, Water quality parameters, Ecosystem services, Water nutrients



## Investigating the Microclimatic Buffering Potential of Submontane Forests in Knuckles Range, Sri Lanka Using Temperature and Relative Humidity

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Microclimatic buffering plays a vital role in maintaining species composition and regulating ecological processes within forest ecosystems. This study aimed to document the ambient temperature (T) and relative humidity (RH) variables to assess the microclimatic buffering potential of tropical submontane forests in Sri Lanka. The study was conducted in the Knuckles Conservation Forest (KCF) which comprises submontane forests (SMF). Microclimatic sensors were placed at nine (n=9) random locations within forest patches at height of 2 m to record temperature and relative humidity at 30-minute intervals over a 24-hour period. Ten (n=10) grassland (GR) locations were selected from within the KCF to function as reference sites. The study was conducted in February 2023. The temperature and relative humidity values were used to calculate the Vapor Pressure Deficit (VPD) which has been used previously for assessing microclimatic buffering potential of ecosystems. The comparison of microclimatic metrics between the SMF and GR revealed significant differences between the two habitats (e.g., T max - SMF=22.9±1.90; GR=28.2±1.90, H=11.21; P<0.05, RH min - SMF=78.1±8.8; GR=56.9±11.3, H=9.89; P<0.05). SMFs exhibited lower variations in both ambient temperature and relative humidity compared to GR. The relationship between VPD max of the GR plotted against the respective values for SMF generated a value of -2.07, indicating a negative buffering potential, i.e., SMF are moister than the reference site (GR). Interestingly, this value was greater than that recorded previously for riverine forests in the dry zone of Sri Lanka. This study provides novel insights into the microclimatic conditions of the central highlands which have, yet not been investigated at a micro-scale. Knowing the buffering capacities of relatively small natural forest patches in Sri Lanka is particularly significant given the high rates of deforestation and the predicted increases in ambient temperatures.

**Keywords:** microclimatic buffering, sub-montane forest, ambient temperature, relative humidity, vapor pressure deficit

**Acknowledgement:** Financial assistance by the Department of Zoology and Environment Sciences, University of Colombo



## Investigating the efficiency of urban trees in alleviating Urban Heat Island effect using Remote Sensing and Geographical Information Systems

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Urban Heat Island (UHI) effect is a phenomenon where urban areas' surface and atmospheric temperatures are higher than the rural areas surrounding them. Colombo Metropolitan Area (CMA) which is the commercial capital and the only metropolitan area in Sri Lanka has been experiencing rapid urbanization over the past few decades degrading its ecology and creating atypical climatic conditions such as extreme heat and fog. Urban vegetation is considered as an effective measure of reducing the UHI and its heat stress. In theory, achieving 1°C drop in urban temperatures is necessitated by a mandatory tree cover of at least 16%. Understanding the changes in temperature with emphasis on vegetation is important to manage the UHI. This study aimed to detect changes in the vegetation cover and Land Surface Temperature (LST) of CMA, and to determine their association from years 2018 to 2021. Pre-processed data sets retrieved by Landsat 8 satellite imagery were used to calculate LST and Normalized Difference Vegetation Index (NDVI) using Google Earth Engine platform and ArcGIS Version 10.8. The mean temperatures of CMA were recorded as 26.99 °C, 28.02 °C, 26.24 °C, 27.06 °C and mean NDVI values were recorded as 0.5778, 0.5829, 0.5711, 0.5880 in years 2018, 2019, 2020 and 2021 respectively. Overall, mean NDVI value has increased by 0.0102 and mean temperature has increased by 0.07 °C from years 2018 to 2021 signifying that, variations in NDVI was not adequate for attenuation of LST. Association analysis distinguished that the variations of LST from years 2018 to 2021 has been explained via NDVI by 23.7% ( $R^2 = 0.237$ ). The relationship between LST and NDVI was deciphered as a moderate negative correlation ( $r = -0.486$ ) with an inversely proportional relationship and statistically presented as  $LST = -4.030 NDVI + 29.612$ . Use of remote sensing and GIS provided a time and cost-effective methodology for valuation of the association between LST and NDVI although the use of freely available low-resolution data is a major limitation the of this study.

**Keywords:** Colombo Metropolitan Area (CMA), Remote Sensing (RS), Geographical Information Systems (GIS), Land Surface Temperature (LST), Normalized Difference Vegetation Index (NDVI)



## Unveiling the secrets of *Stemonoporus*: what lies behind the distribution patterns and ecological niche of Sri Lanka's enigmatic endemic plant genus?

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Sri Lanka is an island in the Indian Ocean, renowned for its unparalleled species diversity and endemism. One of the most species-rich (26 species) endemic genera belonging to the family Dipterocarpaceae in Sri Lanka is *Stemonoporus* Thw. All its members are categorized as critically endangered (CR) or endangered (EN) species in the National Red List and confined to the island's lowland and montane wet zone. This study was performed to determine the distribution patterns and their future predictions of *Stemonoporus* species. The species occurrence data were gathered from the specimens deposited in the National Herbarium, Peradeniya, national and international databases. Suitable habitats of each species were estimated, and the current and future potential distribution was projected under two Shared Socioeconomic Pathways (SSP2-4.5, SSP5-8.5). Highly correlated bioclimatic variables were removed and Isothermality (bio 3), temperature seasonality (bio 4), precipitation of the coldest quarter (bio 19) and elevation were selected to analyse currently suitable habitats. Then the future suitable habitats were determined for 2070 using MaxEnt. All 26 species were further clustered relatively with the floristic zones using R-studio. Niche specialists were identified using restricted niche width and range size. Endemic taxa *Stemonoporus marginalis*, *S. mooni*, *S. kanneliyensis*, *S. affinis* and *S. latisepalum* were identified as crucial range-restricted species. Furthermore, *Stemonoporus mooni* was observed to have both low range size and narrow niche breadth. The present study revealed a reduction of suitable habitats for all 26 species under both current and future climate projections. The species *Stemonoporus cordifolius*, *S. gardneri*, and *S. oblongifolius* were determined by the elevation and *S. affinis* by the coldest quarter's precipitation parameter. Then the remaining *Stemonoporus* species showed a significant correlation with temperature seasonality. Mainly there were 3 clusters observed in the cluster analysis. The suitable habitat predictions and mapping aid the conservation of *Stemonoporus* species.

**Keywords:** *Stemonoporus*, Floristic zones, Ecological niche modelling, Distribution, Cluster analysis.



## Enhancement of the nitrogen level of compost by incorporation of biological nitrogen fixers and nitrogen capture additives

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Nitrogen (N) is one of the crucial macronutrients for plant growth. Even though N is the most abundant element in the atmosphere, crop requirements are not met in most of the agricultural lands. Since high-quality compost has a great potential to enhance the fertility of agricultural soil-eco systems, this study focused on looking into methods that can increase the N content of compost. Free-living heterotrophic N<sup>2</sup>-fixing bacteria were isolated from soil samples from organic farms representing five different ecological zones of Sri Lanka. Bacterial genomic DNA was extracted, and the V4 region of the 16s rRNA gene was amplified for the identification. The bacteria were screened based on their antagonism and N fixing efficacy. Nitrogen capture additive (NCA) was used to reduce N loss from compost. A leaching experiment was performed to study the efficiency of the NCA at different ratios (1% -4%) mixed with the sand matrix. Considerably, the 2% treatment demonstrated the highest efficacy of ammonium adsorption by NCA. Poultry manure, cattle manure, *Gliricidia* leaves, and biochar were used as the feedstock materials for compost production. Composting setups with C:N ratios of 20:1, 25:1, and 30:1 were used with 60% of initial moisture content and 350 g cm<sup>-3</sup> initial bulk density. 2% NCA was added for all treatments. The antagonistic test indicated synergistic growth among selected isolates. According to the N<sup>2</sup> fixation efficacy assessment, the most efficient three isolates which were compatible in coculturing were used for consortium formulation for compost production. According to the final compost sample analysis, C: N, 25:1 treatment showed 38.2±14.7% ( $P<0.05$ ) of significant N enhancement (highest total N: 2.6%) compared to the control.

**Keywords:** Antagonism, Composting, Nitrogen capture additives, Nitrogen fixing bacteria, Sustainable agriculture



## **Spatiotemporal analysis of the impact of open dumping on aquatic vascular plant development: a case study on Karadiyana open dump, Sri Lanka**

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Karadiyana open dumpsite (KOD) is located in the wet-climatic-zone of Sri Lanka. Adjacent to KOD are four surface waterbodies with increased levels of aquatic plant growth. Nutrient rich leachate movement from KOD to surface waterbodies may be the reason for it. The objective of this research is to analyze the impact of open dumping at KOD on accelerated development of aquatic vascular plants in neighboring surface waterbodies using GIS (Geographical information system) and Remote sensing techniques. The current ecological state of said surface waterbodies was visually analyzed and classified into one of five classes (bad, poor, moderate, good, high). The ecological state of two waterbodies were at “poor” state and two were at “moderate” state. Four main land-use classes (open dump, marsh-like vegetation, dense and moderate growth of floating aquatic plants, and visible surface water) were identified in the study area and their spatiotemporal change was compared between 2004 and 2022 using Google Earth imagery. Noteworthy change of land area was recorded in two land use classes: open dump, a 144% increase; and floating aquatic plant (dense growth), a 150% increase. Spatiotemporal distribution of macrophytes after the establishment of the dumpsite was analyzed using Normalized Difference Vegetation Index (NDVI) analysis. Landsat images of the study site from 1995 to 2022 were used for this. Based on the vegetation growth NDVI images of the study area were classified into three classes. The area of two of the three NDVI classes: visible surface water (-65%) and low-density vegetation (-19%) has reduced over the 27-year study period whilst the area of the third land use class: high density vegetation has increased in 73 percent. Strong positive correlation between increase of open dump area and increase of dense aquatic vegetation indicates the possibility of open dumping induced accelerated vegetation growth in the study site.

**Keywords:** MSW, GIS, Aquatic- plants, NDVI





## **Comparison of Major Nutrient Status between Whitefly Non-infected and Infected Coconut Palms of Three Estates: A Case Study in Gampaha Area**

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Coconut Research Institute of Sri Lanka has introduced multiple fertilizer recommendations for coconut palms to balance their nutrient status, thereby enhancing the yield to meet the consumption of the increasing population and exportation of diverse products of the coconut palm. With the unavailability of fertilizers in the country it was found that the palms are not fertilized at proper intervals leaving them with deficiencies. The loss of balance of the nutrient status makes palms vulnerable to pests and diseases and retained sugars in leaves due to less K attracting leaf feeders. Hence, with the currently widespread whitefly infestation, there is a high tendency for a decrease in yield due to damage to leaflets of fronds. Therefore, this case study was focused on assessing the relationship between the nutrient status of palm and whitefly infestation which was categorized under three damage states of fronds; mild(1), moderate(2), and severe(3), non-infested category was considered for the comparison. Randomized Block Design was used with three coconut estates at the bearing stage as blocks differing according to fertilizer application practices followed and whitefly infestation stages as the treatments. Thus, 14th frond leaf samples were collected from infested and non-infested coconut palms of randomly chosen three coconut plantations in Gampaha area. At least 3 leaf samples were collected in each category of the whitefly state from each estate. All leaf samples were analysed for N, P, K, Mg and Ca. In order to find the correlations between the nutrients, Pearson correlation was conducted using Minitab 20 for non-infested and infested all stages. Furthermore, data were analysed through ANOVA to study the relationship of nutrient status with three infested status in comparison with healthy leaf nutrient levels. Analysed data reveals that there is a decrease of N and P from infested stage 1 to 3 (from  $r=+0.46$  to  $r=+0.76$ ). As general coconut plantations show strong K and Mg interaction was also noted with  $r$  value of  $-0.89$  for non-infested palms but the above mentioned correlation became milder from infested stage 1 to 3. However, there were no significant differences among whitefly infestation levels with any of the nutrient levels but nutrient deficiencies of N, K and Mg were 56%, 31% and 64% respectively with the whitefly infestation. However, this study is to be continued with a few more estates to generate more correlations as well as nutrient relationships with whitefly infestations.

Key words: Coconut, Deficiency, Infestation, Nutrition, Whitefly



## **Biochemical characterization of *Oryza sativa* (L.) varieties grown *in vitro* under salinity stress**

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*In vitro* selection based on tissue culture techniques has emerged as a useful approach for screening biotic and abiotic stress tolerance in crops. Rice (*Oryza sativa* L.) varieties with varying levels of salt tolerance (tolerant-Pokkali, medium tolerant – Bg 310, sensitive – Bg 450 and Pachchaperumal) were examined *in vitro* for a number of parameters in an effort to uncover biochemical markers for salt tolerance. Five-day-old *in vitro* grown rice seedlings and six-week-old calli of different rice cultivars were treated with 0, 50, 100, 150 mM NaCl on basal MS medium for 15 days and the responses were evaluated. These included shoot and root lengths of seedlings, weight gain of calli, chlorophyll content, total electrolyte leakage, proline content, total phenolic content, DPPH radical scavenging activity and total flavonoid content. The results were analysed using one-way analysis of variance and differences were considered to be statistically significant if the p values were less than 0.05. The results showed that increasing salt concentrations negatively affected on the growth and development of both seedlings and calli cultures, as evidenced by decreased shoot, root lengths, callus weight and chlorophyll content. The total electrolyte leakage was increased with increasing salt concentration in all varieties and it was significantly high in the sensitive variety Bg 450 at 150 mM salt concentration. The salt tolerant variety Pokkali and moderately tolerant variety Bg 310 successfully tolerated highest salinity level 150 mM by accumulating significantly higher levels of free proline and exhibiting higher DPPH radical scavenging activity, total phenolic content and total flavonoid content than the sensitive genotypes. Interestingly, under salt stress, comparable variation patterns were detected in all biochemical assays in shoots, roots, and callus tissues. According to the results, there was no significant difference in total electrolyte leakage, proline content, total phenolic content, DPPH radical scavenging activity and total flavonoid content among shoots, roots and calli of selected varieties at each salinity level. This implies that callus tissues alone can be tested *in vitro* to screen for metabolic alterations brought on by salinity stress in different rice varieties.

**Keywords:** Rice, calli, DPPH, proline, NaCl, electrolyte leakage



## ***Ipomoea imperati* (Convolvulaceae): A new occurrence record from Manalkaadu, Jaffna, Sri Lanka**

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Family Convolvulaceae, the morning glory family of flowering plants has 14 genera and 39 species in Sri Lanka. Genus *Ipomoea* is the largest of those 14 genera and has 16 species. Among the 16 species, *Ipomoea imperati* is mentioned as 'endangered' in the National red list of Sri Lanka 2020. In a recent study of sand dune plant diversity at Manalkaadu, Jaffna, using belt transects, *I. imperati* was recorded at five of the nine study sites: Katkowlam, Mamunai, Chempianpattu, Thalayadi, and Aliyawalai. Plant identification was done using available keys and with the help of the expertise at National Herbarium at Peradeniya. *I. imperati* is a dicotyledonous flowering plant commonly known as fiddle-leaf morning glory with white flowers. The large white flowers are funnel-shaped with fused white petals and yellow centers. *I. imperati* is a slender, creeping vine with a succulent stem that contains milky latex and trailing stems of the vine are covered with alternately arranged lanceolate, fleshy dark green leaves with a notched apex. *I. imperati* flowers bloom from September to March in the Manalkaadu dune area of Jaffna and the flowers open in the morning and close in the afternoon. The species withstands high substrate temperatures (about 35 °C), salt sprays, strong winds, sand scouring, and moderate burial in accreted sand in the study area. The species *Ipomoea pes-caprae* which is with purple flowers is a common coastal plant which distributed throughout the country's coastal area but the plant of *I. imperati* is confined to Manalkaadu in Sri Lanka and it was recorded for the first time in September 2022 from the Manalkaadu sand dunes of the Jaffna Peninsula of Northern Sri Lanka.

**Keywords:** Convolvulaceae; *Ipomoea imperati*; *Ipomoea pes-caprae*; Jaffna; Sri Lanka



## **Distribution analysis and ecological niche modelling of selected *Shorea* (*Doona*) species in Sri Lanka with special emphasis on range size and niche breadth**

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Sri Lanka is home to 10 endemic *Shorea* species, formerly treated as Genus *Doona*. This study focused on distribution patterns and ecological niche models of these species that help to provide insights into the conservation of these taxa. Distribution data were obtained from the National Herbarium, International Herbaria, and other national level floristic databases. A geo-referenced map was created, to assess the species' spatial distribution across floristic zones. Heat map analysis and Jaccard clustering based on the distribution of species in different floristic zones were used to detect niche dynamic estimations. The study assessed present and future distributions under two socioeconomic pathways. Environmental variables i.e., isothermality, temperature seasonality, precipitation of the coldest quarter, and elevation were selected to address multicollinearity. Models were thresholded to a 95% suitability score, enabling the calculation of habitat changes by 2070. The Southern Sinharaja Hiniduma-Kanneliya and South of Ratnapura-Northern Sinharaja lowland rainforest areas were identified as the key centres of endemism for *Doona* species. Heat map analysis further confirmed this finding. Among the studied species, *Shorea ovalifolia* exhibits the narrowest niche breadth and the limited range size revealing its conservation priority. Jaccard distance analysis revealed that *Shorea gardneri* has distinct distribution characteristics compared to other studied species. *Shorea megistophylla* and *Shorea disticha* exhibit similarities in locality distribution. Models predict an increment in the distribution for all the selected *Shorea* species by 2070 for both socioeconomic pathways.

