Hosted by

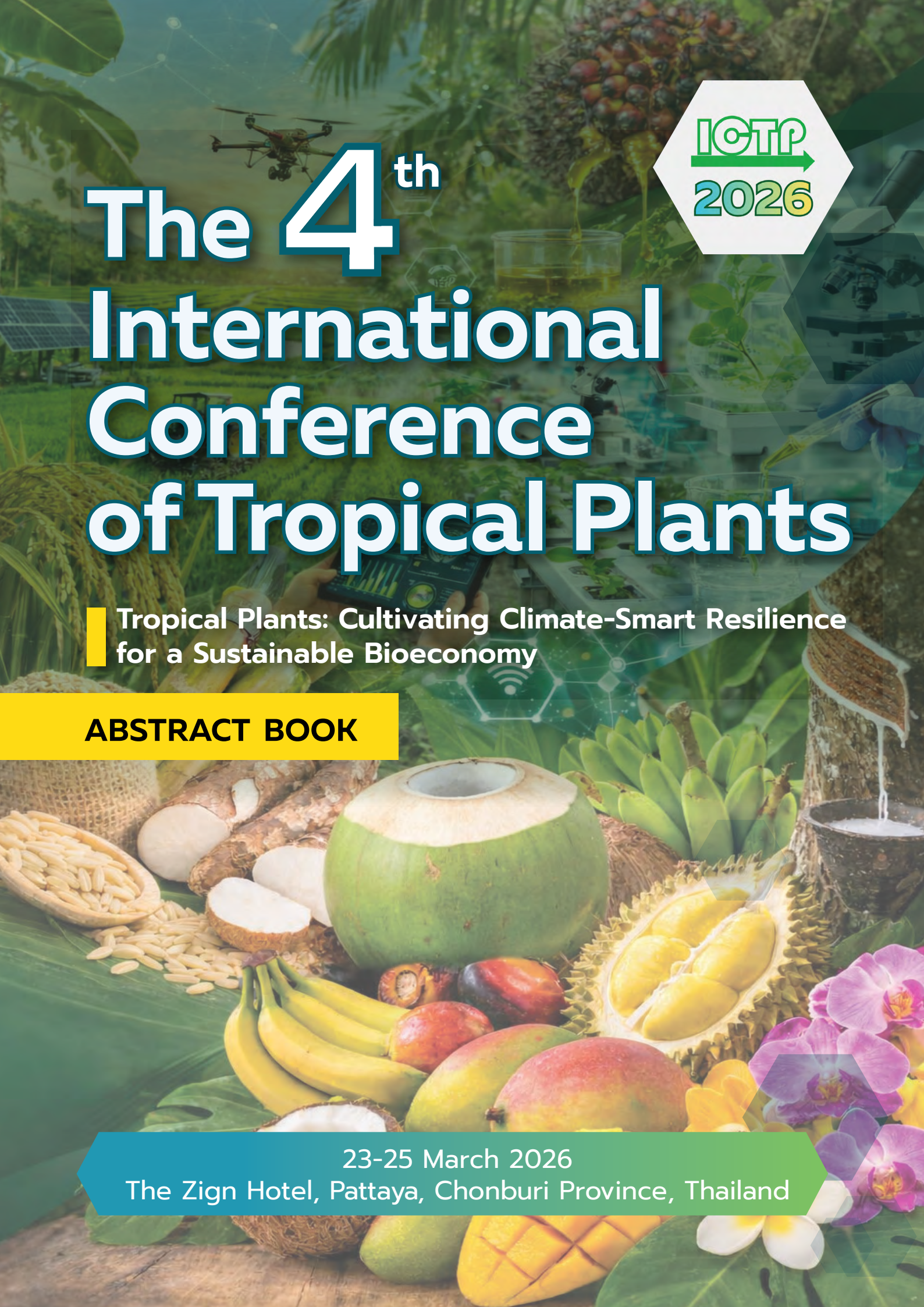
The 4th International Conference of Tropical Plants (ICTP2026)

Tropical Plants: Cultivating Climate-Smart Resilience for a Sustainable Bioeconomy

23-25 March 2026

The Zign Hotel Pattaya, Chonburi, Thailand

ABSTRACT BOOK



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ICTP 2026

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ABSTRACT BOOK

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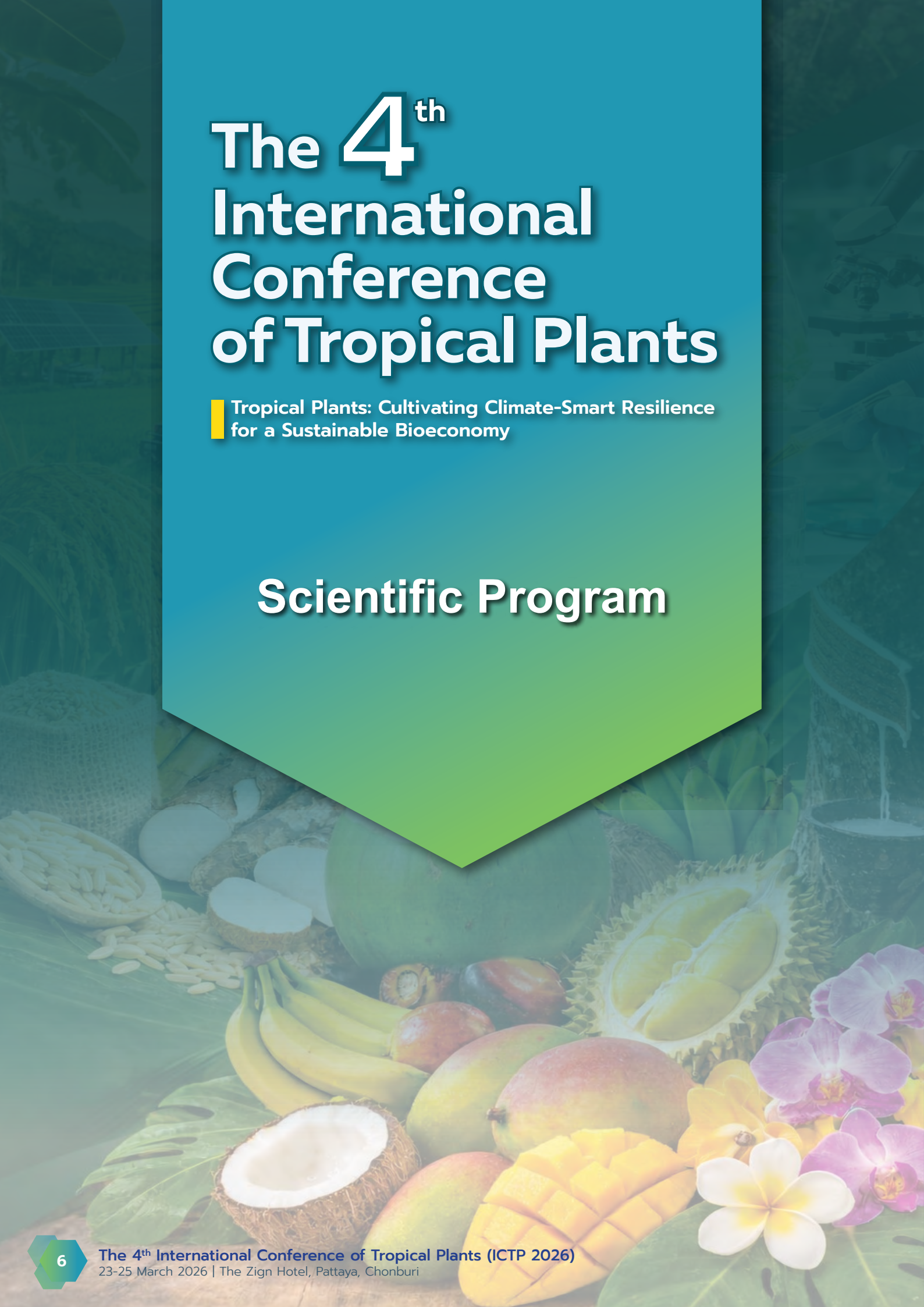
Scientific Program