**Keywords:** *Doona*, *Shorea*, Distribution analysis, Floristic zones, Sri Lanka, Niche modelling



## Reproductive Plasticity of *Miconia crenata* (Vahl) Michelang [syn. *Clidemia hirta* (L.) D. Don] across an elevational gradient

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*Miconia crenata* (Vahl) Michelang [syn. *Clidemia hirta* (L.) D. Don], a member of plant family Melastomataceae is an invasive alien plant species firstly reported from wet lowlands, however had extended its distribution to high elevations in Sri Lanka. It alters the community structure, change microhabitats and ecosystem functions in invaded environments. The noxious nature of *M. crenata* has been partly attributed to its prolific seed production and dispersal strategy. This study aimed to identify the plasticity of reproductive traits of *M. crenata* at different elevation ranges; Low (L, 0–500m), Medium (M, 500m–1000m), High (H, 1000 m–1500m). Composite plant samples were obtained from naturally growing populations of each elevation range. Floral morphological traits, production of ovules and pollen, fruits and seeds were recorded in fully bloomed flowers, ready to open mature flower buds and ripen fruits from each elevation range (n=30) using standard laboratory methodologies. Data were subjected to ANOVA ( $P < 0.05$ ) followed by Tukey's post hoc test using RStudio. Plasticity of reproductive traits varied across elevation. At M, smaller flowers ( $9.713 \pm 0.15$ ) were produced with short receptacles ( $3.353 \pm 0.10$ ), short stamens ( $3.107 \pm 0.09$ ) and increased the stigma – anther distance ( $1.397 \pm 0.13$ ). Diameter of hypanthium receptacle increased with elevation and was broadest at H ( $3.120 \pm 0.10$ ). Pedicel thickness increased between M and H, showing highest at H ( $0.711 \pm 0.02$ ). Shortest sepals ( $2.211 \pm 0.08$ ) and lowest nectar sugar ( $0.25 \pm 0.03$ ) and fruit pulp sugar contents were reported from L, however, the flowers had highest ovule count ( $27493 \pm 2128$ ), hence showed least pollen: ovule ratio ( $5.22 \pm 0.78$ ). At H ( $3.120 \pm 0.10$ ) largest fruits were produced ( $7.902 \pm 0.24$ ) with highest volume ( $149.302 \pm 14.95$ ), fruit weight ( $0.262 \pm 0.02$ ) and seed count ( $8567.2 \pm 459.6$ ). Other reproductive traits investigated; pedicle and style length, number of seeds per unit fruit volume, fresh weight of fruit per unit volume, volume of anther, pollen count, number of pollen per unit volume of anther, ovary length, width and volume, number of ovules per unit volume of ovary did not show statistical differences across elevation ranges. The study revealed that many key traits remain unchanged, and only limited plasticity is exhibited by the reproductive traits to maintain *M. crenata*'s successful reproductive performance despite environmental variations observed from 0–1500m elevations in Sri Lanka.

Key words: *Miconia crenata*, *Clidemia hirta*, invasive alien plant, plasticity, elevation



## **Foliar trait plasticity help *Miconia crenata* (Vahl) Michelang [syn. *Clidemia hirta* (L.) D. Don] to survive from low to high elevations**

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*Miconia crenata* (Vahl) Michelang [syn. *Clidemia hirta* (L.) D. Don], an invasive alien shrub of plant family Melastomataceae is reported in both low and high elevations in Sri Lanka. This study quantified plasticity of foliar anatomical and functional traits of natural populations of *M. crenata* in elevations; Low (L, 0-500m), Medium (M, 500m-1000m), High (H, 1000m-1500m) and VH (1928m). Foliar measurements were obtained from a total 17 sampling locations [L(n=5), M(n=4), H(n=7), VH (1)]. Second and third fully expanded healthy leaves from the top (n=10-30 per location) were subjected to *in situ* measurements of photosynthesis using MultispeQ device v2.0. Leaves were detached, photographed and subjected to image analysis using ImageJ software to obtain leaf area. From half of sample anatomical measurements were obtained through standard laboratory methodologies for stomatal counts and density, guard cell length, leaf thickness, trichome height and density. The Other half of samples were dried in an oven at 110 °C for 3-4 hrs, to obtain dry weight and Specific Leaf Area (SLA) was calculated. Data were subjected to ANOVA followed by Tukey's post hoc test using RStudio. Stomatal density showed an increased trend above 1000m and the length of guard cells were significantly increased at VH ( $16.666 \pm 3.90$ ). Highest SLA was shown at L ( $229.776 \pm 11.93$ ) while lowest was at VH ( $74.34 \pm 45.71$ ). Relative chlorophyll content was highest in M ( $48.559 \pm 0.70$ ). Between 0-3000 PAR, photosynthetic functions behaved differently as quantum yield of photosystem II showed a decreasing trend towards high elevations and exhibited highest at M ( $0.462 \pm 0.02$ ). Plants growing at VH showed significantly highest values for fraction of light energy directed to non-photochemical quenching from photosystem II ( $0.600 \pm 0.10$ ) and the photosynthetic efficacy as reflected by the Linear Electron Flow ( $185.1016 \pm 77.27$ ). No difference was reported in the estimate of non-photochemical quenching, proton conductivity of the chloroplast ATP synthase, steady-state rate of proton flux through the chloroplast ATP synthase, total magnitude of electrochromic shift decay during a light-dark transition, photosystem- I active, open, oxidized and over reduced centers did not show any difference within 0-3000 PAR range. Broad plasticity of foliar traits of *M. crenata* indicates its successful survival at high elevations by increasing gas exchange and maximizing photosynthesis efficiency for better performance alleviating any stress conditions at high altitudes.

**Key words:** Invasive alien plants, *Miconia crenata*, foliar traits, plasticity, elevation range



## Distribution analysis and improved propagation of selected *Eriocaulon* species used for medicinal purposes

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*Eriocaulon quinquangulare* L. (Heen-Kokmota) and *Eriocaulon sexangulare* L. (Kokmota) are widely used in Ayurveda and other traditional treatments in Asian region. Various ecological pressures and intrinsic characteristics of plants such as poor seed germination, slow growth and explicit environmental requirements have caused a drastic decline in the wild populations of these plant species. The main objective of this study was to analyze the distribution and develop an efficient propagation method for the selected *Eriocaulon* species. Species occurrence data and environmental data were collected and species distribution models (SDMs) were developed using Maxent software (v3.4.4). In current SDMs, highly suitable habitats for *E. quinquangulare* and *E. sexangulare* were severely restricted, comprising only 0.17% and 1.65% of the suitable habitats, respectively. Investigations on current conservation status revealed that there were no initiatives for *ex situ* conservation, and *in situ* conservation was restricted to a few protected areas. The identification of *Eriocaulon* species poses considerable challenges due to low interspecific variation. Therefore, a comprehensive pictorial guide including vegetative and reproductive characteristics of the selected species was compiled to facilitate accurate identification. Studies on propagation were conducted according to CRD and data were analyzed using one-way ANOVA in R Studio (v1.4.1106). In investigation of the impact of different potting media on seed germination and subsequent plant growth, *E. sexangulare* exhibited significantly higher ( $p \leq 0.05$ ) seed germination in parent soil (41.7%) and in a potting mixture of sand and coir (2:1) (39.7%) compared to all other media tested. However, *E. quinquangulare* showed no seed germination. Furthermore, the investigation was extended for seed priming treatments with Gibberellic acid (GA), kinetin, and  $KNO_3$ . In *E. sexangulare*, 200 ppm  $KNO_3$  priming resulted in 100% germination. Moreover, seeds soaked in 10 ppm GA exhibited significantly higher ( $p \leq 0.05$ ) germination (95.5%) and seedling growth (20.05 mm) compared to other GA treatments. Although seed priming did not improve seed germination in *E. quinquangulare*, pre-chilling the seeds for 20 days resulted in significantly higher ( $p \leq 0.05$ ) seed germination (31.4%) compared to the control (11.7%). This study revealed the potential of selected seed treatments for overcoming inherent hindrance associated with germination and growth in *E. sexangulare* and *E. quinquangulare*, further providing insights for their conservation and sustainable utilization.

**Keywords:** *E. quinquangulare*, *E. sexangulare*, species distribution modelling, seed priming, pre-chilling.



## Determination of the optimum light conditions to cultivate lettuce in indoor hydroponic systems

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World population is increasing rapidly. Research and development of new technologies to assist and improve crop production is absolutely necessary to fulfil the global food demand in the future. Indoor hydroponic cultivation has proven its effectiveness in urban areas in achieving the above. Here Improved, high quality yield can be obtained without the influence of unfavourable climatic conditions. In an indoor hydroponics system, artificial light plays a crucial role in promoting optimal plant growth. Lettuce (*Lactuca sativa*) is a widely cultivated very popular plant grown hydroponically. The objective of this study was to find out the possibility of cultivating lettuce in indoor and optimizing the provided artificial light conditions to obtain maximum yield. Number of 5 combinations of different spectra and intensities of light (L1=White LED, PPFD at  $200 \mu\text{molm}^{-2} \text{s}^{-1}$ , L2 =White: Blue: Red = 1:1: 1, PPFD at  $200 \mu\text{molm}^{-2} \text{s}^{-1}$ , L3=Blue: Red = 1:1, PPFD at  $200 \mu\text{molm}^{-2} \text{s}^{-1}$ , L4 = natural light, L5 = outdoor control) were tested. The plant height, number of leaves, leaf length, leaf width, chlorophyll content, plant fresh weight and dry weight were measured to determine vegetative growth. Statistical analyses were conducted using the R software. One-way ANOVA and the Duncan multiple range test were performed. According to the results, artificial light had significant impacts on growth of height, number of leaves, leaf width, leaf chlorophyll content, fresh weight of lettuce compared to indoor control. When all data obtained for all 5 weeks are statistically analysed and compared, it was very clear that L1(White LED) and L2 (White: Blue: Red = 1:1: 1) provides significantly higher growth and yield compared to others. The highest numerical data were obtained for L2 (White: Blue: Red = 1:1: 1) indicating, it is the best combination for indoor lettuce cultivation.

**Keywords:** Hydroponics, Indoor cultivation, Artificial lighting, Light intensity, Lettuce





## **A preliminary study deciphering the Bacterial Community Structure in Agroecosystems across the main agro-ecological zones of Sri Lanka via High Throughput Sequencing**

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Soil microbial communities play a vital role in plant growth promotion and productivity. Microbial community structure is represented by the composition of microbial communities and the abundances of its members. Chemical and climatic factors alter microbial community structures. This study assessed the bacterial community structure in organic and conventional Agroecosystems across the three main agro-ecological zones of Sri Lanka via High Throughput Sequencing. Soil was obtained from six organic and three conventional farms. The farms located in Nuwara-Eliya, Gammaduwa (organic farms) and Ja-ela (conventional farm) represented the wet zone; Rangala, Badulla (organic farms) and Kurunegala (conventional farm) represented the intermediate zone; Adaichakal, Pallai (organic farms) and Hambantota (conventional farm) represented the dry zone. The bacterial 16S rDNA was extracted from the nine soil samples, the V4 region was amplified in duplicates as a two-step program, purified and sequenced using High throughput sequencing technique. The metagenomic data showed that the bacterial community was composed of 401 different genera with the most abundant belonging to *Bacillus* (35% of the total sequences), *Streptomyces* (10%) and *Staphylococcus* (8%). The wet zone composed of 221 different genera with *Bacillus* (43.94%), *Clostridioides* (6.81%), *Staphylococcus* (6.76%), *Pseudomonas* (4.52%) and *Bradyrhizobium* (4.05%) being the most abundant and representing >65% of its bacterial community. The intermediate zone composed of 209 genera with *Bacillus* (28.07%), *Staphylococcus* (13.22%), *Burkholderia* (9.61%), *Bradyrhizobium* (6.60%) and *Streptomyces* (6.53%) being the most abundant and representing <65% of its community. The Dry zone composed of 266 genera with *Bacillus* (32.66%), *Streptomyces* (16.99%), *Bradyrhizobium* (7.46%), *Staphylococcus* (6.32%), and *Lysinibacillus* (3.34%) being the most abundant and representing >65% of its community. Interestingly, each zone showed dominance in different genera. The wet zone presented the highest abundance of the genus *Bacillus*; the intermediate zone, *Clostridium*; and the dry zone, *Bradyrhizobium*, *Planococcus*, *Anoxybacillus* and *Sporosarcina*. No distinguishable patterns were observed between the organic and conventional farms.

**Keywords:** Bacterial Community Structure, Agroecosystems, High Throughput Sequencing

**Acknowledgement:** Financial assistance from the National Research Council (Grant No 20-128) is acknowledged.



## **Effect of various processing techniques on nutritional, biological, techno functional, structural and molecular interactions of finger millet (*Eleusine coracana*)**

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The impact of different processing techniques on the characteristic changes of finger millet flour was assessed. It provides additional knowledge of the functionality of finger millet and will increase its utilization and potential in the food industry and contribute to better food security. Anti-nutritional factors, *in vitro* protein and starch digestibility and *in vitro* protein bio-accessibility, molecular and structural interactions of soaked, germinated, fermented and a combination of aforesaid treatments of grains were studied. Alterations of processed finger millet's techno-functional properties were determined as water absorption capacity, water solubility index, oil absorption capacity, paste clarity, swelling power, emulsion activity, emulsion stability, and viscosity. Scanning Electron micrographs and Fourier Transform Infrared spectroscopy revealed structural variations and macromolecular arrangement of processed finger millet. Soaking, fermentation, and the treatment combination showed a reduction pattern of tannin and phytate contents. But saponin content was increased ( $p < 0.05$ ) with time in the germinated finger millet sample (2.03 – 2.50%). All bioprocess techniques increased *in vitro* starch digestibility (6.18 to 9.95 g/100 g) and *in vitro* protein digestibility (65.68 to 90.56 g/100 g). Soaking, Germination, fermentation, and treatment combination significantly increased ( $p < 0.05$ ) water sorption isotherm and oil absorption capacity than the control sample and slightly modified the swelling power, emulsion capacity, and emulsion stability of finger millet flour while water absorption capacity, paste clarity and viscosity were decreased. Among all treatments, the combination of soaking, germination, and fermentation greatly improved most of the functional properties of flour with reduced antinutrients. A combination of treatments could enhance the use of finger millet in novel food product development. And the results are suggesting that processed flour could serve as potential ingredients with improved techno and bio functionality in value-added cereal products such as noodles, cookies, biscuits, and muffins.

**Keywords:** Fermentation, Germination, Saponin, Soaking, Tannin



## Improving multiplication rates for cost-effective micropropagation of *Passiflora edulis*

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Supply of quality planting material at a reasonable price is essential for commercial-scale cultivation of *P. edulis*. Normally, passion fruit is propagated vegetatively using stem cuttings. However, this method is inefficient due to low multiplication rates and the spread of viral diseases. Therefore, propagation of *P. edulis* via *in vitro* shoot tip culture was investigated. The specific objectives were to identify optimal BAP level and light quality for *in vitro* multiplication of shoot tips of *P. edulis* var. Horana Gold, and to evaluate low-cost media for micropropagation. Shoot multiplication was tested on Murashige and Skoog (MS) medium with different BAP concentrations (0.00, 3.00, 4.00, 5.00, 10.00 mg L<sup>-1</sup>) and incubated under white LED light. To test the effect of light quality on *in vitro* growth, explants cultured on MS medium with 5.00 mg L<sup>-1</sup> BAP were exposed to white, red, and blue wavelengths of LED light (PPFD of 31.00 ± 1.00 μmol s<sup>-1</sup> m<sup>-2</sup>). Suitability of alternative nutrient sources (half-strength MS, Albert's nutrient media of two different salt-strengths; 5.00 and 7.50 g L<sup>-1</sup>), and gelling agents (sago flour, mung flour, food-grade agar) were tested for culturing *P. edulis* shoot tips. In all experiments, a minimum of 15 replicate culture bottles with four shoots per bottle were maintained in a completely randomized design. After six weeks, mean shoot height, number of shoots and leaves per explant were obtained and the data analyzed using SPSS (Version 22.0). Mean number of shoots per explant was significantly higher ( $P \leq 0.05$ ) on media containing 3.00, 4.00, and 5.00 mg L<sup>-1</sup> BAP (4.0, 4.6, 3.8) than on media with 0.00 or 10.00 mg L<sup>-1</sup> BAP (1.6, 2.4). Shoot tips cultured under red light showed significantly higher values ( $P \leq 0.05$ ) for mean number of shoots (1.9), mean shoot height (3.0 cm), and number of leaves (2.6) than those cultured under blue or white light. MS medium at half-strength could replace full-strength MS medium without significantly affecting growth and multiplication of cultured explants, thus reducing media cost by 50%. However, shoot multiplication was significantly lower ( $P \leq 0.05$ ) on media containing alternative gelling agents compared with phytigel (3.8 shoots per explant). From the results it can be concluded that half-strength MS medium supplemented with 3.00 - 5.00 mg L<sup>-1</sup> BAP can support shoot multiplication of *P. edulis* up to 4.6 shoots per explant and incubation under red light results in better shoot growth.

**Keywords:** *P. edulis* (Passion fruit), shoot tip culture, 6-benzylaminopurine (BAP), red Light-Emitting Diode (LED) light, gelling agent



## **Prediction of new candidate proteins and analysis of protein hubs associated with seed development in *Oryza sativa* using a network-based approach**

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Rice, a vital staple food for most of the world's population, is facing challenges such as low yield and an increasing population that threatens its production. To enhance rice yield and quality, understanding the seed development process is important, though information on important proteins and their interactions underlying rice grain development is lacking. Protein-protein interaction (PPI) network analysis is a powerful approach for studying developmental phenotypes like seed development, but it has not been fully utilized in rice research despite its potential to uncover new findings to improve grain yield and quality. This study aimed to identify novel candidate proteins for rice seed development from a pool of differentially expressed proteins (DEPs) and already annotated seed proteins from literature. From the overall PPI network obtained from the STRING database, the sub-network for seed development was extracted using an ensemble of network-based algorithms. The extracted sub-network was partitioned into modules using the Louvain community detection algorithm. Functional overlap between these modules and known seed development-related pathways was analysed using Gene Ontology analysis. Using the Z-score and partition coefficient, module hubs and inter-modular hubs were identified, respectively. This resulted in the formation of a sub-network with 14 sub-modules representing seed development pathways, which comprised 196 DEPs identified as novel candidates, as well as 95 previously annotated seed development proteins. Among these modules, 17 proteins were identified as module hubs, while 6 proteins were identified as inter-module hubs. These hub proteins are useful as future genetic engineering and genetic breeding targets as they are important for the stability of the grain development subnetwork. Thus, this research provides valuable guidance for future genetic engineering and plant breeding efforts aimed at improving rice grain yield and quality.

**Keywords:** Protein-protein interaction network, Network-based algorithms, Sub-modules, Hubs.



## **Antibacterial properties of essential oil extracted from *Acronychia pedunculata* (Ankenda) leaves and bark**

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The increasing expenses of healthcare due to antibiotic resistance in bacterial species have become a worldwide problem. One solution to this issue is the identification of alternative antibacterial drugs, particularly from natural herbs. *Acronychia pedunculata* (Ankenda), a common medicinal plant in Sri Lankan traditional medicine, has shown promising antibacterial properties, particularly in its leaves and bark. This study aimed to evaluate the antibacterial activity of the Essential oils (EO) extracted from *Acronychia pedunculata* (*A. pedunculata*) against different bacterial species using Agar well diffusion method. Additionally, phytochemical analysis of the EO was conducted using Gas Chromatography-Mass Spectrometry (GC-MS). *A. pedunculata* fresh leaves and bark (intermediate maturity stage) were collected from Gampaha, Sri Lanka, air-dried at room temperature for 5 days, hydro-distilled for 5 hours at atmospheric pressure and subjected to GC-MS. Essential oils extracted from leaves and bark of *A. pedunculata* have been tested for in vitro antibacterial activity against gram-negative *Escherichia coli*, *Salmonella enterica*, and gram-positive *Staphylococcus aureus*, *Staphylococcus epidermidis*. EO from dry leaves resulted in the most effective antibacterial activity against *Staphylococcus aureus* (86.66%) whereas the EO extracted from bark demonstrated its highest inhibition against *Staphylococcus epidermidis* (71.88%) when compared with the control, ciprofloxacin (5 µg/ml). There was no inhibition shown against *E. coli* for both dried leaves bark. EO extracted from dry bark has shown less antibacterial activity than leaves. However, both dried leaves and bark have shown considerable antibacterial activity against gram-positive and negative bacteria. GC-MS analysis showed that most abundant compound present in EO of dry leaves as 1R-alpha-pinene (87.78%), caryophyllene (2.39%) and there were 1S-alpha-pinene (91.5%) and beta-myrcene (2.37%) present in the dry bark. The EO derived from the dried leaves and bark of *A. pedunculata* have demonstrated significant antibacterial properties against various pathogenic bacteria. These findings suggest that *A. pedunculata* has the potential to be used in the pharmaceutical industry to develop effective antibacterial drugs.

**KEYWORDS:** *Acronychia pedunculata*, Agar well diffusion, Antibacterial, Essential oil, Gas Chromatography-Mass Spectrophotometry (GC-MS)



## Morpho-molecular characterization of commercially grown *Pleurotus* spp. in Sri Lanka

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Oyster mushrooms (*Pleurotus* spp.) are commercially cultivated and consumed worldwide for their flavour, high nutritional content, and certain therapeutic characteristics. In Sri Lanka Oyster mushroom cultivation is practiced as a self-employment cottage industry. However, Sri Lanka has a huge potential for export quality oyster mushroom farming gaining the advantage of the low-cost resources readily available within the country but proper species identification is essential prior to cultivation attempts. Therefore, this study aims at characterizing the commercially cultivated *Pleurotus* species in Sri Lanka using morpho-molecular analysis to confirm their species identity. For that, the fruiting bodies of morphologically different oyster mushrooms were purchased and collected from growers in the western province. The morphological features of the collected specimens were recorded. The genomic DNA of the mushrooms was extracted using a modified CTAB method, and the rDNA - ITS fragment of the genomic DNA was amplified using ITS1 and ITS4 primers which were subjected to nucleotide sequence determination followed by Maximum likelihood analysis available at the CIPRES science gateway to generate the phylogenetic tree. It was evident that the close resemblance of different *Pleurotus* species at the fruit body stage is due to changes in environmental factors, the substrate used for cultivation, and cultivation methods. According to the resulted phylogenetic tree, there is considerable species diversity present among the strains of Oyster mushrooms cultivated in Sri Lanka. Molecular characterization confirmed the occurrence of *Pleurotus djamor*, *Pleurotus eous*, *Pleurotus ostreatus*, and *Pleurotus cystidiosus* in Sri Lanka as the most abundant commercially grown species. This study can be used as a pilot study towards developing a sustainable cultivation plan for mushroom cultivation which is assisted by the accurate species identification for commercially growing oyster mushroom species in Sri Lanka.

**Keywords:** Oyster mushrooms, DNA extraction, Phylogeny, *Pleurotus* species, Mushroom cultivation

**Acknowledgement:** Financial assistance from the University of Kelaniya Internal research grant.



## Extraction and characterization of phycobiliproteins from the red alga *Gracilaria hikkaduensis* (Rhodophyta)

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*Gracilaria hikkaduensis* Durairatnam, is an underexplored red seaweed species found in Sri Lanka, which contains phycobiliproteins (PBPs) as their photosynthetic pigments. Phycobiliproteins are vividly coloured water-soluble pigment proteins which have commercial potential in many industries due to their bright hue, availability, and bioactive properties. The present study is aimed at extracting and characterizing phycobiliproteins from *G. hikkaduensis*. Seaweed specimens were collected from the shallow water near to Talpe, Galle, Southern coast of Sri Lanka and taxonomy has been confirmed by studying the morphology. Phycobiliproteins were extracted using an aqueous extract in a 0.1 M phosphate buffer, followed by centrifugation and filtration. The obtained freeze-dried powder was used to calculate the yield. The presence of phycobiliproteins was investigated through the Ultraviolet (UV)-Visible spectrum. Chemical properties, including protein concentration and phycobiliprotein quantity, were determined using Lowry's assay and UV-Visible spectrophotometric absorbance values. The crude phycobiliprotein extract (CPE) has resulted in a yield of 6.09% (w/w of fresh weight) of crude phycobiliprotein and the presence of phycobiliproteins was confirmed by characteristic UV-Visible spectral pattern of phycoerythrin, displaying a trimmer state and absorption peaks at 496, 547, 570 nm wavelengths. Concentration of total protein content calculated as 1.42 mg/g of fresh weight (FW), while individual phycobiliproteins (Phycoerythrin, Phycocyanin, and Allophycocyanin) were measured spectrophotometrically as 0.25 mg/g (FW), 0.14 mg/g (FW) and 0.18 mg/g (FW), respectively. The documented concentrations of total protein and various phycobiliproteins in the extraction highlight the significant availability of phycobiliproteins sourced from *G. hikkaduensis* across multiple disciplines. Ongoing analyses are being conducted to gather data pertaining to the purification and fractionation of the extracted phycobiliproteins.

**Keywords:** Seaweed, *Gracilaria hikkaduensis*, Phycobiliproteins, Phycoerythrin, Phycocyanin



## Study on micropropagation of native shrub *Catunaregam spinosa* (Thunb.) Triveng. in Sri Lanka: Conservation strategy

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Micropropagation is a successful platform for producing new plants using small pieces of plant tissues which are grown under controlled laboratory conditions. The method provides healthy materials and enables to reintroduce plants that have drawbacks in conventional propagation. *Catunaregam spinosa* (Family Rubiaceae) is a native medicinal plant in Sri Lanka with rare abundance yet with crucial pharmacological properties. Conventional constraints such as low reproduction rate and seed desiccation caused by increasing global warming, demand novel strategies to ensure the future sustainability of *C. spinosa*. Seeds, leaves, nodes and internodes of the plant were *in vitro* propagated as an alternative *ex situ* conservation method. Explants were sterilized using 10 % Clorox<sup>®</sup>, 15 % Carbendazim<sup>®</sup> and 70 % ethanol for 10, 15 min and 30 sec respectively each followed by two successive washings in sterile distilled water and cultured in Murashige and Skoog (MS) medium supplemented with (1.0,4.0), (2.0,3.0), (3.0,2.0) and (4.0,1.0 mg L<sup>-1</sup>) concentration combinations of 6-Benzylaminopurine (BAP) and Gibberellic acid (GA<sub>3</sub>) respectively. Completely randomized design was used with ten replicates per treatment. Nodal explants showed highest mean number of leaves (11.2±0.1), highest mean shoot height (4.66±0.25 cm) with 100 % germination in MS medium supplemented with 3.0 mg L<sup>-1</sup> BAP and 2.0 mg L<sup>-1</sup> GA<sub>3</sub> after four months of incubation. Seeds produced seedlings with 3.1±0.12 cm of mean shoot height and 6.89±0.23 of mean leaf number with 60 % germination within two months in the medium supplemented with 2.0 mg L<sup>-1</sup> BAP and 3.0 mg L<sup>-1</sup> GA<sub>3</sub>. Results revealed the potential of *in vitro* germination of seeds for reintroduction of *C. spinosa* through acclimatization before introducing to the natural environment. The developed protocol will facilitate the safeguarding of *C. spinosa* missing from the natural population.

**Keywords:** *Catunaregam spinosa*, conservation, micropropagation, shoots, sterilization

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## Assessing the anthocyanin and carotenoid contents in selected *Phalaenopsis* cultivars

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Flower colour is an important aspect in the floriculture industry. With the changing consumer demand, enhancing the visual appeal and suitability of floricultural crops for market applications is one of the major targets among breeders. In addition to providing aesthetic value for the flower, floral pigments are crucial in insect pollination. The flower colour is determined by several pigments, including chlorophylls, anthocyanins and carotenoids. *Phalaenopsis* is one of the most popular and top-traded genera in the family Orchidaceae. Large flowers in various colours are the most popular in the *Phalaenopsis* market. *Phalaenopsis* flower colouration is in the range of orange to red and is determined by a combination of carotenoids and anthocyanins. Assessing the major pigments in the flowers of selected *Phalaenopsis* cultivars and identifying cultivars with higher pigment contents are important for future breeding programs for cultivar development with diverse colour combinations. Seven self-pollinated *Phalaenopsis* cultivars were selected from the growers considering the demand. Anthocyanin and carotenoid content of powdered floral parts were analysed using UV-spectrophotometer. The data was analysed using SPSS 19 package. The anthocyanin and carotenoid contents ranged from 0.1909 mg g<sup>-1</sup> DW to 14.051 mg g<sup>-1</sup> DW and 1.9455 mg g<sup>-1</sup> DW to 12.016 mg g<sup>-1</sup> DW, respectively. Among the selected cultivars, *Phalaenopsis* cv. Shu Long 'F89322' had shown the highest anthocyanin content (14.0351 ± 0.23753 mg g<sup>-1</sup> DW), while *Phalaenopsis* cv. Golden Sands 'Canary' had the highest carotenoid content (12.1016 ± 0.25763 mg g<sup>-1</sup> DW). The two cultivars, *Phalaenopsis* cv. Shu Long 'F89322' and *Phalaenopsis* cv. Golden Sands 'Canary' can be recommended as potential parents in future breeding programmes for cultivar improvement.

**Keywords:** Anthocyanins, Carotenoids, *Phalaenopsis* cultivars, Floral pigments, Floriculture

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## ***In silico* analysis of genes differentially expressed in fruits of black pepper (*Piper nigrum* L.)**

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The pungency of black pepper (*Piper nigrum* L.) fruits is primarily attributed to the presence of piperine. Until now, only a limited number of studies have investigated the underlying genes involved in black pepper fruit development. Thus, the present study aimed to identify and characterize genes differentially expressed in fruits of black pepper using a range of bioinformatic tools. Transcriptomes of eight different tissues of black pepper (root, stem, leaf, and flower tissues and berries at four different developmental stages) were retrieved from a previously published dataset (BioProject number: PRJNA529760). A total of 1,493 genes with  $|\log_2 \text{ Fold Change}| \geq 2.0$  of expression between berries and other tissue samples were considered as differentially expressed genes in berries ('berry-specific (BS)-genes'). K-means clustering of expression profiles of these genes identified two clusters with different expression patterns, shedding light on gene expression changes in the early and later black pepper fruit development. Functional enrichment analysis showed that BS-genes may be involved in various biosynthetic and metabolic processes, including phenylpropanoid, terpenoid, flavonoid, isoquinoline alkaloid, tropane, piperidine and pyridine alkaloid biosynthesis. Protein-protein interaction (PPI) network analysis of proteins encoded by BS-genes identified distinct clusters and 55 hub proteins. Integrated analysis of conserved domain architectures, PPI networks, and functional enrichment identified 129 BS-genes that may be involved in the regulation of piperine biosynthesis including 24 genes from isoprenoid biosynthesis C1 superfamily, 14 from cytochrome P450 superfamily, 02 from glycosyl hydrolases family 32, 03 from glycosyltransferase GTB-type superfamily, 18 from AdoMet-dependent methyltransferases family, 05 from terpene cyclase plant C1 family, 01 from terpene synthase C family and 02 from WRKY family. These genes could provide novel insights into the fruit development and biosynthesis of piperine in black pepper. However, further studies are necessary to validate the roles of these genes, as many of them remain functionally uncharacterized.

**Keywords:** Black pepper, Fruit development, Transcriptomes



## ***In silico* prediction and analysis of transcription factors in black pepper (*Piper nigrum* L.)**

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Prediction of transcription factors (TFs) and their binding sites is crucial for understanding gene regulation. Experimental identification of TFs is expensive and time-consuming. Therefore, computational methods for predicting TFs have become increasingly valuable in recent years. The present study aimed at predicting and analyzing the full complement of TF-encoding genes in the black pepper (*Piper nigrum* L.) genome based on the Hidden Markov Model (HMM) profiles of DNA-binding domains (DBDs). HMM profiles of conserved DBDs from 62 distinct TF families were used to scan the proteome of black pepper with the HMMER tool. This resulted in 2,503 putative TF-encoding genes (herein PnTFs) in the black pepper genome. These PnTFs were further analyzed to determine their physicochemical properties, subcellular localizations, gene structures, genomic distribution, distribution of regulatory elements in their gene promoters, and protein-protein interaction (PPI) networks. The majority of PnTFs were found to be localized in the nucleus, and the members of PnTF families were distributed randomly throughout the genome. As expected, functional enrichment analysis revealed that most PnTFs were involved in DNA-templated regulation of transcription. Interestingly, 471 intronless PnTFs were identified; more than 50% of the members of the Dof, ERF, GeBP, GRAS, NF-YB, RAV, TCP, Trihelix, and ZF-HD TF families were intronless. Additionally, most of the members of PnTF families contained stress-responsive elements in their promoter regions. Furthermore, analysis of PPI networks of PnTF families identified 171 hub PnTFs that may play vital roles in regulating multiple biological processes. Collectively, the findings of this study provide insights for further experimental characterization of the predicted PnTFs and their potential roles in regulating important biological processes in black pepper. Moreover, the predicted TF-encoding genes and their interactions can serve as a valuable resource for genetic crop improvement in black pepper and related crops.