Day 1: Monday, March 23, 2026

Time	Code	Room	Title	Speaker / Presenter
8:00 - 9:00		Fineen	**Registration**	
9:00 - 9:30		Fineen	**Opening Remarks**	**Dr. Damrong Sripraram** Acting President of Kasetsart University **Ms. Sirinporn Deotrakul** Deputy Executive Director, National Research Council of Thailand (NRCT)
9:30 - 10:00		Fineen	**Keynote Speaker (1)** "Advancing Thai Agriculture: Genome Editing for Global Sustainability and Economic Resilience"	**Dr. Piyarat Thammakijjawat** Director of Biotechnology Research and Development Office, Department of Agriculture, Ministry of Agriculture and Cooperatives"
10:00 - 10:30		Fineen	**Keynote Speaker (2) : Online** "The evolution and domestication of coconut"	**Prof. Jie Luo** Hainan University, Chief scientist of Multi-omics platform of Yazhoubay Laboratory, China
10:30 - 10:45		Fauna	**Coffee Break**	
10:45 - 11:15		Fineen	**Keynote Speaker (3)** "Engineering Tropical Plants to Replace Fossil Carbon"	**Prof. Robert Henry** Academician of Australian Academy of Technology and Engineering, University of Queensland, Australia
11:15 - 11:45		Fineen	**Keynote Speaker (4)** "Cryptochromes and plant highlight responses"	**Prof. Chengtao Lin** Fujian Agriculture and Forestry University, China
11:45 - 12:15		Fineen	**Keynote Speaker (5)** "From Germplasm to Global Markets: Advancing Coconut Research Excellence, Crop Protection, and Evidence-Based Governance"	**Dr. Jelfina Alouw** Director General International Coconut Community (ICC)
12:15 - 13:15			**Lunch**	
Oral Presentation			Session 4: Smart Agriculture, Forestry, & Plant Protection in Tropical Regions	Convener: **Prof. Youxiong Que** **Prof. Huang Xi**
13:15 - 13:30		Fineen	Areca palm velarivirus 1 encoded proteins suppress antiviral RNA silencing by mediating the degradation of SGS3 and disrupting the SGS3–RDR6 interaction	**Prof. Huang Xi**
13:30 - 13:45		Fineen	Epigenetic regulation of chilling injury in banana fruit	**Prof Peitao Lu**, Institute of Tropical Biosciences & Biotechnology, CATAS
13:45 - 14:00	O05	Fineen	Regenerative Design for Agriculture Service Providers in Thailand: A Structured Analytical Review of Ecological, Economic, Organizational, Social, and Governance Transitions	**Nutchanon Phichadul**, Ubon Ratchathani University
14:00 - 14:15	O12	Fineen	Enhancing Tea Oil Yield of Camellia oleifera Through Optimized Root Zone Soil Management	**Nattaporn Prakongkep**, Land Development Department
14:15 - 14:30	O14	Fineen	Association Between Canopy Size from RGB Images and Destructively Measured Biomass for Growth Assessment in Holy Basil	**Thanapat Nilwaranon**, Kasetsart University, Kamphaeng Saen Campus
14:30 - 14:45	O30	Fineen	Synergistic Effects of Pre-harvest UV-A Supplementation and CO2 Enrichment on Physiological Traits and Phytonutrient Profiles of Kale	**Jutiporn Thussagunpanit**, Kasetsart University
14:45 - 15:00	O31	Fineen	Loss and Recovery Dynamics of Mitochondria in Laticifers of the Rubber Tree During Repeated Latex Harvesting	**Jiaming Zhang**, Chinese Academy of Tropical Agricultural Sciences