**Keywords:** Black pepper, Transcription factors, Genome-wide analysis, HMM profiles



## Evaluation of fungicidal effects of selected plant extracts for controlling Leaf Blight Disease in coconut

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Leaf blight disease is one of the main fungal diseases, caused by *Pestalotiopsis palmarum* reported to be lethal to coconut palms. With the application of several chemical fungicides, disease could be controlled but the hazardous impacts of such products in human health and environment are well known. Natural plant products have been effective and could be safely incorporated as suitable alternatives for synthetic fungicides. In an approach toward the development of eco-friendly antifungal compounds for controlling leaf blight disease, crude aqueous plant extracts of 20 plant species were preliminary screened to identify the most effective extracts using the percentage of inhibition (PI value) that was calculated based on the 7<sup>th</sup> day radial growth of fungus. The major phytochemical compounds were investigated within the selected extracts. The evaluation of antifungal properties was followed for the dilution series to determine the most effective and economical concentration at which they exhibited maximum efficacy for the practical use. The synergistic effect of the selected plants was investigated by preparing cocktail solution. Determination of antifungal efficacy was performed using food poisoning technique. Experiments were arranged in complete randomized design with six replicates and the data was statistically analysed using ANOVA. Presence of tannins, alkaloids, flavonoids and terpenoids in extracts were found to have antifungal properties effective in suppressing fungal growth. *Clitoria ternatea*, *Piper nigrum*, *Citrus aurantiifolia*, *Tamarindus indica* and *Helianthus annuus* extracts exhibited the maximum antifungal potential at 100% concentration. *Alstonia scholaris* was most effective at 10% concentration, while *Allium sativum*, *Allium cepa* L. and *Aloe vera* were most effective at 0.1%. Furthermore, *Zingiber officinale* showed the highest potential at 0.01% and *Curcuma longa* at 0.001%. The cocktail solution exhibited maximum antifungal potential at 0.001% enhancing its efficacy with the maximum synergistic effect. (P<0.03) Further studies are underway to isolate and characterize the active ingredients in these extracts.

**Keywords:** Minimum inhibitory concentration, Maximum antifungal potential, Plant extracts, PI value, Phytochemicals

**Acknowledgement:** Financial assistance provided by Coconut Research Institute, Sri Lanka.



## **A study on fungal endophytic communities of wild rice species in Sri Lanka as a potential source of biocontrol and growth-promoting agents**

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Fungal endophytes confer many beneficial properties to the host plant and are transmitted to subsequent generations of plants. Wild relatives of rice and its microbiome could serve as a genetic pool that could be used as a biotechnological tool to improve commercial rice cultivation. Thus, this study was focused on the isolation of fungal endophytes from wild rice species in Sri Lanka, evaluate their potential antagonism against sheath blight caused by *Rhizoctonia solani* and the ability to produce Indole-3-Acetic Acid (IAA). Fungal endophytes from wild rice plants (*Oryza nivara* and *O. eichingeri*) collected from 3 different sites in the dry and intermediate zones of Sri Lanka were isolated during this study. A total of 192 putative fungal isolates were obtained, out of which 64 were classified into 20 morphotypes based on their morphological characters such as colony shape, colour, and the growth rate. The occurrence of endophytic fungi in each sampling part was determined using the frequency of colonization (FC%) and the relative abundance (RA%) of the isolates. Furthermore, 12 isolates of different morphotypes were selected and their antagonism against *R. solani* (ITCC No. 6491) were determined *in vitro* using dual culture assay and their IAA production ability was screened. According to the results, *Oryza nivara* plant samples had the highest diversity of fungal endophytes with morphotypes 2, 10, 13 and 20 equally having the highest RA% (6.25%). Isolate WRA 001 showed the highest percentage inhibition (76.3%) of *R. solani*. Out of the 12 isolates 5 were found to produce IAA in culture and isolate WRA 001 produces the highest (106.68 µg/mL). The study carried out thus far has shown that the putative fungal endophytes isolated from wild rice can be used to control rice sheath blight and as a growth-promoting agent due to their ability to produce IAA.

**Keywords:** Endophytes, Wild rice, Biocontrol, Sheath blight, Indole Acetic Acid



## Antioxidant activities of lichen-associated fungi of mangrove ecosystems in Sri Lanka

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Most synthesized antioxidants have cytotoxic or carcinogenic effects. Thus, there is a very high demand for naturally occurring antioxidants. The less explored lichen inhabiting fungi associated with mangrove ecosystems are bound to exhibit potent antioxidant activities due to the strenuous environment they inhabit. Hence, this study was conducted to determine the antioxidant potential of lichen-associated fungi in a mangrove environment. Seventeen lichen samples were collected from NARA Regional Research Centre, Kalpitiya in Sri Lanka (8.25° or 8° 15' North latitude, 79.7707° or 79° 46' 15" East longitude). Among them nine samples were fruticose (*Rocella* spp.), and the rest were crustose lichens. Lichen-associated fungi were isolated by plating surface-sterilized thallus pieces onto water agar medium and subsequent hyphal tip transfer. A total of 121 putative fungal isolates were obtained and coded for convenience. Colony characteristics and micromorphology of the pure cultures of the fungi were noted. Crude extracts were prepared from 33 isolates using ethyl acetate (EtOAc) as the solvent. The antioxidant activity of crude extracts was tested using 2,2-diphenyl-1-picrylhydrazyl (DPPH) radical scavenging assay with 0.25 mM methanolic DPPH solution in a flat bottom 96-well microtiter plate. Using the optical density values, the scavenging concentration at 99% inhibition (SC99) of crude extracts was calculated and compared with the SC99 of Ascorbic acid. Isolates LIF1211, LIF1501, LIF1312, LIF1504, and LIF1514 showed promising antioxidant activities. Out of those, extracts of LIF 1211 isolated from *Rocella* sp. and LIF 1501 from unknown crustose with SC99 value of  $5.34 \pm 0.43$  and  $5.39 \pm 0.20$  mg/mL, respectively showed comparatively higher radical scavenging activities. According to the two sample t-test, these SC99 values were significantly different ( $p < 0.05$ ) compared with that of the positive control, ascorbic acid (SC99  $3.40 \pm 0.40$  mg/mL). From molecular identification by DNA barcoding through Internal Transcribed Spacer (ITS) sequencing, LIF 1211 was identified as *Daldinia eschscholt*. Therefore, this study proved that lichen-associated fungi of mangrove ecosystems are one of the less explored groups of microbes with high potential antioxidant activities. Moreover, studies are required to identify the other best fungal isolates that show the highest radical scavenging activities, determine the compounds with antioxidant properties and screen the putative agents against a standard.

**Keywords:** *Daldinia eschscholt*, Bioactivities, DPPH assay, Radical scavenging ability, *Rocella* sp.



## Anti-fungal activity of secondary metabolites extracted from endophytic fungal isolates of *Plumeria rubra* leaves.

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Endophytes are symbiotic microbes that reside within a host plant while providing them with certain advantages. The benefits conferred by host plants are reported to be as results of the secondary metabolites (SMs) produced by the endophytes. These SMs are known to possess beneficial biological properties including anticancer, antibacterial, antifungal, insecticidal, antiviral, and antioxidant. The current study was conducted to investigate the anti-fungal effects of SMs produced by endophytic fungi isolated from *Plumeria rubra* leaves against a potential pathogenic fungus isolated from diseased leaves of *Epiphyllum oxypetalum*. Of the isolated 5 endophytes, three colonies were selected based on morphological and growth characteristics and presence of secretions for further investigations. Extracted SMs of each endophyte were used to conduct anti-fungal assay at concentrations of 10,000 µg/mL, 1000 µg/mL, 100 µg/mL, 10 µg/mL and zones of inhibition were measured at each 24-hour time interval. Phytochemical detection assays were conducted to evaluate the presence of saponins, flavonoids, tannins, terpenoids, steroids and phenols. Statistical analysis of the obtained results was carried out using R-studio version 4.2.3. The growth rates of the endophytes were recorded as PL1C- 0.25 cm/day, PL2C- 0.14 cm/day and PL3C- 0.56 mm/day. Although zones of inhibition were recorded in both secondary metabolites PL1C and PL2C, only PL2C SM showed significant anti-fungal activity at 10 µg/mL and 100 µg/mL concentrations ( $p < 0.05$ ). Also, PL2C SM showed positivity for the presence of flavonoids, saponins, terpenoids and steroids, whereas the remaining two SMs showed negative results. Thus, secondary metabolite of PL2C isolate has the potential to be utilized as an inexpensive, and effective anti-fungal agent for disease causing fungi in economically important plants. Further validation of the SM, on shelf life and other beneficial effects on the crops, would result in a natural product which would support towards much needed local economic prosperity.

**Keywords:** endophytic fungi, *Plumeria rubra*, secondary metabolites, phytochemicals, anti-fungal

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## **Predicting the structure and active site of a putative xylanase in *Mycobacterium tuberculosis*.**

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Tuberculosis is one of the most common diseases that causes many deaths around the world. As a result of the continuous evolution of *Mycobacterium tuberculosis*, some novel strains show high resistance to most anti-TB drug therapies. Antibiotic resistance associated with *Mycobacterium tuberculosis* can be resolved by the development of anti-virulence drug targets. The MarR gene family is one of the major transcriptional regulation families in *Mycobacterium tuberculosis*, and this family mainly contributes to controlling several bacterial responses, such as bacterial virulence. The regulator Rv 3095 which was identified as a virulence gene regulator, mainly regulates the expression of Rv 3096 gene that codes for a putative xylanase enzyme. The main objective of this study is to determine the structure and active site of the putative xylanase enzyme. Molecular docking was conducted to identify possible antibiotic ligands that can block the active site of putative xylanase enzyme. The FASTA sequence of Rv 3096 was downloaded from the NCBI database, and the structure of the protein was predicted by using alpha fold and Robetta fold protein prediction servers. The active site of the Rv 3096 protein was determined by using CoachD active site prediction server. The molecular docking was done by using PyRx software, and ligand libraries were downloaded from the Zinc 15 database. The structure of the N-terminal end of the protein was predicted by both protein prediction servers with high confidence levels. However, both protein prediction servers were unable to predict the structure of the C-terminal end of the protein with high confidence levels. The pocket which has the highest C score is considered an active site of the predicted protein. In the virtual screening, the highest binding affinities to the active site of the xylanase enzyme were recorded by drug ligands that belong to the penicillin and doxycycline drug groups.

**Keywords:** *Mycobacterium tuberculosis*, Rv 3096 protein, MarR gene family, Bacterial virulence, Virtual drug screening

**Acknowledgement:** Financial assistance by the Department of Zoology and Environment Sciences, University of Colombo.





## Anti-hypertensive, anti-diabetic and anticancer potential of selected edible flowers available in Sri Lanka

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Edible flowers have recently gained popularity as sources of antioxidants. Though they are being consumed in various forms, bioactives entering the body from edible flowers undergo physical and chemical changes upon gastro-intestinal digestion, which influence their bioactivities. In Sri Lanka, though the use of edible flowers were in prevalence, only a narrow spectrum of flowers has been investigated up to date and there are no ample scientific evidences about the digestive recovery of bioactives from these flowers. To investigate anticancer property and the impact of gastro-intestinal digestion on the content of bioactive compounds, anti-hypertensive activity and anti-diabetic activity of selected species of edible flowers in Sri Lanka. Ethanolic extracts (EE) and *in-vitro* digested fractions (DF) of eight flowers were evaluated for their total phenolic, total flavonoid contents, anti-hypertensive activity (angiotensin converting enzyme [ACE] inhibitory assay) and anti-diabetic activity ( $\alpha$ -amylase and  $\alpha$ -glucosidase inhibitory assay). For each assay a control was prepared by replacing the sample with the solvent or phosphate buffered saline. Sulphorodamine-B assay was used to measure the cytotoxicity of the EE on 4 cancer cell lines (Heptocarcinoma, lung carcinoma, oral carcinoma and colon carcinoma cell lines). Individual phenolic compounds present in the EE and DF were quantified using high performance liquid chromatography-mass spectrometry. SPSS software was used for statistical calculations, and the mean separation was carried out using Turkey's multiple variance test. Chromatographic results reveal that kaempferol-3-O-glucoside and apigenin was detected in all raw flower extracts. The highest bioaccessible phenolics and flavonoids were observed in *Hibiscus rosa-sinensis* (85.93%) and *Ocimum sanctum* (85.08%) respectively. Highest  $\alpha$ -amylase ( $2.20 \pm 0.14\%$ ) and  $\alpha$ -glucosidase inhibitory ( $49.77 \pm 0.56\%$ ) activity after dialysis was expressed by *O.sanctum* flowers. After dialysis ACE inhibitory activity of the samples were in the range of  $11.53 \pm 0.43$  to  $47.96 \pm 0.32\%$ . *Calendula officinalis* flowers exerted the most potent anticancer activity against oral carcinoma cells after 48 h of treatment ( $IC_{50}$ : 40ppm). In conclusion, investigated edible flowers are good sources of bioactive compounds with significant bioactivities and are able to retain the bioactivities after digestion.

**Keywords :** Anticancer, anti-diabetic, bioactives, edible flowers, *in vitro* digestion

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## Antifungal susceptibility of *Candida* isolates from cancer patients

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*Candida* species cause systemic Candidiasis, leading to high morbidity and mortality. In recent years, experience in increasing resistance of *Candida* species to antifungal agents and antifungal drug resistance is becoming a major problem in effective management of immunocompromised cancer patients in Sri Lanka. If a rapid and effective methodology to test drug susceptibility pattern is available, it allows clinicians to use the most appropriate antifungal agent in-order to decrease the mortality and morbidity rates of their patients and thereby decrease antifungal resistance. In this study, 52 *Candida* isolates collected and identified from cancer patient at the Apeksha Hospital, Maharagama, Sri Lanka were employed to antifungal susceptibility testing using the disk diffusion method on Mueller-Hinton agar medium. The testing was carried out in accordance with the CLSI guidelines (CLSI document M44-A) and the manufacturer's instructions (HiMedia Laboratories). Six antifungal drugs, including Fluconazole, Itraconazole, Clotrimazole, Miconazole, Ketoconazole, and Amphotericin B, were utilized in the susceptibility testing. Out of the 52 *Candida* isolates analysed, 41 isolates were resistant to Amphotericin B and only two of the *Candida* isolates resistant against Fluconazole. Thus, according to this study Fluconazole (96.15%) was the most susceptible drug against *Candida* isolates and Amphotericin B (0%) was the least susceptible drug. Ketoconazole (23.08%), Clotrimazole (21.15%), Itraconazole (38.46%) and Miconazole (82.69%) showed varying degrees of susceptibility depending on the *Candida* isolates. The study concludes that Fluconazole is the best antifungal drug against *Candida* infections, while caution is advised when considering Amphotericin B as a treatment option due to low susceptible rates. Clinicians can use these findings to better manage *Candida* infections.

**Keywords:** Antifungal drugs, Susceptibility, Fluconazole, Amphotericin B, *Candida* isolates

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## Antibacterial and anti-inflammatory activities of a polyherbal formulation based on traditional Sri Lankan medicine for diabetic wound healing

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Diabetic wounds are a global health issue that has affected many populations worldwide owing to its severity, slow recovery, and economic burden. Despite the considerable efforts made in its treatment, they remain a challenge in many nations partly due to its last-resort treatment of lower-leg amputations, which is burdensome to patients in the long-term. Therefore, the rationale of this study was to explore a topical application prepared in traditional Sri Lankan medicine as a natural and more cost-effective alternative treatment for diabetic wounds. The topical application (TA) was prepared into two extracts, TA water and TA oil, and this study aimed to analyse the wound healing potential of the extracts by means of their antibacterial and anti-inflammatory activities. The antibacterial activity of both extracts was determined by performing a disk diffusion assay against four skin pathogens that inhabit diabetic foot, namely *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Streptococcus spp.*, and *Escherichia coli* with tetracycline antibiotic as the positive control to obtain the diameter of the zones of inhibition. The anti-inflammatory activity of TA water was determined using the albumin denaturation method with reference to the known NSAID, Ibuprofen to obtain the percentage inhibition of protein denaturation, which was further assessed using IC<sup>50</sup> values (GraphPad Prism 9.5.1). The findings indicated that both extracts possessed sufficient antibacterial potential against all four bacteria. However, in comparison to tetracycline, the antibacterial activity of the extracts against *Pseudomonas aeruginosa* was greater than that of *Staphylococcus aureus*, *Streptococcus spp.*, and *Escherichia coli*. Moreover, TA water possessed the highest anti-inflammatory activity at a 0.1 dilution (143.75 mg/ml) of the concentrated extract (1437.5 mg/ml), which was comparable to that of Ibuprofen (40 mg/ml), and its effectiveness was further confirmed by its IC<sup>50</sup> value (5.14 mg/ml). Therefore, the study concluded that the topical application prepared possesses substantial antibacterial activity and anti-inflammatory activity validating its potential use in diabetic wound healing.

**Keywords:** Traditional Sri Lankan medicine, Diabetic wounds, Topical application, Antibacterial activity, Anti-inflammatory activity



## **Evaluation of the contribution of facultative anaerobes for domestic biogas production: A microbial approach**

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Despite the existence of biogas technology in Sri Lanka for several decades, its adoption at the domestic scale remains limited and challenging. Analysing facultative anaerobes (FA) involves standard microbiological methods, while strictly anaerobes (SA) require specialized methods due to their sensitivity to oxygen. The aim of this study is to explore the feasibility of enhancing domestic biogas production through the utilization of FA as a low-cost approach with the prevailing economic difficulties. During the biogas generation stage, a substrate was thoroughly examined and characterized. Subsequently, colonies displaying significant abundance were isolated, and cultured using aseptic techniques. The experimental setup comprised two medium-scale laboratory reactors (10 L each). One reactor served as the control and contained cow dung, while the other reactor included cow dung supplemented with cultured FA. Three replicates were employed for each treatment to ensure the accuracy of the results. The reactor utilizing cow dung as the substrate produced biogas with a methane composition ranging from 51% to 55% and a mean flame time of 3.7 seconds(s) from a 50 ml volume of biogas. Conversely, the reactor employing cow dung supplemented with cultured FA substrate generated biogas with a slightly higher methane composition, ranging from 55% to 58% and exhibited a mean flame time of 3.6 seconds(s) from the same 50 ml volume of biogas. The observed differences in methane composition and mean flame time between the two types of reactors are relatively small ( $P > 0.05$ ). It can be concluded that the presence of SA is crucial for efficient biogas generation. Consequently, the study suggests that basic microbial techniques may not be effective in significantly improving methane production on a domestic scale and further studies regarding anaerobic behaviour are required. From an economic perspective, the observed level of improvement may not have a substantial impact on the overall cost-effectiveness of biogas production.

**Keywords:** Cow dung, Culture media, Flame time, Methane composition, Substrate

**Acknowledgement:** Financial assistance and the laboratory facilities provided by the Department of Zoology & Environment Sciences, University of Colombo is acknowledged.



## **The Last Laugh: Could an evolutionary-plastic cytochrome oxidase subunit II enzyme from the cyanobiont of *Azolla pinnata* be a contender to better control Nitrous Oxide released from paddy fields?**

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Cyanobacteria are not equipped with nitrous oxide reductases (NosZ enzymes) but the *Trichormus azollae* cyanobiont of *Azolla* has a plastic cytochrome oxidase subunit II enzyme (WP\_013192178.1) that is hypothesized to be a factor for the conversion of nitrous oxide into di-nitrogen gas, acting as a sensor, a catalyst and a transcription factor. Nitrous and nitric oxides are known to bind to cytochrome oxidase subunit II enzymes, which share marked sequence homology with the NosZ counterparts. To shed insight on this unprecedented biology, the author used PCR to amplify full length open reading frames of homologs of the WP\_013192178.1 in the major cyanobiont of *Azolla microphylla* (TA-CoxM), a northern hemisphere *Azolla* species, and *Azolla pinnata* (TA-CoxP), the predominant *Azolla* plant of urea-opulent Asia. Both PCR products when sequenced and translated using the ExPasy Translate tool, showed key transformative mutations, none more so than twin mutations of a putative DNA-binding, glycine-rich, structurally-disordered loop region, to a motif enriched in Alanines, only in TA-CoxP. Alanine-rich low complexity regions (LCRs) are known for neo-functionalization, such as gifting a DNA binding loop a mechanism to be a transcription factor. A serine to tyrosine mutation (S160Y) - a substitution mutation - is found in the region with the highest structural disorder, perhaps acting as a candidate for NO-dependent site specific nitration. NO or N<sup>o</sup>O or both may be signaling molecules acting on an emerging, periplasmic, sensory Y\_Y\_Y domain identified by bioinformatics. 60% of anthropogenic nitrous oxide is produced from agriculture lands and urea may well be the trigger for the evolution of a new NO or N<sup>o</sup>O sensitive transcription factor within the cyanobiont of *Azolla pinnata*. What genes are influenced by the TA-CoxP transcription factor are not known, and pathway of converting nitrous oxide to dinitrogen gas is proposed to include TA-CoxP, partner and regulatory proteins.

**Keywords:** Nitrous Oxide, *NosZ* gene, cytochrome oxidase subunit II enzyme, nitrous oxide reductase, climate change



## Studying the microbial community interactions of Sri Lankan milk microbiota for different cattle breeds

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Since the early 1940s, the global dairy industry has been ever-improving due to technological advancements, especially since the inclusion of genomics. In Sri Lanka, local dairy production is increasing yearly, but still only meeting around 45% of market demand. Most cattle in Sri Lanka are European and their cross breeds prevalent in mid-country farms. Indian and local breeds are equally distributed across the country. For the first time in Sri Lanka, Industrial Technology Institute conducted a 16S rRNA gene sequencing on 82 Sri Lankan milk samples collected from 18 different farms representing 03 different agro-climatic zones. These data were used in our study to construct microbial co-occurrence networks, to identify keystone genera, and to study the pathogen distribution across milk samples of different cattle breeds. SparCC, a correlation-based association measure was used to estimate the co-occurrences between taxa. All the network constructions, analysis, and comparisons were done using the NetCoMi package in R programming language. The 03 microbial co-occurrence networks that were constructed contained 17 clusters altogether. Some of these clusters were enriched with different bacterial genera performing similar functions in the natural environment. For the first time, targeting microbial data, an enrichment analysis tool was developed using Fisher's exact test to validate these findings. Constructed networks were subjected to identification of keystone taxa and their functions in the milk microbial community. According to pathogen distribution analysis, 75% of Asian breed network clusters indicated the presence of pathogenic genera; therefore, it is safe to speculate that the milk produced by European cattle breeds is a healthier option for human consumption. The pipeline developed in the present study lays the foundation for numerous future studies to be conducted on Sri Lankan milk microbiota using different variables such as farm size and cleanliness.

**Key words:** co-occurrence networks, keystone genera, cluster analysis, enrichment analysis, pathogens



## **Isolation and characterization of pigmented bacteria from the Phycoplane of the marine alga *Padina minor* Yamada (Phaeophyta), with special emphasis on UV-blocking and antioxidant properties of their pigments**

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The concept of 'seaweed-bacteria holobiont' has gained interest in the scientific community due to the importance of their interaction in seaweed-based industries. Sri Lanka, being an island with limited scientific exploration, provides ample opportunity to study the phycoplane-associated bacterial communities. Therefore, the present study was aimed at isolating pigmented phycoplane bacteria from a common brown seaweed, *Padina minor* Yamada, and investigating the antioxidant and ultraviolet radiation (UVR) blocking activities of the bacterial pigments to have a better understanding of host-bacterial interactions. Six different phycoplane bacteria were isolated with vibrant color profiles using the dilution spread plate method. They were morphologically characterized using Gram staining, cell morphology, and colony morphology tests, while biochemical characterization was carried out by evaluating 11 different biochemical parameters. Methanol (99.5%) was used to extract their pigments from three selected isolates by incubating harvested cells with the solvent overnight. The antioxidant activity of crude pigments was tested using the 2,2-diphenyl-1-picrylhydrazyl (DPPH) assay. The sun protection factor (SPF) for three crude extracts was calculated using the Mansur equation (1986), with their absorbance readings ( $p$  value < 0.05) ranging from 290 to 320 nm. All the pigment samples demonstrated antioxidant activities ( $p$  value < 0.05), while 678f showed the highest antioxidant activity ( $IC_{50} = 0.7276 \pm 0.001$  mg/mL). All three pigment samples displayed significant SPF values even at low concentrations (0.1 mg/mL). Among them, 456d showed the highest SPF value ( $2.548 \pm 0.001$ ). While having better UV-protective properties, algae may need their bacterial partner for their survival, and with lower antioxidant activity, bacteria may need their algal partner for their survival. This study sheds light on the seaweed-bacteria holobiont concept, and these pigments hold promising potential in the textile, cosmetic, and pharmaceutical industries with their antioxidant and UV-blocking abilities.

**Keywords:** effective concentration, epiphytic bacteria, free radical scavenge, phycosphere, UV filters



## Isolation and molecular identification of *Listeria monocytogenes* serotypes from raw milk collected from Polonnaruwa District, Sri Lanka.

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*Listeria monocytogenes* is an opportunistic food-borne pathogenic bacterium causing listeriosis among humans. *L. monocytogenes* contamination of milk and dairy products is a significant issue for the entire world, including Sri Lanka. Because *L. monocytogenes* can multiply in both ambient and chilled temperatures, making even the existence of small amounts of this bacterium is dangerous. The main goal of this study is to identify and determine the abundance of different serotypes of *L. monocytogenes* contamination in raw milk in Polonnaruwa District to focus on the safety of dairy products and disease prevention. Specific objectives are to identify the contamination of *L. monocytogenes* isolates found in raw milk samples from the Polonnaruwa District, and common serotypes using PCR technique. First raw milk samples were collected from four areas of Polonnaruwa District and bacterial isolates were isolated using *Listeria* selective growing culture media. DNA was extracted from isolated bacterial colonies using Wizard genomic DNA extracted kit. A nested PCR test was conducted for molecular identification. Then multiplex PCR was conducted for positive samples from identification PCR to identify serotypes. From eighty samples ninety-eight bacterial strains were isolated. Out of eighty, thirty-seven samples were positive for *L. monocytogenes* (46.25%). When considering serotypes, 7.5% of 1/2a, 15% of 1/2b, 10% of 1/2c and 32.5% of 4b were found. The percentage of *Listeria monocytogenes* contamination in raw milk from Polonnaruwa District is 46.25%. Serotype 4b, which is mostly responsible for *Listeria* related food borne diseases, shows the highest percentage of contamination (32.5%). And next highest percentage of contamination is shown by 1/2b serotype and this serotype also commonly cause to the listeriosis. Hence it is important to take effective measures to avoid raw milk contamination by *L. monocytogenes*.

**Keywords:** *Listeria monocytogenes*, Milk, Nested PCR, Serotyping, Polonnaruwa

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## Diversity of fungal endophyte morphotypes of Mangrove plant *Avicennia marina* in the Puttalam Lagoon, Sri Lanka.

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Mangrove ecosystems have unique environmental conditions characterized by high temperature, high salinity, tidal waves and waterlogged and anaerobic soils. Thus, the mangrove flora and the mycobiota inhabiting these extreme conditions are considered unique with characteristics that enable them to survive in these environments. The study aimed to isolate and characterize fungal endophytes from *Avicennia marina* plants in the National Aquatic Resources Research and Development Agency-Kalpitiya (NARA) site located in the Puttalam lagoon, Sri Lanka. During the study, fungal endophytes were isolated from leaves, stems and root samples of three *A. marina* plants collected on 28th December 2021. The three plants were located within the intermediate zone of the lagoon (2 m, 12.1 m and 18 m from the lagoon water level). Plant segments were surface sterilized and placed on Potato Dextrose Agar (PDA) medium. The resulted putative endophyte isolates were purified via tip purification and separated into 13 morphologically distinct isolates. The highest number of morphotypes (11) was identified in plant leaves and the diversity indices Simpson's Index and Shannon - Weiner Index were 0.20917 and 0.585671 respectively. A single isolate, AV001, dominated *A. marina* plants with an 84% relative percentage occurrence. Root endophyte morphotypes were tested for their abiotic stress tolerance. Under salinity (PDA medium infused with NaCl) and simulated drought stress (PDA medium infused with PEG) conditions, morphotype AV001 did not show a significant change in growth rate in a wide range of salinity and drought stress conditions, indicating its ability to tolerate similar stress conditions. Based on the preliminary analyses, a number of putative mangrove fungal endophytes with antifungal, antibacterial and antioxidant properties, were identified, using dual culture method, agar well diffusion method and DPPH assay respectively. In addition, 3 fungal morphotypes were identified to have the ability to produce protease enzymes and one isolate with the ability to solubilize phosphate in Pikovskayas medium.

**Keywords**–Fungi, Endophytes, *Avicennia marina*, Diversity, Puttalam Lagoon



## **Extracellular enzymatic activities of halophilic fungi in Kalpitiya area of Puttalam Lagoon, Sri Lanka**

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Halophilic fungi are those which can thrive, survive, grow and reproduce in environments with extreme salt concentrations. Halophilic fungi have become an area of interest for research due to the potential biotechnological applications of their secondary metabolites. However, research related to halophilic fungi is still novel to Sri Lanka. This study was conducted with the aim to reveal the extracellular enzymatic activities of halophilic fungi isolated from the Kalpitiya area of Puttalam lagoon in Sri Lanka (8°15' N 79°46' E). Fungi were isolated from the soil, sediment and water samples collected from the Kalpitiya area of Puttalam lagoon in Sri Lanka using the serial dilution method on alkaline potato dextrose agar medium. Among them, thirty one isolates were screened for extracellular enzymatic activities including cellulase, lipase, laccase and L-glutaminase. Fungi were screened for extracellular enzyme activities by inoculating them on a specific substrate medium (carboxymethylcellulose for cellulase, Tween 20 for lipase, tannic acid for laccase and L-glutamine for L- glutaminase). Enzyme activity was calculated using the enzymatic index (EI). The normality of the data was tested by Shapiro-Wilk test and mean enzymatic indexes were analyzed by one-way ANOVA with the SPSS program version 26. Positive cellulase activity was observed as yellow colour zone around the colony in 19 isolates. Among them, 11 isolates exhibited a higher enzymatic activity (EI >2). Twenty-four isolates showed opaque precipitate around the colonies, and they were recorded as positive for the lipase activity whereas 11 isolates showed higher activity with Enzymatic index greater than two. In 5 isolates, the production of laccase was observed as yellow brown colour zones around the colonies. Out of these, two isolates demonstrated a higher enzymatic index greater than two (EI>2). L- glutaminase production was detected in 4 isolates with reddish-pink zones around the colony and their L-glutaminase production was quantitatively determined. The highest L-Glutaminase activity was recorded as 4.63U/mL by a fungal isolate extracted from the lagoon water sample. Accordingly, these results provide evidence for the potential of halophilic fungi to be used as better candidates for various biotechnology-based industries.

**Keywords:** Cellulase, Extra-cellular enzymes, Halophilic fungi, L-glutaminase



## ***In vitro* evaluation of the antioxidant activity of selected fungal endophytes isolated from two species of family Pandanaceae in Sri Lanka**

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Fungal endophytes are a group of organisms, which inhabit plant tissues, rendering various benefits to the host plants, without causing any apparent signs of infection during their life cycles. They are important sources of natural bioactive products as they occupy unique biological niches found in different types of environments. This study focused on the antioxidant activity of 30 selected fungal morphotypes isolated from the foliage of two selected plant species of the family Pandanaceae, i.e. *Pandanus odorifer*, *P. thwaitesii* from coastal areas of north western Province, Sri Lanka. The identities of the plants were confirmed by the standard authentication process with the Peradeniya herbarium. Fungal endophytes were isolated from healthy leaves according to a published protocol. The fungal cultures were allowed to grow in Czapek-Dox Broth media. After incubation the resulting filtrate was extracted with ethyl acetate. To evaluate the antioxidant activity, 2,2-diphenyl-1-picrylhydrazyl (DPPH) free radical scavenging assay was performed for the ethyl acetate crude extracts after dissolving them in methanol. A crude extract of fungal morphotype isolated from *P. thwaitesii* exhibited the highest inhibition percentage (85.86 ( $\pm 1.86$ ) %) at a concentration of 12.5 mg/mL. It was significantly ( $p < 0.05$ ) higher than the positive control (84.89 ( $\pm 1.64$ ) %), L-Ascorbic acid (1 mg/mL). Out of the 30 fungal crude extracts tested, four from *P. odorifer* and ten from *P. thwaitesii* exhibited more than 70% inhibition percentage. Further,  $IC_{50}$  values were obtained from linear regression plots and the crude extracts had  $IC_{50}$  values ranging from 4.10 - 289.12 mg/mL. The lower the  $IC_{50}$  values, it implies a higher antioxidant activity and values ranging from 10-50 mg/mL are considered to exhibit strong antioxidant activity generally. Crude extracts of eight fungal endophytic isolates of this study exhibited  $IC_{50}$  values less than 10 mg/mL. Thus, there is a high potential to use these fungal endophytes from the plant species of the family Pandanaceae as possible candidates for the pharmaceutical industry.