Scientific Program

Day 1: Monday, March 23, 2026

Time	Code	Room	Title	Speaker / Presenter
Oral Presentation			Session 2: Physiological and Molecular Mechanisms of Stress Tolerance in Tropical Plants	Convener: **Prof. Dr. Yinghua Chen** **Assoc.Prof. Sutkhet Nakasathien**
13:15 - 13:30	O03	Flavio	Single Nucleus RNA-sequencing for Understanding Secondary Cell Wall Patterning of Xylem Vessels	**Elvian Indah Nilamsari**, Nara Institute of Science and Technology
13:30 - 13:45	O09	Flavio	Molecular regulation of sugar accumulation in citrus under cold stress	**Liu, Ji-Hong**, Huazhong Agricultural University
13:45 - 14:00		Flavio	Regulation of Cassava Immune Response by Xpm typeIII effectors	**Yinhua Chen**, Hainan University
14:00 - 14:15		Flavio	Mechanisms of Xanthomonas phaseoli pv. Manihotis effector XopAG in Regulating Cassava Immune Response	**Liyun Yang**, Hainan University
14:15 - 14:30	O07	Flavio	Effect of chitosan coating combined with 1-Methylcyclopropene on postharvest quality and storage life of MD2 pineapple under low-temperature conditions	**Peerasak Chaiprasart**, Naresuan University
14:30 - 14:45	O25	Flavio	Toward Climate-Smart Rice: Integrative Genomic Approaches for Candidate Gene Discovery Under Drought-prone Environments	**Phanchita Vejchasarn**, Rice Department
14:45 - 15:00	O29	Flavio	Multi-omics approach reveals the mechanisms of salt tolerance in rice	**Supatthra Narawatthana**, Thailand Rice Science Institute, Rice Department, MOAC
15:00 - 15:15		Fauna	**Coffee Break / Poster Session**	
Oral Presentation			Session 6: Tropical Plants in Carbon Sequestration and the Bioeconomy	Convener: **Prof. Peng Xu**
15:15 - 15:30		Fineen	Aboveground Biomass of urban Trees and Its Driving Factors in Tropical Cities of Hainan	**Prof. Huafeng Wang**, Hainan University **online**
15:30 - 15:45		Fineen	The mechanism of grain amaranth tolerance to salt and alkali stress and its potential application in improving saline-alkali soil	**Dr. Jinpeng Wan**, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences
15:45 - 16:00		Fineen	Genetic basis of coordinated sugar and amino acid accumulation during abiu fruit ripening revealed by a T2T haplotype-resolved genome	**Dr. Yuhua Chen**, Hainan University
Oral Presentation			Session 2: Physiological and Molecular Mechanisms of Stress Tolerance in Tropical Plants	Convener: **Prof. Dr. Yinghua Chen** **Assoc.Prof. Sutkhet Nakasathien**
15:15 - 15:30	O02	Flavio	Pushing through: QTL-Seq insight into root penetration under soil compaction in rice	**Suparad Klinsawang**, Kasetsart University Kamphaeng Saen Campus
15:30 - 15:45	O06	Flavio	Uncovering the Genetic Basis of Mega-Papillae Formation in Rice (*Oryza sativa* L.) Through QTL-seq and Genome-Wide Association Studies	**Watchara Phetluan**, Center of Excellence on Agricultural Biotechnology: (AG-BIO/MHESI)
Oral Presentation			Session 5: Discovery and Characterization of Novel Bioactive Compounds from Tropical Plants	Convener: **Asst. Prof. Dr. Srihunsa Malichan**
15:45 - 16:00	O13	Flavio	Effect of CPPU and Boric Acid on Flower Induction of Off-season Lychee	**Thanarut Chinnapan**, Maejo University
16:00 - 16:15	O24	Flavio	From Aroma to Preference: Linking Volatile Profiles and Consumer Acceptance in Landrace Chilli (*Capsicum* spp.)	**Chutchamas Kanchana-udomkan**, Kasetsart University, Kamphaeng Saen Campus
16:15 - 17:15		Fauna	**Poster Session**	
19:00 - 21:30		Z Beach	**Welcome Dinner**	

Day 2: Tuesday, March 24, 2026

Time	Code	Room	Title	Speaker / Presenter
9:00 - 9:30		Fineen	**Keynote Speaker (6)** "Improving Rice to Sustain One Health"	**Prof. Apichart Vanavichit** Rice Science Center Kasetsart University Kamphaeng Saen Campus
9:30 - 10:00		Fineen	**Keynote Speaker (7)** "From wild plants to novel calcium-rich vegetables"	**Prof. Hongwen Huang** Director of Lushan Botanical Garden The Chinese Academy of Sciences, China
10:00 - 10:15		Fauna	**Coffee Break**	
10:15 - 10:45		Fineen	**Keynote Speaker (8)** "Thai Sugar Industries: Toward Sustainability"	**Assoc. Prof. Wirat Vanichsriratana** Faculty of Agro-Industry, Kasetsart University
10:45 - 11:15		Fineen	**Keynote Speaker (9)** "The efficiency myth of polycrossing in cassava: evidence from the crossing nursery"	**Dr. Sean Fenstemaker** The Alliance of Bioversity International and CIAT, Columbia
11:15 - 11:45		Fineen	**Keynote Speaker (10)** "Sugarcane breeding: theoretical thinking and practical exploration"	**Prof. Youxiong Que** Institute of Tropical Biosciences & Biotechnology, CATAS
11:45 - 12:15		Fineen	**Keynote Speaker (11)** "Storage of the difficult mango, a climacteric fruit that refuses to play by the rules"	**Prof. Dr. Randy Beaudry** Michigan State University, USA
12:15 - 13:15			**Lunch**	
Oral Presentation			Session 7: Resilient Coconut Futures: Bridging Genetics, Smart Agriculture, and the Bioeconomy	
9:00 - 9:15		Vermillion	**Opening Remarks**	**Dr. Jelfina C. Alouw**, DG, ICC & KU president
9:15 - 9:45	O16	Vermillion	Coconut Germplasm Resources & Breeding for market competitiveness	**Dr. Niral Vittal**, CPCRI – India
9:45 - 10:15	O17	Vermillion	Coconut Tissue Culture: Present Developments and Future Opportunities	**Dr. Bart Panis**, Katholieke Universiteit te Leuven, Belgium
10:15 - 10:30		Vermillion	**Coffee Break**	
10:30 - 11:00	O18	Vermillion	Coconut agronomy and the evolving landscape of international trade	**Dr. Anjana Atapattu**, CRI – Sri Lanka
11:00 - 11:30	O15	Vermillion	Genomic & Molecular Breeding	**Dr. Samart Wanchana**, NSTDA, Thailand
11:30 - 12:00	O19	Vermillion	AI & Digital Technologies: Advancing Basic Molecular Research	**Dr. Andria Garavito**, CIRAD, France
12:00 - 13:00			**Lunch**	
Oral Presentation			Session 7: Resilient Coconut Futures: Bridging Genetics, Smart Agriculture, and the Bioeconomy	
13:00 - 13:30	O23	Vermillion	Sustainable Production and Dissemination of Three-Way Hybrid Coconuts to Thai Farmers	**Ms. Tippaya Kraitong** Director of Chumphon Horticulture Research Center, Horticulture Research Institute, Thailand
13:30 - 14:00	O20	Vermillion	Navigating molecular diagnostics to strengthen pest surveillance for resilient trade and shared prosperity	**Dr. Justine Milado**, Visayas University, Philippines
14:00 - 14:30	O27	Vermillion	Innovation-Driven and Sustainable Development of Thai Coconut Products	**Ms. Sarapee Yuadyong**, Managing Director of Chiwadi Productss, Thailand
Oral Presentation			Session 1: Climate Change Impacts and Adaptive Strategies for Tropical Agriculture	Convener: **Prof. Dr. Simon Wang** **Prof. Yun Zheng**
13:15 - 13:30		Flavio	A Weatherman's Take on Future Climate Extremes in Southeast Asia	**Prof. Dr. Simon Wang**, Kasetsart University

Scientific Program

Day 2: Tuesday, March 24, 2026

Time	Code	Room	Title	Speaker / Presenter
13:30 - 13:45	O01	Flavio	Multiomics analysis of flowers reveals that enlarged epidermic cell of petal is the major reason of large flowers of *Gypsophila paniculata* L.	**Prof. Yun Zheng**, Yunan Agriculture University
13:45 - 14:00	O08	Flavio	Inoculation of wheat seeds with spore-forming bacteria as a novel approach to enhance growth under climate change-induced stress conditions	**Shafiqullah Aryan**, Tokyo University of Agriculture and Technology
14:00 - 14:15	O10	Flavio	Prospects of Plant Growth-Promoting Rhizobacteria from Different Plant Rhizospheres as Biofertilizers for Diverse Crops in Japan	**Safiullah Habibi,** Tokyo University of Agriculture and Technology
14:15 - 14:30	O11	Flavio	Growth Responses of Rice to Viable and Non-Viable Bacillus Spores	**Ali Yawar Seerat**, Tokyo University of Agriculture and Technology
14:30 - 14:45	O28	Flavio	Performance of Alginate-Gelatin Hydrogel-Coated Maize Seed during Germiantion and Seedling Establishment under Limited Water Condition	**Panuphun Boonsuebsakoon**, Kasetsart University
Oral Presentation			Session 3: Advanced Breeding and Biotechnology for Climate-Resilient Tropical Crops	Convener: **Prof. Dr. Zhiqiang Xia**
13:15 - 13:30		Fineen	AI for Plants: Research on Tropical Plant Genomes Driven by Artificial Intelligence	**Prof. Dr. Zhiqiang Xia**, Sanya Institute of Breeding and Multiplication
13:30 - 13:45		Fineen	Research Progress on the Genome of Sesbania Genus and its Breeding Application	**Assoc.Prof. Fuqiang Wang**, Hainan Seed Industry Laboratory
13:45 - 14:00		Fineen	Multi-omics decipher the metabolic basis of flavor and nutritional quality in tropical fruits	**Prof. Wenquan Wang**, Hainan University
14:00 - 14:15	O21	Fineen	NKI17196-102-2-1-1-1-SKN-1: A Promising Photoperiod Insensitive Glutinous Rice Line with Blast and Bacterial Blight Resistance for Irrigated Lowland Area in Northeastern Thailand	**Surachet Chamontri**, Sakon Nakhon Rice Research Center
14:15 - 14:30	O22	Fineen	Carotenoid Accumulation and Regulation of Carotenogenic Gene Expression During Ripening of Red-Fleshed 'Siam Red Ruby' Pumelo (Citrus grandis)	**Assoc. Prof. Dr. Samak Kaewsuksaeng**, Thaksin University
14:30 - 14:45	O26	Fineen	Reconceptualizing Cassava: Regional Approaches to Breeding, Processing, and Market Integration	**Vishnuvardhan Reddy Banda**, International Institute of Tropical Agriculture (IITA)
14:45 - 15:00		Fineen	Genetic Dissection of Root Crown Architecture Using 3D Modelling for Yield Improvement	**Assoc. Prof. Supachai Vuttipongchaikij**, Kasetsart University
15:00 - 15:15		Fauna	**Coffee Break / Poster Session**	
Oral Presentation			Session 3: Advanced Breeding and Biotechnology for Climate-Resilient Tropical Crops	Convener: **Prof. Dr. Zhiqiang Xia**
15:15 - 15:30		Fineen	Cassava Breeding for Cassava Mosaic Disease Resistance at Kasetsart University	**Asst. Prof. Piya Kittipadakul**, Kasetsart University
15:30 - 15:45		Fineen	Driving Genome Innovation: Complete T2T Genomes and Multi-Omics Solutions	**Xiaojun Su**, Sailgene Technology (Hong Kong) Co., Ltd.
15:45 - 16:00		Fineen	Application of Multi-omics in Tropical Crop Research	**Dr. Xiaoyun Wu**, SanshuBio, China
16:00 - 16:15	O04	Fineen	QTL-seq Identifies a Wall-associated Kinase as a New Resistance Gene to Bacterial Leaf Streak in Rice	**Moe Moe Kyi Win**, Kasetsart University Kamphaeng Saen Campus
16:15 - 16:45		Fineen	**Closing Remarks**	

Day 2: Tuesday, March 24, 2026

Time	Code	Room	Title	Speaker / Presenter
			The Fouth Editorial Board Meeting of Tropical Plants Theme: Summarize and enhance to approach top-tier publication status"	
17:30 - 17:50		Vermillion	(EiC), Development Report of Tropical Plants	**Wenquan Wang**
17:50 - 18:20		Vermillion	Seminar on Problems and Opportunities of TPs.	**Fei Chen** (Organizer)
18:20 - 18:40		Vermillion	Summary of the meeting	**Max Cheng, Robert Henry, Jie Luo**

Day 3: Wednesday, March 25, 2026

Time	Room	Title	Speaker / Presenter
		Field Trip Program	
7:00 - 9:00		Depart from The Zign Hotel Pattaya to Kubota Farm	
9:00 - 12:00		Educational tour and exploration of Kubota Farm	
12:00 - 13:00		**Lunch**	
13:00 - 14:15		Depart from Kubota Farm to Rayong	
14:15 - 15:30		Site Visit at Farm Ruenrom	
15:30 - 17:30		Depart from Farm Ruenrom to The Zign Hotel Pattaya	
		Workshop on Coconut Genomics: “From Coconut DNA to Breeding Applications”	Moderators: **Dr. Siwaret Arikit**, Associate **Professor, KU, Dr. Ste phanie Bocs**, CIRAD, France, **Dr. Samart Wanchana**, NSTDA, **Dr. Wasin Ponchewin**, NSTDA, Thailand
9:00 - 16:45	Vermillion	Session 1: Coconut Genomics Landscape Session 2: SNP Data Handling & Quality Control Session 3: Genetic Diversity & Population Structure Session 4: GWAS and Trait Mapping in Coconut Session 5: Genomic Selection for Coconut Session 6: Data Sharing & International Collaboration Session 7: Discussion & Future Roadmap	

The 4th International Conference of Tropical Plants

Tropical Plants: Cultivating Climate-Smart Resilience for a Sustainable Bioeconomy

Keynote Speaker

Advancing Thai Agriculture: Genome Editing for Global Sustainability and Economic Resilience

Dr. Piyarat Thammakijjawat

Thailand's agricultural sector remains a cornerstone of national economic development, food security, and rural livelihoods. However, increasing climate variability, emerging pests and diseases, and rising global demand for nutritious and high-quality food are posing significant challenges to sustainable agricultural production. Addressing these complex challenges requires innovative approaches that integrate science, technology, and policy to strengthen agricultural resilience and long-term sustainability.