**Keywords:** *Pandanus*, Endophytes, Antioxidant activity, Inhibition percentage,  $IC_{50}$  value



## Investigation of leaf litter fungal diversity and their enzyme profiles in a selected *Eucalyptus* plantation in Sri Lanka

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*Eucalyptus* spp. (Family Myrtaceae) are native to Australia and Tasmania and are now extensively distributed globally including Sri Lanka. However, the fungal diversity associated with *Eucalyptus* spp. in Sri Lanka is unknown. As part of an ongoing broad study on fungi associated with *Eucalyptus* spp., this study was conducted to determine the leaf litter fungal diversity in a selected *Eucalyptus* plantation in Sri Lanka and investigate their role in leaf litter decomposition. Leaf litter samples belonging to two decomposition stages (early and late) were collected from an *Eucalyptus* plantation situated in Bandarawela, Sri Lanka (GPS coordinates–802123,80.96283). Twenty-seven morphologically distinct fungal isolates were isolated from surface-sterilized leaf litter and coded for convenience. So far six isolates have been molecularly identified as *Phyllosticta* sp., *Dothideaceae* sp., *Nigrospora* sp., *Penicillium citrinum*, *Cytospora eucalypticola*, and *Pseudopezalotiopsis theae*. Diversity analysis revealed that Shannon (early-1.32769±0.48507, late-1.41022±0.65650) and inverse Simpsons (early-3.49408±1.26898, late-4.01176±2.38865) indices were greater in advanced decomposition stages. However, the diversity indices' difference was not significant according to ANOVA (p value > 0.05). Percentage abundance of fungal morphotypes indicated that each decomposition stage was dominated by a few pioneer species and others were less prevalent. Accordingly, fungal isolates EUGSF02 and EUGSF05 dominated the litter assemblage during the early and late stages of decomposition, respectively. Preliminary screening for various enzymatic activities revealed 85.19%, 62.96%, 48.15%, 25.92%, 44.45%, and 37.03% of all isolates exhibiting amylase, pectinase, cellulase, lipase, protease, and laccase activity, respectively. Furthermore, studies were carried out to ascertain whether leaf litter fungi's individual extracellular enzyme profiles relate to the fungal community shift that occurs during the two decomposition stages using ANOVA or Kruskalwallis test. Results revealed that majority of amylase and protease-producing fungi colonize leaf litter in early decomposition stages whereas, fungal isolates involved in lipase, cellulase, and laccase production were prominent in advanced decomposition stages. Furthermore, pectinase-producing fungi were found to be distributed in both stages. Therefore, it can be concluded that the dynamics of fungal communities dwelling within leaf litter undergo alterations over time as the leaf litter matures.

**Keywords:**Diversity index, fungi, extracellular enzymes, amylase, microbial-succession.



## Investigating the mycobiome of Welsh onion under biotic stress through metabarcoding

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Welsh onion (*Allium fistulosum* L.) is an important flavoring vegetable cultivated in Taiwan. Stemphylium leaf blight disease (SLB) or black rot in Welsh onions is caused by a fungal plant pathogen, *Stemphylium vesicarium*. This project constitutes a preliminary metabarcoding based mycobiota study conducted to decipher any difference in the endophytic fungal communities associated with healthy and SLB infected Welsh onion plants. Metabarcoding sequences for the study were provided by the National Taiwan University, Taiwan. Sequencing was done at BioTools Co., Ltd, Taiwan. Sequence data of four samples; leaves (HL), roots (HR) of healthy onion plants and leaves (DL), roots (DR) of diseased onion plants were received. The sequence data was analyzed using the QIIME 2 (Quantitative insights Into Microbial Ecology) pipeline and R program with modifications as necessary. The analysis revealed a total of 153 ASVs (amplicon sequence variants) at 97% similarity, and a total of 50 sequence reads were identified with taxonomic annotations; only 19 were identified to the species level from the four samples. In terms of diversity, DL had the highest value followed by DR > HR > HL. The 50 different taxa identified belonged to the three phyla Ascomycota, Basidiomycota, and Mucoromycota, and eight classes: Agaricomycetes, Dothideomycetes, Eurotiomycetes, Mucoromycetes, Orbiliomycetes, Sordariomycetes, Tremellomycetes, and Ustilaginomycetes. Under disease condition, the relative abundance of Ascomycota phylum seemed to increase while Basidiomycota phylum seemed to decrease. There were 26 and 8 different taxa identified as unique for diseased leaves and roots respectively. There were 4 and 5 unique taxa identified in healthy leaves and roots respectively. *Moesziomyces aphidis*, *S. vesicarium* and *Fusarium proliferatum* showed high abundance in diseased leaves. *M.aphidis* has been reported as a natural antagonist against pathogenic fungi. However, *S. vesicarium* and *F. proliferatum* have been identified as plant pathogens. The preliminary results indicated that there is a difference in the fungal communities between healthy and diseased plants understanding their implications is underway.

**Keywords:** Amplicon Sequence Variants, Stemphylium leaf blight disease, Next Generation Sequencing, Endophytic fungi, Relative abundance



## Diversity and industrial potential of endophytic fungi isolated from *Avicennia marina* in the Puttalam Lagoon, Sri Lanka

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Endophytes reside in plant tissues without causing any apparent symptoms and provide the host with numerous benefits. Fungi in challenging environments are known to entail unique properties that improve the stress resilience of the plants and may have potential applications in various industries. Therefore, this study aimed to determine the fungal endophyte diversity of a selected mangrove plant, *Avicennia marina* and explore their properties. A total of 38 morphologically distinct putative fungal endophyte isolates were obtained from leaf, stem and root segments of three *Avicennia marina* plants situated in the Puttalam lagoon, Sri Lanka. The highest Shannon Weiner diversity index (H') value of 2.520 was seen in stem tissues. According to the percentage occurrence data, the most dominant fungus in *A. marina* was identified as isolate AV011. Five isolates have been identified as *Candida* sp., *Acremonium* sp., *Phialophora* sp., *Preussia* sp. and a Dothideomycetes species via rDNA ITS sequences thus far. Preliminary screening of the morphotypes revealed that over 97% of them could produce siderophores at different levels and majority of the fungal endophytes produced the hydroxamate type of siderophores. More than 68% of the isolates produced Indole-3-acetic acid (IAA) at varying concentrations. Out of 38 putative endophytic fungal isolates tested, 14, 8 and 5 isolates showed promising amylolytic, cellulolytic and phosphate solubilizing activity, respectively. Furthermore, the crude extract of the fungal isolate AV023 showed promising antibacterial activity against both gram (+) and (-) bacteria. The findings thus far have revealed that some of the isolates (i.e. AV027), have multiple beneficial properties such as phosphate solubilization, and IAA and siderophore production at appreciable amounts making them suitable candidates for applications in agricultural and related industries.

**Keywords:** amylase, cellulase, IAA, phosphate solubilization, endophytes



## **ITS rDNA Phylogeny Based Identification of *Ganoderma* sp. (Ganodermataceae, Polyporales) in Gampaha, Kegalle, and Colombo Districts, Sri Lanka**

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*Ganoderma* P. Karst. has been used in traditional Chinese medicine for thousands of years to maintain vivacity and longevity. This group of fungi can cause root and butt rot diseases on many woody plants and species show a cosmopolitan distribution. *Ganoderma* is a species-rich genus, and many members are found in subtropical and tropical regions. *Ganoderma* species are abundant sources of highly active bioactive substances like polysaccharides, proteins, steroids, and triterpenoids. Products made from *Ganoderma* have been marketed as potent food and nutrition supplements with positive health effects. Over the past three decades, the *Ganoderma* market has grown significantly, and hundreds of products are available. However, in Sri Lanka, there has not been much research on *Ganoderma*. The key objective of the study is to identify *Ganoderma* species in Sri Lanka based on their molecular characteristics. Moreover, this study attempts to pique interest in the field, assess current advancements, and fill in the missing gaps in *Ganoderma* research in Sri Lanka. Fresh samples were collected from Colombo, Kegalle, and Gampaha districts. The CTAB method was used to extract genomic DNA from the fruiting bodies. The Internal Transcribed Spacer (ITS) sequence data acquired from the fresh specimens were used to identify the species based on the maximum likelihood (ML) criterion using RAxML- HPC BlackBox in the CIPRES portal. Based on the resulting phylogenetic tree, four *Ganoderma* species namely, *Ganoderma angustiporum*, *G. ellipsoideum*, *G. orbiforme*, and *G. sinense* were identified. This research will provide valuable insights into the evolutionary history and genetic makeup of *Ganoderma* species in Sri Lanka while contributing to the fungal systematics and potential applications in various fields such as medicine and biotechnology.

**Keywords:** Fungal systematics, Internal Transcribed Spacer (ITS), Medicinal mushrooms, Molecular phylogeny, Sri Lankan mycota

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## **An *in silico* approach to study the secretome of *Rhizoctonia solani***

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*In silico* analysis of the secretomes and effectomes is one of the valuable approaches available to understand the dynamics of fungal infections. Fungal pathogens secrete effector proteins to suppress host defences and promote infection. However, identifying the most likely secretory and effector candidates from a large proteome dataset poses challenges due to the extensive data volume. This study aimed to screen conventionally secreted proteins of *Rhizoctonia solani* AG1 IA (NCBI Acc. No. PRJNA51401), a necrotrophic plant pathogen, using a validated fungal-specific secretome pipeline. In addition, this study aimed to functionally characterize the predicted secretome and effectome, with the goal of identifying key features that define the distinct lifestyle of *R. solani*. The pipeline was created through the tandem use of favorably evaluated set of bioinformatics tools: SignalP 3.0, combined Phobius and TMHMM 2.0, TargetP 2.0, Pred GPI, Scanprosite, and combined WoLF PSORT with Protcomp 9.0. The pipeline demonstrated high sensitivity (90.00%), specificity (98.15%), and accuracy (97.37%), along with a Matthews' correlation coefficient of 85.45%. The constructed pipeline was applied to screen the secretome of *R. solani* AG1 IA. To identify the effector proteins, six key effector traits, EffectorP 3.0 and PHI database were used. The functional annotations of the predicted secretory proteins were performed using BLAST2GO/OmicsBOX software, based on the information given by Gene Ontology annotation and InterProScan. In *R. solani*, out of 10,489 proteins, 671 representing 6.4% of the proteome were identified as secretory proteins. Among the secretory proteins, 95, 175 and 316 proteins were identified as highly probable, moderately probable and low probable effector proteins respectively. Most of the effector proteins were cysteine-rich and contained more lysines in the final two-thirds region. Additionally, two effector proteins exhibited known motifs, LyzM and CFEM2, while four effector proteins displayed novel conserved motif patterns. Among the carbohydrate-activated enzymes found in secretome of *R. solani*, GH152 family and GH16\_1 subfamily were abundant. Among the proteases, the peptidyl-Lys metallo endopeptidase and fungalysins were the most abundant. Furthermore, a significant number of proteins were predicted to participate in oxidation-reduction interactions. The results of this investigation seemed to be consistent with *R. solani*'s robust necrotrophic lifestyle and pathogenesis. The accuracy metrics of the pipeline used in this study further demonstrated that it was suitable for secretome prediction, offering a crucial resource for studying fungal secretomes and their impact on host-pathogen interactions..

**Keywords:** *Rhizoctonia solani* AG1 IA, Fungi, *In silico*, Pipeline, Secretome, Effectome





## Preparation of tea using stevia syrup extracted from fresh and dry leaves of stevia ( *Stevia rebaudiana* Bertoni )

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There is an emerging demand for low-calorie natural sweeteners such as Stevia with the increasing cases of Type 2 diabetes. The non-communicable disease like diabetics is influenced by lifestyle and dietary factors such as higher consumption of saturated fats and sugars. This study attempted to optimize the recovery of stevia syrup from the stevia leaves with different ethanol percentages. Fresh and dry stevia in two different ratios (1:25 and 1:50) were used in the development of syrups. The best ethanol percentage as the solvent was selected based on the contents of total carbohydrates, total steviosides, total flavonoid and total chlorophylls using standard methods. The syrups were evaluated for their physiochemical and microbial stability. Stevia tea formulated with stevia syrup was subjected to sensory evaluation. A shelf-life study was conducted for a period of 28 days. The total carbohydrate, steviosides and flavonoids contents did not show any significant change ( $p>0.05$ ) with increasing percentage of EtOH, however they significantly ( $p<0.05$ ) increased with increasing solute: solvent ratio. The total chlorophyll contents significantly ( $p<0.05$ ) decreased with increasing EtOH. However, considering extractability and palatability 30% EtOH was selected for further development into syrup. Throughout a one-month period of storage at ambient temperature and in the refrigerator, physiochemical and microbial quality parameters of final products did not significantly ( $p>0.05$ ) change. The tea formulation with the 0.5 mL dry powder syrup showed significantly ( $p<0.05$ ) highest sweetness – 1.75 and overall acceptability – 1.62. Similarly, 1 mL of fresh leaf syrup showed significantly ( $p<0.05$ ) highest sweetness – 1.75, and overall acceptability – 1.59. Thus, the developed stevia syrup can successfully be incorporated into food as a non-caloric sugar substitute.

**Keywords:** Low-calorie, Stevia leaf powder, Stevia syrup, Stevia fresh leaves, Alcoholic extraction

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## Re-analysis of the R2R3-MYB transcription factor family in *Theobroma cacao*

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In plants, myeloblastosis (MYB) transcription factors (TFs) play vital roles in regulating various processes such as plant growth and development, primary and secondary metabolism, and responses to biotic and abiotic stresses. MYBs are divided into four classes based on the number and type of highly conserved MYB domain repeats (Rs): 1R, R2R3-, 3R-, and 4R-MYB proteins. Of these, plant- and yeast-specific R2R3-MYBs comprise the largest group of MYB TFs. Although a recent study reported a genome-wide analysis of the R2R3-MYB gene family in *Theobroma cacao*, a comprehensive analysis of this gene family is still lacking. The analysis of R2R3-MYBs in *T. cacao* (TcR2R3-MYBs) employing a range of bioinformatics tools and databases identified a total of 121 R2R3-MYBs, which were classified into 25 subfamilies (1-25). Eight MYBs that were not reported previously as R2R3-MYBs in *T. cacao* were detected in the present study (i.e., TCM\_007672, TCM\_021750, TCM\_042604, TCM\_043101, TCM\_012262, TCM\_041160, TCM\_041362, and TCM\_041672). Within the same subgroup, the majority of genes shared a similar domain and motif architecture and exon/intron structures. The identified *TcR2R3-MYBs* were unevenly distributed over 10 chromosomes. The subcellular localization analysis revealed that TcR2R3-MYBs are mainly localized in the nucleus. It was evident that TcR2R3-MYBs may be involved in regulating various biological processes, including cell differentiation, and stomatal movement. In addition, protein-protein interaction network analysis of TcR2R3-MYBs demonstrated interactions among proteins, and several proteins with high degrees of freedom were detected (i.e., TCMYB119 (TCM\_041672) and TCMYB49 (TCM\_021750)); these could be potential hub proteins. The findings of this study may provide valuable information for further elucidating the functional roles of R2R3-MYB TFs in *T. cacao*, as well as for promoting their use in genetic crop improvement.

**Keywords:** *Theobroma cacao*, R2R3-MYBs, Genome-wide identification



## Evaluation of protocols for the extraction of high-quality genomic DNA from black pepper (*Piper nigrum* L.) leaves

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Black pepper (*Piper nigrum* L.) is one of the most economically important spice crops, primarily cultivated in tropical regions. In recent years, there has been an increasing interest in conducting population genetic studies and investigating piperine biosynthesis at the molecular level. Isolation of pure, intact, and high-quality DNA from black pepper tissues is technically challenging due to the presence of high amounts of secondary metabolites, such as oxidized polyphenolic compounds, in tissue samples, especially in berries and leaves. The majority of the existing DNA extraction protocols require long incubations, multiple purification steps, or commercially available expensive kits to yield DNA of high purity. Here we evaluated six extraction protocols to investigate the impact of the grinding method and the component of the lysis buffer to obtain high molecular weight DNA from black pepper leaves. The quality of extracted DNA samples was assessed by PCR amplification using the primers specific for the Internal Transcribed Spacer (ITS) gene and visualization of the amplified products on agarose gels. It was evident that the presence of sodium chloride (NaCl), lithium chloride (LiCl), and polyvinylpyrrolidone (PVP) together in the cetyltrimethylammonium bromide (CTAB)-containing lysis buffer greatly improved the DNA yield of black pepper compared to using LiCl and PVP alone in the lysis buffer ( $102.3 \pm 6.5$  ng/ $\mu$ L), regardless of the grinding method employed. However, the addition of  $\beta$ -mercaptoethanol to the lysis buffer containing NaCl, LiCl, and PVP did not significantly improve the DNA yield ( $65.6 \pm 10.9$  ng/ $\mu$ L). Although black pepper leaves ground using acid-washed sand yielded a higher DNA concentration, those extracts failed to produce amplified products during PCR. In conclusion, our study demonstrated that the sample disruption using liquid nitrogen, and cell lysis using CTAB buffer containing NaCl, LiCl, and PVP can effectively isolate a sufficient yield of black pepper DNA with better quality for downstream analyses.