Genome editing has emerged as a transformative biotechnology that enables precise, efficient, and rapid crop improvement. Recognizing its strategic potential, Thailand has incorporated genome editing into national development strategies under the Bio-Circular-Green (BCG) economy model, which seeks to leverage the country's rich biodiversity, promote innovation, and enhance value creation in agricultural products while advancing environmentally sustainable production systems. To support responsible innovation, the Ministry of Agriculture and Cooperatives has established a science-based regulatory framework for genome editing. Ministerial and departmental notifications issued during 2024–2025 define transparent criteria and certification mechanisms for genome-edited plants, animals, and aquatic species, ensuring biosafety, regulatory clarity, and alignment with international standards. In parallel, Thailand is strengthening research and development through collaborative genome editing projects across several research institutions, supported by national funding agencies.

The genome editing innovation forum provides a valuable platform to strengthen international collaboration, exchange knowledge, and foster research partnerships, highlighting the potential of genome editing to advance resilient agricultural systems, enhance food security, and support sustainable bioeconomy development at both national and global levels.

Keynote Speaker

Engineering Tropical Plants to Replace Fossil Carbon

Robert J Henry

ARC Research Hub for Engineering Plants to Replace Fossil Carbon, University of Queensland, Brisbane QLD 4072 Australia

Reductions in the use of fossil carbon is a key target of efforts to limit climate change. Plants provide an alternative option providing a renewable source of carbon for use in the production of chemicals (e.g. for plastic production) and fuels that cannot be replaced by electrification (e.g. sustainable aviation fuels). The production of plants for this purpose needs to avoid significant competition with food production and biodiversity conservations. This requires highly efficient capture of carbon from that atmosphere by high yielding crops that allow production on a relatively small land footprint. Tropical plants are the most promising options that might allow production on the scale needed. Conversion of the biomass of these crops to chemicals and fuels requires improved conversion technologies but will benefit greatly from improved biomass composition. Genomics and gene editing offer technologies that could deliver the genetic modifications needed. Progress towards genetic improvement of these traits in key tropical crops will be discussed.

Cryptochromes and plant highlight responses

Chentao Lin

Basic Forestry and Plant Proteomics Research Center,
Fujian Agriculture and Forestry University, Fuzhou, China

Tropic plants are characterized by molecular mechanisms responsible for highlight adaptation. Plant cryptochromes (CRYs) are nuclear blue light receptors that mediate almost all responses. We recently found that Arabidopsis CRYs are essential for the survival of young seedlings grown in highlight. According to our current understanding, plant CRYs exist as monomers in darkness, the photoexcited CRYs oligomerize to form photobody that contain various CRY-interacting proteins. CRYs physically interact with non-constitutive or the constitutive CRY-interacting proteins to form the non-constitutive or the constitutive CRY complexes, respectively. The non-constitutive CRY complexes exhibit different affinity to CRYs in response to light, and they act by the light-induced fit (lock-and-key) mechanism. The constitutive CRY complexes exhibit similar affinity to CRYs regardless of light exposure, and they act by the light-induced Liquid-Liquid Phase Separation (LLPS) mechanism. Plant CRY complexes contain >100 CRY-interacting proteins, including transcription factors, chromatin remodelers, splicing factors, ubiquitin ligases, protein kinases, mRNA methyl-transferases, hormone receptors, etc. However, how this large number of CRY complexes work together to regulate plant highlight responses remain unclear. Possible molecular mechanisms underlying plant highlight response will be discussed.

From Germplasm to Global Markets: Advancing Coconut Research Excellence, Crop Protection, and Evidence-Based Governance

Jelfina C Alouw

International Coconut Community (ICC)

The coconut (*Cocos nucifera* L.) stands as a fundamental pillar of the global circular bioeconomy, uniquely positioned to address escalating market demands through its vast and resilient genetic diversity. As the "Tree of Life," every anatomical component of the crop serves as a high-value feedstock for zero-waste industrialization, offering healthy and nutritious foods and a sustainable alternative to synthetic materials in sectors ranging from renewable energy to green infrastructure. However, the global industry currently navigates a "Production-Demand Paradox," where consumer interest is soaring, but primary productivity remains stagnant. This supply-side vulnerability is exacerbated by aging plantations and a heavy geographic concentration of production, presenting a significant risk to the global supply chain. To resolve this paradox, the International Coconut Community (ICC) and Coconut Genetic Resource Networks (COGENT) advocates for a strategic transition from traditional subsistence agriculture to high-precision, evidence-based governance. Central to this shift is the preservation of germplasm through our network of International Coconut Genebanks (ICGs) and the deployment of advanced biotechnologies such as micro-propagation to scale elite, climate-resilient clones. By maximizing the mechanical and chemical valorization of all coconut derivatives, including the integration of lignocellulosic fibers and ash into sustainable construction materials, the industry can unlock its full economic potency. Transitioning from low-value raw exports to high-precision processing of coconut-based products provides a roadmap to double the sector's global valuation from US$20 billion to US$41 billion. This systemic evolution ensures that the coconut remains a resilient driver of food security and economic stability in a decarbonizing world.

Keywords: Coconut, COGENT, ICGs, coconut-based products

Improving Rice to Sustain One Health

Apichart Vanavichit[1], Siriphat Reungphayak[1], Anuchart Sawasdeeand[1] and Siwaret Arikit[1,2]

[1] Rice Science Center, Kasetsart University, Kamphangsaen, Nakhon Pathom, 73140, Thailand
[2] Agronomy Department, Faculty of Agriculture, Kamphangsaen; Nakhon Pathom, 73140, Thailand

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One Health is a holistic approach to health that encompasses humans, animals, and the planet. In the Thai context, rice is a key element, serving as the starting point of the food chain that shapes a single health context. Thailand has more than half of its total agricultural land dedicated to rice cultivation—possibly as much as 75 million rai, with about 80% on main-season and 20% on off-season rice paddies. Therefore, the rice cultivation system directly and inevitably impacts One Health. Consequently, rice-based food products affect the health of consumers globally, as well as livestock that consume rice straw, and microorganisms in the soil and surrounding plant and animal remains. All these factors contribute to a chain reaction, from popular chemical-driven rice farming methods to biochemical-driven farming systems, impacting the environment, microorganisms, and ultimately humans and animals. Of course, organically grown rice often yields less and is more susceptible to disease and pest outbreaks. This forces breeders to improve photosynthetic efficiency, disease and pest resistance, nitrogen and water use efficiency, and, at the same time, nutrient density. However, rice production that fails to account for greenhouse gas emissions inevitably contributes to global warming, particularly affecting the agricultural environment. Alternating wetting and drying techniques to reduce irrigation water use and prolonged waterlogging have resulted in a 30-40% reduction in greenhouse gas emissions. However, this is compounded by decreased weed competition and higher soil temperatures, leading to reduced rice yield unless rice varieties are developed that are water-saving but have high photosynthetic rates, possess methane-inhibiting properties, promote nitrogen-fixing bacteria, and reduce CH4-emission bacteria populations. These improvements would increase rice productivity and mitigate global warming by developing carbon-neutral and net-zero rice production systems. Efforts to reduce rice straw burning can be addressed by processing it into various materials or by improving its biodegradability (brittle stems) by reducing lignin accumulation in the stem and leaf structures (cellulose). This results in more easily digestible, nutrient-rich forage straw (bioavailability) that is suitable for innovative food and feed products. However, the impact on grain and leaf quality, disease and pest susceptibility, and lodging remains an area for improvement. Therefore, suitable rice varieties, environmentally friendly cultivation systems, and effective straw management are key to a One Health approach.

Keywords: One Health, Oryza sativa, GHG Emission, Nutrient-dense Rice, Climate-ready Rice

Thai Sugar Industries: Toward Sustainability

Wirat Vanichsriratana[1,2] and Naiyasit Yingkamhaeng[1,3]

[1] Center of Knowledge and Technology for Cane and Sugar, National Research Council of Thailand (NRCT)
[2] Thailand Society of Cane and Sugar Technologists (TSSCT)
[3] Kasetsart Agricultural and Agro-Industrial Product Improvement Institute (KAPI), Kasetsart University

The Thai sugar industry is a major agro-industrial sector in Thailand. This consists of sugarcane production in field and sugar production in the mills. At its peak, Thailand produced up to 134.9 million tons of sugarcane (year 2017) and has been one of the world's leading sugar exporters and used to be ranking second globally. In recent years, Thai sugar mills have adopted zero-waste practices, ensuring that nearly all by-products from the production process are utilized as valuable co-products. For example, bagasse is used for cogeneration of heat and electricity, molasses is processed into ethanol, and filter cake is applied as fertilizer. These practices align with Thailand's government policy promoting the Bio-Circular-Green (BCG) economic model, which aims to enhance sustainability and strengthen national competitiveness. In sugarcane cultivation with environmental concerns, particularly PM2.5 pollution associated with sugarcane burning, have driven changes in farming practices. Agricultural mechanization is increasingly adopted to reduce dependence on manual labor and minimize burning. In addition, green leaves and cane tops collected during mechanical harvesting can be utilized as biomass or converted into biochar. Returning these materials to the soil helps increase organic matter and recycle carbon, supporting the principles of regenerative agriculture. Together, these approaches contribute to forwarding of sustainability of the sugar industry in Thailand.

Keywords: Sugarcane industry; Bio-Circular-Green economy; Biomass utilization; Sustainable agriculture

The efficiency myth of polycrossing in cassava: evidence from the crossing nursery

Sean Fenstemaker[1], Alex Ferris[2], Nelson Morante[1] and Xiaofei Zhang[1]

[1] The Alliance of Biodiversity International and the International Center for Tropical Agriculture (CIAT), Apartado Aéreo, Cali, 6713, Colombia
[2] Agricultural Development Division, Gates Foundation, Seattle, WA, USA

Polycross nurseries have traditionally been used in cassava breeding to overcome poor and asynchronous flowering, increase seed production, and generate large, genetically diverse seedling populations with less labor, while fitting phenotypic recurrent selection systems where unknown paternity was acceptable. However, modern breeding approaches based on genomic selection, pedigree tracking, and quantitative genetic analysis require known parentage and therefore favor controlled biparental crosses. To evaluate mating patterns in a polycross system, we genotyped progeny using 30 KASP markers distributed across the 18 cassava chromosomes along with three trait-linked markers for CMD resistance, provitamin A, and starch content. Five half-sib families with known maternal parents—CR63 (N=58), GM7672-7 (N=189), PER221 (N=157), SM2775-4 (N=100), and SM2828-28 (N=105)—were genotyped together with all 40 potential parents in the polycross nursery. Paternity assignment identified a single pollen donor for 73% of progeny, multiple donors for 13%, no matching donor for 12%, and mismatched maternal identity for 1%. Self-pollination rates among the maternal parents ranged from 14% to 52% (mean 27.8%). Month effects were modest: selfing rates remained relatively stable from February to May (~0.15–0.20) and increased slightly in June (~0.28), suggesting only limited seasonal influence despite the six-month crossing period. This pattern may reflect modest changes in flowering overlap or pollen availability through time, but genotype effects were clearly stronger. For example, SM2775-4 exhibited consistently high selfing (~52%), while GM7672-7 remained modest (~14%). Pollen contribution among outcrossed progeny was highly uneven, with many potential donors contributing <1% of offspring and fertilization dominated by a small subset of males. Together, these results indicate that mating in the polycross nursery is strongly non-random, with genotype-specific selfing and skewed pollen success substantially reducing the effective number of male parents and overall recombination among breeding parents. Consequently, a significant fraction of progeny assumed to be outcrossed may actually be selfed, implying that breeding programs may allocate substantial resources to screening populations with limited recombination. Given an average evaluation cost of **$0.52 per m²**, the inadvertent inclusion of selfed progeny in half-sib families may represent a meaningful inefficiency in early-stage field evaluation.