**Keywords:** *Piper nigrum*, DNA extraction, modified CTAB method



## **Genome-wide analysis and characterization of the LAZY gene family in *Oryza sativa***

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Rice was used as a more efficient target for whole genome sequence analysis because of its small genome size. Rice faces a variety of abiotic stressors, including drought, salinity, cold, and submersion. Plants use a variety of signals to optimize shoot and root architecture to overcome these stresses. The root growth angle is particularly important for tolerating drought conditions, with deep rooting playing a significant role. The LAZY gene family in rice (*Oryza sativa*) plays a crucial role in regulating plant growth, in response to environmental stresses. However, no prior studies have focused on the LAZY family in rice. Through genetic analysis, we identified six LAZY gene sequences in rice, located on four different chromosomes namely 3,7,9 and 11, three of which were reviewed (TAC1, LAZY1, DRO1), and three were uncharacterized (NP\_001390067, EEC74632, XP\_025880192). These genes control various aspects of plant architecture, including tiller development and root growth angles. Functional analysis done using MEGA11, HMMER, UGENE, DAVID, WoLF PSORT, GSDS tools, etc. revealed that the reviewed gene sequences are associated with the regulation of auxin polar transport, while the functions of the uncharacterized sequences require further investigation. Phylogenetic analysis demonstrated that the uncharacterized LAZY gene sequences are evolutionarily closer to the DRO gene group, which is responsible for drought tolerance of *Arabidopsis thaliana*. In contrast, another uncharacterized sequence is related to the TAC gene group which responds to photosynthetic cues and increases downward branch angles. LAZY1 and DRO1 sequences in rice share evolutionary proximity to genes in *Panicum virgatum*. Nuclear localization was found within 2 uncharacterized sequences. XP\_02580192 and LAZY1 are modified for the same functions, regulating polar auxin transport. Overall, this comprehensive analysis provides valuable insights into the LAZY gene family in rice, shedding light on its role in regulating plant growth and development. Understanding these genes can contribute to crop improvement strategies, enhancing crop yield and resilience to environmental stresses.

Keywords – LAZY, DRO1, TAC1, Reviewed, Uncharacterized



## An investigation on plant based, non-toxic, anti-aging compounds for cosmetics

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The strategies aimed at preventing or reversing signs of skin aging include the use of sunscreens, anti-oxidants to scavenge or neutralize free radicals and many others. Herbal compounds play a prominent role in preventing skin aging, and influence the biological functions of the skin while providing necessary nutrition for its health. Recent developments in cosmetics industry have focused on creating new products with non-toxic botanicals which have anti-aging and other bioactive properties. The use of plant materials that have been used in traditional medicine or cosmetics is advantageous as the majority of those are known to be harmless. This study aimed to investigate the potential anti-aging properties of some selected plant species that have been traditionally used in cosmetic formulations or medicine, by determining their antioxidant-, free radical scavenging- and UV-shielding capacities. Aqueous extracts were obtained from different parts of six medicinal plant species, namely, *Aloe vera* (L.) Burm.f., *Etilingera elatior* (Jack) R. M. Sm., *Nelumbo nucifera* Gaertn., *Curcuma zedoaria* (Christm.) Roscoe, *Commelina benghalensis* L. and *Nyctanthes arbor-tristis* L. The 2,2-Diphenyl-1-picrylhydrazyl radical scavenging activity, total phenolic content (TPC), total flavonoid content (TFC) and the Sun Protection Factor (SPF) of the plant extracts were determined using standard methods to identify their anti-aging potential which may be helpful to be used as ingredients in herbal cosmetics. *E. elatior* flower extract showed the highest ascorbic acid equivalent radical scavenging capacity ( $99.10 \pm 7.34$  mg AAE/g) and its leaf extract showed the highest TPC of  $36.13 \pm 0.31$  Gallic acid equivalent mg (GAE)/g and highest TFC of  $49.48 \pm 10.90$  mg Rutin equivalent (RE)/g. The *Nyctanthes arbor-tristis* L. flower extract showed the highest SPF value of  $39.33 \pm 0.12$ . Overall, this study provides valuable insights into the cosmetic potential of the selected medicinal plants as natural antiaging ingredients for the development of new products.

**Key words:** herbal extracts, cosmetic potential, anti-aging, SPF, antioxidant

**Acknowledgement:** The authors acknowledge the University of Colombo for facilitating undergraduate research work and the Herbal Care Industries (Pvt) Ltd., Kelaniya, for providing chemical reagents for the research.



## Molecular Characterization of Wild Edible Mushrooms in Colombo and Rathnapura Districts, Sri Lanka

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Wild edible mushrooms are traditionally used worldwide as a food source. Identification of mushrooms based on morphological characteristics can often be misleading to discriminate variations among species and strains that are closely related. Molecular characterization allows for a more accurate and reliable identification of mushrooms compared to morphological identification. Sri Lanka provides significant potential for having a rich and unique collection of mushrooms owing to its high biodiversity. However, Sri Lankan wild edible mushrooms have not been extensively studied based on molecular characterization. The main objective of the present investigation was to identify the collected wild edible mushrooms using molecular markers, with an emphasis on the internal transcribed spacer (ITS) region of the ribosomal DNA (ITS-rDNA) sequence data. A total of eight specimens of wild edible mushrooms were collected from Colombo and Rathnapura districts based on information from local communities regarding their edibility. Genomic DNA was extracted using the CTAB method from the fresh fruiting bodies of the collected mushrooms. The data obtained from sequencing the mushroom strains were used to construct phylogenetic trees based on the Maximum Likelihood method using RAxML-HPC BlackBox in the CIPRES portal. The phylogenetic analyses revealed six different mushroom species, which were identified as *Calvatia candida*, *Pleurotus giganteus*, *Schizophyllum radiatum*, *Termitomyces heimii*, *T. microcarpus* and *Volvariella volvacea*. Among these species, *C. candida* and *S. radiatum* are reported for the first time in Sri Lanka. The molecular characterization using the ITS-rDNA sequence data would aid in the identification of these wild edible mushrooms in Sri Lanka, thereby facilitating their cultivation, commercialization, and conservation of existing bioresources. However, multi-gene molecular characterization and detailed morphological analyses are recommended for more accurate species identification.

**Keywords:** Basidiomycetes, DNA barcoding, Internal Transcribed Spacer (ITS), Molecular phylogeny, Taxonomy

**Acknowledgement:** The authors are thankful to GeneLabs Medical, Sri Lanka for providing DNA sequencing facilities. Center for Plant Materials and Herbal Product Research and Centre for Biotechnology, Faculty of Applied Sciences, University of Sri Jayewardenepura are acknowledged for their resources and laboratory facilities. Special thanks are extended to the local communities at the sampling locations in Rathnapura and Colombo districts for assisting with the sample collection.



## Evaluation of *in vivo* effects of traditional Sri Lankan spice mix on inflammation and the production of reactive oxygen species by peritoneal cells

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The traditional Sri Lankan spice mix (TSSM) also known as raw curry powder is prepared by combining the seeds of coriander (*Coriandrum sativum*), cumin (*Cuminum cyminum*), and fennel (*Foeniculum vulgare*). Generally, spices contain bioactive compounds like phytochemicals with therapeutic potential that can boost immunity. As studies on TSSM are scarce, the potential effects of TSSM on inflammation and the production of reactive oxygen species (ROS) by peritoneal cells were investigated here. Two groups (test - TSSM; n=4, control - distilled water; n=4) of healthy adult male Wistar rats were orally gavaged daily for 6 weeks during this study. At the end of the 6<sup>th</sup> week, the carrageenan-induced rat paw oedema model was utilized in assessing the anti-inflammatory properties whereas the Nitroblue tetrazolium (NBT) assay was performed on carrageenan-induced infiltration of peritoneal cells to determine the effect of TSSM on the ROS production of peritoneal cells. The assessment of anti-inflammatory properties resulted in different rates of change in hourly paw volume between the two groups following the carrageenan administration. The mean peak volume displacement for the test group was observed at the 3<sup>rd</sup> hour of carrageenan treatment and for the control group, it was recorded at the 4<sup>th</sup> hour. This manifests better anti-inflammatory powers in the test group. Nevertheless, there was no significant difference between the changes in the volume displacement of the two groups in each hour ( $p < 0.05$ ). The statistical comparison of optical density values of NBT assay at 620 nm revealed no significant difference ( $p < 0.05$ ) in ROS production of peritoneal cells between the test and control groups. These results indicate that there is a window for higher concentrations of TSSM to possess better anti-inflammatory properties that could make TSSM a food adjunct that acts against hyperinflammation although no significant relationship between the TSSM and oxidative stress was unveiled.

**Keywords:** Anti-inflammation, Reactive oxygen species, Peritoneal cells, *In vivo*, Spices

**Acknowledgement:** Department of Zoology & Environment Sciences, Faculty of Science, University of Colombo.



## **Application of *Allium cepa* bioassay for examining the status of potential cytogenotoxicity of two selected Sri Lankan rice varieties**

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Being the staple food of many Asian countries, rice is used for many cosmetic treatments due to its high nutritional value and cleansing properties. Rice water obtained during washing and cooking is known to be traditionally applied as a skin cleanser. However, potential agrochemical contaminations including heavy metals may affect these cleansing properties while additionally causing toxic effects. This study aims to investigate the suitability of the use of rice water extracts for cosmetic purposes via the assessment of cytogenotoxic activity based on the *Allium cepa* bioassay. After 48 hours of direct exposure of the grown *A. cepa* roots to the second washing water with a tight rubbing of two selected rice varieties (rice water of Rathukekulu-RK, Steamed rice-ST) along with the dechlorinated water control, root tips were harvested, processed, and stained with acetocarmine to observe the mitotic division of the meristematic cells. The Mitotic index and percentage chromosomal aberrations were evaluated by scoring 1000 meristematic cells. Macroscopic observations indicated that some roots exposed to RK were slightly coiled with necrotic appearance while upper parts of some roots in ST were brownish yellow colour. The mitotic index of the control, RK and ST were 50.7%, 51.83%, 66.7%, respectively. The percentage of chromosomal aberrations were 3.07%, 6.96%, 2.43%, respectively. Among the recorded aberrations polyploidy (75.75%), sticky chromosomes (21.81%) and bridging chromosomes (1.81%) were common. When comparing the two rice varieties the ST- steamed rice seems more favourable for cleansing and revitalizing effects resulting in higher mitotic index and lower percentage aberration effects. The present study validates the traditional use of rice water on cosmetic purposes, highlighting the importance of nature-based treatments and practices. Further studies are warranted to investigate the most suitable methods of rice water preparation in this concern.

**Keywords:** *Allium cepa* bioassay, cytogenotoxicity, Sri Lankan rice varieties

**Acknowledgement:** Department of Zoology, Faculty of Natural Sciences, The Open University of Sri Lanka is greatly acknowledged for providing the necessary facilities.





## Harnessing the soil conditioning ability of Sesame (*Sesamum indicum* L.) crop wastes

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During processing of crops and crop products, generated wastes are disposed ineffectively causing many environmental issues and hence, a timely intervention is needed to explore the alternative ways of utilizing such crop wastes. Sesame (*Sesamum indicum* L., Family Pedaliaceae) is a nutrient rich oil seed crop cultivable under drought conditions. The objective of this study was to investigate soil conditioning ability of sesame crop wastes (oil cake) resulted from oil extraction process. Grounded samples of Black and White-seeded oil cake (60 g) were separately placed on 140 g of sieved garden soil in 3:7 (w/w) ratio of oil cake: soil in plastic pots with garden soil as the control and arranged according to complete randomized block design (n=3x24). Soil from 3 random pots representing each treatment and control were tested weekly over eight consecutive weeks for nutrients [available Nitrogen (N), Phosphorus (P), and Potassium (K), pH, electrical conductivity and soil organic matter]. Three-week old Chilli (*Capsicum annum* L. variety M2) seedlings were exposed to soil treated with black and white seeded oil cake decomposed for 5 weeks, and the control arranged according to complete randomize design (n= 10x3) in the green house. Growth of Chili was monitored over eight weeks. Growth data were subjected to ANOVA using SPSS 26.0 software. Available N, P, K contents of black oil cake were 4.77%, 0.88% ,1.21%, respectively while it was 5.31%, 0.78%, 1.14% for white sesame oil cake. The available N, P, K, pH, electrical conductivity and soil organic matter were significantly higher in treatments than the control (p<0.05) especially after 6<sup>th</sup> weeks. Plant height, leaf length and number of leaves of chili plants were significantly increased according to One-Way ANOVA test using SPSS 26.0 software (p<0.05) when treated with oil cake, and the black seeded oil cake was much effective. It can be concluded that sesame oil cake samples improved the soil characteristics and direct application of partially decomposed oil cake residues can stimulate the growth of chili seedlings.

**Keywords:** Sesame, *Sesamum*, oil cake, nutrients, soil parameters





## Schedule of the Scientific Sessions

43<sup>rd</sup> Annual Sessions of the Institute of Biology, Sri Lanka  
22<sup>nd</sup> September, 2023  
Orchid Hall, Ariyana Reach Hotel - Maharagama

### Parallel Session A

TIME	ABSTRACT NUMBER	Zoology and Environmental Science
1.30-4.20 p.m.	A_01	Evaluation of anti-inflammatory and antioxidant activity of of <i>Fromia indica</i> (a common starfish) crude extract. <i>By K.K.K. Perera, K.V.K. Gunathilake</i>
	A-02	Heavy metal loads in the dung of wild Asian Elephants ( <i>Elephas maximus</i> ) in Sri Lanka <i>By K.K.K. Perera, M.R. Wijesinghe, R.D. Wijesekara, S.M. Vithanarachchi</i>
	A-03	Herbivory of mangrove crabs ( <i>Sesarmidae</i> ) in regenerating mangrove ecosystems - A study from Southern Sri Lanka <i>By H.M.M.D. Dedunupitiya, D.H.N. Munasinghe, K.V.S.N. Bandara</i>
	A-04	Molecular characterization and the record of host range of Rugose Spiraling Whitefly ( <i>Aleurodicus rugioperculatus</i> Martin): A newly emerging pest of coconut in Sri Lanka <i>By D.H. Dilrukshika, D.P.M. Silva, P.H.P.R. De Silva, N.S. Aratchige, N.T.M. Wijewardana, A.D.T.D.S. Kulasinghe, S.A.C.N. Perera</i>

A-05	A preliminary study of rs4913269 in IFNG-AS1 gene as a genetic risk factor for susceptibility to cutaneous leishmaniasis in a selected endemic cohort in Sri Lanka <i>By M.N.K. Nuha, I.P. Kahawita, N. Perera, G. Galhena</i>
A-06	Parasitic profiles of edible fish catch from selected inland water bodies and culture systems in Sri Lanka <i>By W.A.P. Thathsarani, M.M.K.I Marasinghe, V.K. Fernando</i>
A-07	New record of <i>Knemodynerus coriaceus</i> ( <i>Giordani Soika, 1970</i> ) (Hymenoptera, Vespidae, Eumeninae), a vespid wasp from Sri Lanka <i>By T.D. Ranasinhe, D.L. Abeywardhana, A. Nugaliyadde, C.D. Dangalle</i>
A-08	Potential of the aqueous extract of <i>Terminalia chebula</i> ('Aralu') powdered dry fruit in reducing serum triglyceride levels – A pilot study in albino Wistar rats <i>By M.G.K. Madhavi, K.B.S. Gunawickrama, R.P. Hewawasam</i>
A-09	Influence of land use and land cover attributes on population dynamics of Indian Peafowl ( <i>Pavo cristatus</i> ) in a selected expanse of peafowl accident susceptible zone of the Southern Expressway <i>By T.S. Wickramasinghe, C.M.K.N.K. Chandrasekara, N. Dayawansa</i>
A-10	Patterns of distribution in endemic birds along a one-kilometer elevational gradient in the submontane zone of Sri Lanka <i>By A. S. Adikari, S.J. Perera, S. S. Seneviratne</i>
A-11	The study investigating the population dynamics of a critically endangered hog deer ( <i>Axis porcinus</i> ) population in Honduwa island sanctuary in the wet zone of Sri Lanka <i>By G.P. Harischandra, C.M.K.N.K. Chandrasekara, P.K.P. Perera, N. Dayawansa</i>