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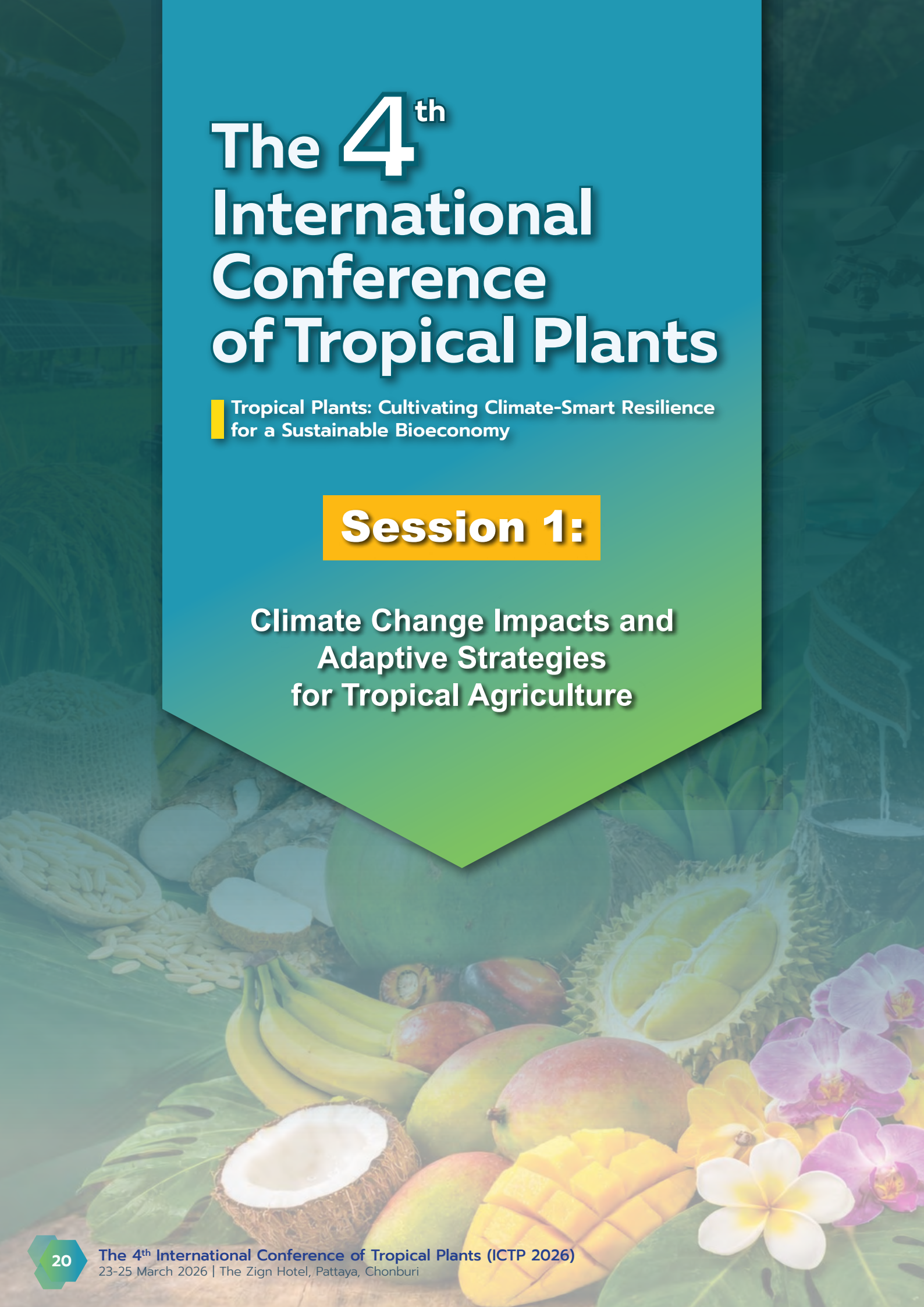
Session 1:

Climate Change Impacts and Adaptive Strategies for Tropical Agriculture



Multiomics analysis of flowers reveal that enlarged epidermic cells of petals as the major reason of large flowers of *Gypsophila paniculata* L.

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ABSTRACT:
Gypsophila paniculata L. is an important cut flower, often used as decorating flower or processed into eternal (or dry) flower. *Gypsophila paniculata* L. with double petals (GPDP) is of very high ornamental and economical value. However, the flower of GPDP is very small, with average diameters of 10 to 14 mm, which severely hinders the elevation of its economic value. To understand the molecular mechanism of the enlargement of flowers of GPDP, we produced RNA-Seq, small RNA-Seq and degradome profiles of petals of two GPDP cultivars, one with small flowers of diameters of 10 mm and the other with flowers of diameters of 14 mm. Our results indicate that the gene expression profiles of these two GPDP cultivars are very different. We also characterized the miRNA-mediated gene network in *Gypsophila paniculata* L. Importantly, we found that the epidermic cells of petals were significantly enlarged in the cultivar with large flowers. Our results also suggest that an MYB gene is a key regulator for the enlargement of epidermic cells in the GPDP cultivar with large flowers. In summary, our results indicate that the enlargement of epidermic cells of petals is the main reason for the larger flowers of *Gypsophila paniculata* L., which provide clues for breeding of more valuable cultivars of baby's breath.

Inoculation of wheat seeds with Spore-Forming Bacteria as a Novel Approach to Enhance Growth under Climate Change-Induced Stress Conditions

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ABSTRACT:
Spore-forming bacteria (SFB) survive various environmental stress conditions by transforming into dormant endospores. In this study, we isolated 243 strains of SFB from the roots and rhizosphere soils of crops. The 16 S rRNA sequences of the selected 62 isolates identified *Bacillus* (45%), *Priestia* (31%), and *Paenibacillus* (24%). These *Priestia* and *Paenibacillus* isolates showed the capability for P solubilization, *Priestia* strains were capable of K solubilization and exhibited higher indole-3-acetic acid, while *Bacillus* strains showed strong siderophore production. Whole genome analysis of isolates, TTREn1 and TCCSREp1, classified them as *Priestia aryabhattai* and *Paenibacillus* sp. Inoculation of wheat seedlings with the spores of 13 selected isolates improved shoot and root biomass under control and stress conditions (heat and drought) compared to uninoculated controls. *Bacillus* species, which showed higher biofilm formation among the three genera, colonized roots endophytically when inoculated as spores under drought stress, whereas the other isolates tested did not. Furthermore, spore inoculation modulated the expression of stressrelated genes such as *APX*, *CAT*, and *P5CS*, with strong induction observed under heat stress and suppression under drought stress in most isolates. Our findings demonstrate the potential eaicacy of spore inoculation in enhancing wheat plant growth resilience under heat and drought stress conditions.

Keywords: Heat stress, Drought stress, PGPR, Spore-forming bacteria, Spore inoculation, Wheat

Prospects of Plant Growth-Promoting Rhizobacteria from Different Plant Rhizospheres as Biofertilizers for Diverse Crops in Japan

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ABSTRACT:
Increasing plant productivity is a major challenge, and excessive use of chemical fertilizers has caused many environmental problems. Microbial inoculants are considered effective biotechnology to promote plant growth and mitigate environmental pollution. Thus, a total of 166 bacteria were isolated from different plant rhizospheres at Tokyo University of Agriculture and Technology, and their physiological and genetic characterization, as well as their effects on rice growth, were analyzed. Out of 166 isolates, 115 produced Indole-3-Acetic Acid (IAA) (0.04 -231 µg L^{-1}), 122 showed nitrogen fixation activity (0.04- nmole C_2H_4 h^{-1}), and thirty-six exhibited P solubilization (0.4-4.5 mm). 16S rRNA gene analysis categorized the isolates into the genera *Enterobacter*, *Pseudomonas*, *Stenotrophomonas*, *Bacillus*, *Allorhizobium*, *Caulobacter*, *Agrobacterium*, and *Klebsiella*. Inoculation of isolates on rice resulted in a significant increase in growth attributes, indicating their potential to enhance rice growth and productivity. Among the isolates, JR5 from paddy soil and JW191 from upland soil (wheat rhizosphere) exhibited high physiological characteristics of nitrogen fixation and IAA production, respectively. Hence, the genomes of those isolates were sequenced for further genetic analysis. Interestingly, the isolates were found to harbor numerous genes associated with key physiological traits, particularly phosphate solubilization, IAA production, nitrogen fixation, biofilm formation, and other important plant growth-promoting characteristics. In this study, most of the isolates effectively promoted rice growth *in vitro* conditions and are planned to be further evaluated under field conditions for biofertilizer development across diverse environments.