A-12	Vitamins, minerals, and fatty acids composition of Mackerel scad ( <i>Decapterus macarellus</i> ): a common edible fish from Sri Lanka <i>By N.D. Wimalagunaratna, B.G.D.N.K. De Silva, I. Wijesekara and K.V.K. Gunathilake</i>
A-13	Investigation of haemoparasites in avian communities along an altitudinal gradient <i>By H.D.J.M. Karunaratne, M.S. Mapalagamage, S. N. Weerakkody, V. R Gunasekara, S.S. Seneviratne</i>
A-14	Investigating the potential of <i>Scenedesmus</i> sp. isolated from Beira Lake, cultivated under non-axenic, ambient conditions in open bioreactor systems, for biodiesel production in Sri Lanka. <i>By J. K. D. M. Jayasekara, L. Wanasekara, S. Perera and P. S. Saputhanthri</i>
A - 15	Conventional and modern methods of measuring N, P and K levels in the soils around the world and their adaptability in Sri Lanka <i>By Y.G.D.Kithmini, T.A Perera</i>
A-16	Carbon footprint calculation for scope-2 indirect emissions of a knowledge-based institution and its impacts under the post covid-19 conditions <i>By Udadini K.M.E., Perera P. and Halwatura D.</i>
A - 17	The impacts of the lockdown and economic crisis on energy-related greenhouse gas emissions from selected apparel industry factories in Sri Lanka <i>By D.M.T.S. Dissanayake and E.Y.K. Lokupitiya</i>
A - 18	A Socio-Economic Investigation of Landslide Disasters in the Kegalle District <i>By G.A.M. Eragama, D. Halwatura, P. Hudson, D. D. Wickramasinghe</i>
A - 19	Water quality analysis based on physical-chemical parameters in selected urban wetlands in the Colombo district, Sri Lanka <i>By W.D.H. Weerasinghe and H.I.U. Caldera</i>

A - 20	Investigating the Microclimatic Buffering Potential of Submontane Forests in Knuckles Range, Sri Lanka Using Temperature and Relative Humidity <i>By S.S.Samaramanna, H.H.E.Jayaweera, M.R.Wijesinghe</i>
A - 21	Investigating the efficiency of urban trees in alleviating Urban Heat Island effect using Remote Sensing and Geographical Information Systems <i>By S.S Wimalakeerthi, I.A.J.K. Dissanayake, M. Ranagalage</i>
A - 22	Unveiling the secrets of <i>Stemonoporus</i> : what lies behind the distribution patterns and ecological niche of Sri Lanka's enigmatic endemic plant genus? <i>By M. S. K. Perera, S. A. C. Harshanie, H. S. Kathriarachchi</i>
A - 23	Enhancement of the nitrogen level of compost by incorporation of biological nitrogen fixers and nitrogen capture additives <i>By D.C.L. Mendis, R. Vinushayini, K.R.E. Padmathilake and L. Herath</i>
A - 24	<i>Spatiotemporal analysis of the impact of open dumping on aquatic vascular plant development: a case study on Karadiyana open dump, Sri Lanka</i> <i>By L. D.R Samarawickrama and D. Halawatura</i>

## Parallel Session B

TIME	ABSTRACT NUMBER	Agriculture and Plant Sciences
1.30–4.30 p.m.	B-01	Comparison of Major Nutrient Status between Whitefly Non-infected and Infected Coconut Palms of Three Estates: A Case Study in Gampaha Area <i>By A.A.R.W. Abeysinghe, D.H. Dilrukshika, D.P.M. Silva, P.H.P.R. De Silva, M.K.F. Nadheesha, C.S. Ranasinghe</i>
	B-02	Biochemical characterization of <i>Oryza sativa</i> (L.) varieties grown in vitro under salinity stress <i>By S.M.Y.P.Dharmarathna and H.D.D.Bandupriya*</i>
	B-03	<i>Ipomoea imperati</i> ( <i>Convolvulaceae</i> ): A new occurrence record from Manalkaadu, Jaffna, Sri Lanka <i>By Kasunthi Amarasekara, Chintha Perera, Mangala Yatawara, H.B.Jayasiri</i>
	B-04	Distribution analysis and ecological niche modelling of selected <i>Shorea (Doona)</i> species in Sri Lanka with special emphasis on range size and niche breadth <i>By U.D.S.K.Ruwanjana, S.M.Rajapaksha, W.S.S.N.Fernando, H.S. Kathriarachchi</i>
	B-05	Reproductive Plasticity of <i>Miconia crenata</i> (Vahl) Michelang [syn. <i>Clidemia hirta</i> (L.) D. Don] across an elevational gradient <i>By K.D.A.G. Jayarathne and S.M. W. Ranwala</i>
	B-06	Foliar trait plasticity help <i>Miconia crenata</i> (Vahl) Michelang [syn. <i>Clidemia hirta</i> (L.) D. Don] to survive from low to high elevations <i>By K.D.A.G. Jayarathne and S.M. W. Ranwala</i>
	B-07	Distribution analysis and improved propagation of selected <i>Eriocaulon</i> species used for medicinal purposes <i>By O. W. Ketakela, W. A. A. D. M. Viduranga, D. M. R. G. Mayakaduwa, H. S. Kathriarachchi, S. K. M. K. Herapathdeniya</i>
	B-08	Determination of the optimum light conditions to cultivate lettuce in indoor hydroponic systems

	By <u>M.P.C.K Divyanjalee</u> and <u>T. A Perera*</u>
B-09	A preliminary study deciphering the Bacterial Community Structure in Agroecosystems across the main agro-ecological zones of Sri Lanka via High Throughput Sequencing By <u>B. D. Tissera</u> , <u>M. M. G. P. G. Mantilaka</u> and <u>H. M. L. I. Herath</u>
B-10	Effect of various processing techniques on nutritional, biological, techno functional, structural and molecular interactions of finger millet ( <i>Eleusine coracana</i> ) By <u>P.S.R. Fonseka</u> and <u>K.D.P.P Gunathilake</u>
B-11	Improving multiplication rates for cost-effective micropropagation of <i>Passiflora edulis</i> By <u>S.A.D.L. Senanayake</u> and <u>T.D. Silva</u>
B - 12	Prediction of new candidate proteins and analysis of protein hubs associated with seed development in <i>Oryza sativa</i> using a network-based approach. By <u>M.R.P. De Silva</u> , <u>J.W.J.K. Weeraman</u> , <u>S.P.C. Fernando</u>
B - 13	Antibacterial properties of essential oil extracted from <i>Acronychia pedunculata</i> (Ankenda) leaves and bark By <u>R.P.D.M. Rajapaksha</u> , <u>G.D. Liyanaarachchi</u> , <u>J.K.R.R. Samarasekara</u> and <u>K.M. Mewan</u>
B - 14	Morpho-molecular characterization of commercially grown <i>Pleurotus</i> spp. in Sri Lanka By <u>I. Y. Nawarathne</u> , and <u>D. A. Daranagama</u>
B - 15	Extraction and characterization of phycobiliproteins from the red alga <i>Gracilaria hikkaduensis</i> (Rhodophyta) By <u>M.E.N. Saumya</u> , <u>I.U.Kariyawasam</u> , and <u>K.V.K.Gunathilake</u>
B - 16	Study on micropropagation of native shrub <i>Catunaregam spinosa</i> (Thunb.) Triveng. in Sri Lanka: Conservation strategy



	<i>By P.K. Lawrence and W.T.P.S.K. Senarath</i>
B - 17	Assessing the anthocyanin and carotenoid contents in selected <i>Phalaenopsis</i> cultivars <i>By Y.K.D.D. Thathsarani, A.I.S. Priyadarshan, H.M. Herath, R.A.S.P. Senanayake</i>
B - 18	In silico analysis of genes differentially expressed in fruits of black pepper ( <i>Piper nigrum L.</i> ) <i>By M.A.U Karunaratne and A.M. Wickramasuriya</i>
B - 19	In silico prediction and analysis of transcription factors in black pepper ( <i>Piper nigrum L.</i> ) <i>By D.R.R. Wijewardene and A.M. Wickramasuriya</i>
B - 20	<i>Evaluation Of Fungicidal Effects Of Selected Plant Extracts For Controlling Leaf Blight Disease In Coconut</i> <i>By D.L.V. Kaushalya , V.K. Gunathilake , P. Madhushani, P.H.P Roshan De Silva</i>
B - 21	A study on fungal endophytic communities of wild rice species in Sri Lanka as a potential source of biocontrol and growth-promoting agents <i>By U. C. Galagoda and K.G.S.U. Ariyawansa</i>
B - 22	Antioxidant activities of lichen-associated fungi of mangrove ecosystems in Sri Lanka <i>By H.A.D.N.N Happitiya, C. M. Nanayakkara, K. G. S. U. Ariyawansa, S. S. Ediriweera, N. N. Wijayawardene, R. P. P. K. Jayasinghe, Don-Qin Dai, S. C. Karunathna</i>
B-23	Evaluation of Fungicidal Effects of Selected Plant Extracts For Controlling Leaf Blight Disease in Coconut <i>By Kaushalya D.L.V., Gunathilake V.K., Madhushani P., Roshan De Silva P.H.P</i>
B-24	<i>Anti-fungal activity of secondary metabolites extracted from endophytic fungal isolates of Plumeria rubra leaves.</i> <i>By M.K.S.R. Fonseka, Nandasena. K.D, Suriarachchi. C., A. V. K. Udalamaththa.</i>

## Parallel Session C

TIME	ABSTRACT NUMBER	Microbiology and Biochemistry
1.30–4.30 p.m.	C-01	Predicting the structure and active site of a putative xylanase in <i>Mycobacterium tuberculosis</i> . <i>By T.R.M. Madusanka, I.C. Perera</i>
	C-02	Anti-hypertensive, anti-diabetic and anticancer potential of selected edible flowers available in Sri Lanka <i>By G.Janarny, K.D.P.P Gunathilake, K.K.D.S Ranaweera</i>
	C-03	Antifungal susceptibility of Candida isolates from cancer patients. <i>By S. C. Ganguli, W. A. S. Wijendra, P. N. Dasanayaka, R. Ramesh, A. G. G.kaushalya and S. Gunasekara</i>
	C-04	Antibacterial and anti-inflammatory activities of a polyherbal formulation based on traditional Sri Lankan medicine for diabetic wound healing <i>By J. A. T. D. Peiris, S. P. N. N. Senadeera, K. R. Weerasekara, I. C. Perera</i>
	C-05	Evaluation of the contribution of facultative anaerobes for domestic biogas production: A microbial approach <i>By J.M.S. Jayalath, K.K.A. Sirisena, A. Witharana</i>
	C-06	The Last Laugh: Could an evolutionary-plastic cytochrome oxidase subunit II enzyme from the cyanobiont of <i>Azolla pinnata</i> be a contender to better control Nitrous Oxide released from paddy fields? <i>By D. Gunawardana</i>
	C-07	Studying the microbial community interactions of Sri Lankan milk microbiota for different cattle breeds <i>By M. A. Udara, D. U. Rajawardana, I. G. N. Hewajulige, C. M. Nanayakkara, S. P. C. Fernando</i>

C-08	Isolation and Characterization of Pigmented Bacteria from the Phycoplane of the Marine Alga <i>Padina minor</i> Yamada (Phaeophyta), with Special Emphasis on UV-Blocking and Antioxidant Properties of Their Pigments <i>By W. A. Malith, C. L. Jayasinghe, Lakshani S. Pathirana, Dinendra Dhanapala, Isurika R. Fernando, Isuru U. Kariyawasam</i>
C-09	Isolation and molecular identification of <i>Listeria monocytogenes</i> serotypes from raw milk collected from Polonnaruwa District, Sri Lanka. <i>By H.A.T.K.D. Perera, W.A.S. Wijendra, R. Wimalasekara, A.G.G. Kaushalya</i>
C-10	Diversity of fungal endophyte morphotypes of Mangrove plant <i>Avicennia marina</i> in the Puttalam Lagoon, Sri Lanka. <i>By M. K. D. Fernando, S. S. Ediriweera, C. M. Nanayakkara, N. N. Wijayawardene, R. P. P. K. Jayasinghe, Don-Qin Dai, S. C. Karunarathna, K. G. S. U. Ariyawansa</i>
C - 11	Extracellular enzymatic activities of halophilic fungi in Kalpitiya area of Puttalam Lagoon, Sri Lanka <i>By P. H. H. J. Bandara, D. A. Arokkiyam, S. S. Ediriweera, C. M. Nanayakkara, K. G. S. U. Ariyawansa, N. N. Wijayawardene, R. P. P. K. Jayasinghe, Don-Qin Dai, S. C. Karunarathna</i>
C - 12	In vitro evaluation of the antioxidant activity of selected fungal endophytes isolated from two species of family Pandanaceae in Sri Lanka <i>By D.P.T.H.De Silva, W.N.N. Dabarera, S.S. Ediriweera, C.M. Nanayakkara, K.G.S.U. Ariyawansa, N.N. Wijayawardene, R.P.P.K. Jayasinghe, S.C. Karunarathna, D.Q. Dai</i>
C - 13	<i>Investigation of leaf litter fungal diversity and their enzyme profiles in a selected Eucalyptus plantation in</i>

		<p><i>Sri Lanka</i></p> <p>By <u>G. L. S. N De Silva</u>, C. M. Nanayakkara, S. S. Ediriweera, N. N. Wijayawardene, Dong-Qin Dai, K. G. S. U. Ariyawansa</p>
	C - 14	<p>Investigating the mycobiome of Welsh onion under biotic stress through metabarcoding</p> <p>By <u>D.P.B. Hendalage</u>, H. Jayasinghe, H.A. Ariyawansa, K.G.S.U. Ariyawansa</p>
	C - 15	<p>Diversity and industrial potential of endophytic fungi isolated from <i>Avicennia marina</i> in the Puttalam Lagoon, Sri Lanka</p> <p>By <u>R.G.S. Anurangi</u>, C.M. Nanayakkara, S.S. Ediriweera, N.N. Wijayawardene, R.P.P.K. Jayasinghe, Dong-Qin-Dai, S.C. Karunarathna, K.G.S.U. Ariyawansa</p>
	C- 16	<p>Molecular Characterization of Wild Edible Mushrooms in Colombo and Rathnapura Districts, Sri Lanka</p> <p>By <u>H.M.N. Dasanthi</u>, H. Munasinghe, K.M. Thambugala</p>
	C-17	<p>ITS rDNA Phylogeny Based Identification of Ganoderma sp. (<i>Ganodermataceae</i>, <i>Polyporales</i>) in Gampaha, Kegalle, and Colombo Districts, Sri Lanka</p> <p>By <u>K.M.U.A.K. Konara</u> and K.M. Thambugala</p>
	C - 18	<p>An in silico approach to study the secretome of <i>Rhizoctonia solani</i></p> <p>By <u>B.M.G.G.K. Rajapaksha</u> and K.G.S.U. Ariyawansa</p>
	C -19	<p>Preparation of tea using stevia syrup extracted from fresh and dry leaves of stevia (<i>Stevia rebaudiana</i> Bertoni)</p> <p>By <u>R.P.N.S. Randeni</u>, J.M.N. Marikkar, N.S. Weerakkody</p>
	C - 20	<p>Re-analysis of the R2R3-MYB transcription factor family in <i>Theobroma cacao</i></p> <p>By <u>A.T.S. Wekada</u> and A.M. Wickramasuriya</p>

C-21	Evaluation of protocols for the extraction of high-quality genomic DNA from black pepper ( <i>Piper nigrum</i> L.) leaves  By <u>K.C.T. Peiris</u> , D.S. Kumanayaka, N.A.D.K. Deshani, U.G.S. Malka, K.L.S. Perera, H.A.D.G. Rathnasiri, L.A. Udeshika, W.G.N.A. Wimalarathna, R.R.P.W.M.R.U.C. Galagoda, H.D.D. Bandupriya, A.M. Wickramasuriya	
C - 22	<i>Evaluation of in vivo effects of traditional Sri Lankan spice mix on inflammation and the production of reactive oxygen species by peritoneal cells</i>  By <u>S.S. Gunasekara</u> , I.C. Perera, M.S. Mapalagamage	
C - 23	Genome-wide analysis and characterization of the LAZY gene family in <i>Oryza sativa</i>  By <u>D.S.Muthmala</u> and S.P.C. Fernando	
C - 24	An investigation on plant based, non-toxic, anti-aging compounds for cosmetics  By <u>K. I. L. De Silva</u> , L. Wanasekara, S. Perera and P. S. Saputhanthri	
C - 25	Application of <i>Allium cepa</i> bioassay for examining the status of potential <i>cytogenotoxicity</i> of two selected Sri Lankan rice varieties  By <u>A.M.P.E.K. Atapattu</u> , A.A.D.N. Thathsarani, U.A. Jayawardena	
C - 26	Harnessing the soil conditioning ability of Sesame ( <i>Sesamum indicum</i> L.) crop wastes  By <u>W.G.S.M. Rupasinghe</u> , I.A.J.K. Dissanayake, S.M.W. Ranwala	



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