Keywords: Rice, Plant growth-promoting rhizobacteria, IAA production, Nitrogen fixation, Phosphate solubilization, Genetic characterization

Funding: The Cabinet Office, Government of Japan, Moonshot R&D Program for Agriculture, Forestry and Fisheries (JPJ009237, funding agency: Bioriented Technology Research Advancement Institution)

Growth Responses of Rice to Viable and Non-Viable Bacillus Spores

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ABSTRACT:
Biofertilizers based on plant growth-promoting bacteria (PGPB) are increasingly recognized as sustainable alternatives to chemical fertilizers for improving crop productivity. Among PGPB, *Bacillus* species receive particular attention due to their spore-forming ability, which provides high environmental tolerance and formulation stability. This study evaluated the effects of live spores and dead spores (spore-related materials) of different *Bacillus* species on the growth responses of japonica rice cv. Hitomebore, with the aim of clarifying how both viable and non-viable spores contribute to rice growth-related traits and their applicability in biofertilizer development.

Rice seeds were inoculated at the coleoptile emergence stage with live spores or spore-related materials derived from *Bacillus altitudinis* (TUAT1, JR4, JR198), *B. pumilus* (JM52, MAFF118530, MAFF301706), and *B. megaterium* (MAFF301694, MAFF520023). Seedlings were harvested two weeks after sowing, and growth parameters associated with yield potential were measured. Live spores significantly promoted root growth in response to several strains, including TUAT1. Notably, dead spores significantly increased root dry weight across all tested strains.

The growth-promoting effects observed in this study emphasize the importance of *Bacillus* spores, including non-viable spores, in stimulating rice growth through spore-associated components rather than bacterial viability. These effects are likely mediated by structural molecules of Gram-positive spores, such as peptidoglycan components recognized by plant LysM receptors (e.g., LYM3) (Islam et al., 2024). Overall, both live and dead *Bacillus* spores can promote rice growth and support the development of stable and reliable spore-based biofertilizer formulations for sustainable rice production.

Performance of Alginate-Gelatin Hydrogel-Coated Maize Seed during Germination and Seedling Establishment under Limited Water Condition

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ABSTRACT:
Hydrogel have been widely applied as the soil conditioner to improve soil water availability for plant growth and development. In contrast, the application of hydrogel-assisted seed enhancement during seed germination remains limited. This experiment evaluates the effects of two hydrogel seed coating formulations (SC1 and SC2) relative to uncoated seed (SC0), on physiological and molecular responses during seed germination and on subsequent seedling establishment under two initial water-holding capacity (IW) levels (IW1 = 30% IW and IW2 = 60% IW) in sand culture system. The results showed that SC1 and SC2 improved seed imbibition (SI) during 0 to 24 HAI and 30 to 36 HAI compared with SC0, except at 27 and 48 hours after imbibition (HAI). IW significantly influenced the entire imbibition period, with reduced SI observed under IW1. At 36 HAI, Malondialdehyde (MDA) content was higher at IW1 than IW2 in SC0 and SC1, except for SC2. Seed coating with SC1 and SC2 reduced *ZmSOD4* expression compared with SC0. In contrast, *ZmSOD4* and ZmCAT2 expressions were higher at IW1 than at IW2, irrespective of whether seed were coated or uncoated. At 48 HAI under IW1, the percentage of radicle emergence (%RE) of SC2 was significantly inhibited, whereas SC1 showed a comparable %RE to that of SC0. Under IW2, the %RE of SC1 remained lower than that of SC0 but higher than that of SC2, and SC2 exhibited lowest germination percentage (%GR) at 96 and 168 HAI. At 168 HAI, SC0 showed the highest seedling vigor indices (SVI-I and SVI-II) under IW2. In contrast, under IW1, SC1 exhibited higher SVI-II as well as higher root and total conversion rates than SC0, except for shoot conversion rate. Neither seed coating formulation nor IW did not significantly affect seed reserve utilization efficiency at this stage.

Keywords: Drought, Hydrogel, Seed Coating, Imbibition, MDA, Gene Expression

Soil–Plant Nutrient Dynamics Assessment of Regenerative Practices in Thai Aromatic Coconut Orchards

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ABSTRACT:
The adoption of regenerative practices in Thai aromatic coconut orchards promotes a bio-circular system designed to enhance soil fertility and crop productivity while strengthening environmental resilience. However, data on the long-term impact of these practices on soil-plant nutrient dynamics remains limited. This study evaluated the soil-plant nutrient dynamics across eight diverse orchards in the central lowland delta of Thailand (Ratchaburi and Samut Sakhon). Soil physico-chemical properties (at 0–15 and 15–30 cm depths) and leaf macronutrient status (via index leaf 14) were quantified to assess spatial variability and the sustainability of current regenerative transitions. Results revealed that the majority of the sites were heavy clays with alkaline pH (7.10–7.67) and high CEC (> 21.4 cmol/kg). Of the eight sites, S8 had higher levels of potassium (647.63 ppm) and available phosphorus (1,032.1 mg/kg), while S2 (2,588.5 ppm) and S1 (2,148.9 ppm) had exceptionally high levels of exchangeable sodium, all of which were significantly higher than those of the other sites ($p < 0.001$). Organic matter and total nitrogen were significantly higher in topsoil (0–15 cm) than in subsoil (15–30 cm) at $p < 0.001$. Soil micronutrients such as iron (Fe), zinc (Zn), and manganese (Mn) were also sufficiently high, with the exception of copper (Cu), which was consistently deficient in all sites. In contrast, leaf tissue analysis failed to reflect the high soil concentrations, showing a weak correlation between soil and leaf nutrient status except for Mg and Fe. Although total N (1.26–1.67%) and total Ca (0.30–0.41%) concentrations were slightly lower than the optimal range, total P (0.17–0.22%), total Mg (0.25–0.38%), and total S (0.577–0.617%) were sufficiently higher compared to the standard requirements across all locations. The findings show that regenerative practices work as adaptive strategies to climate change by maintaining soil fertility, while underlining the need for site-specific management of soil fertility in the context of increasing climatic variability.

Keywords: Regenerative, aromatic coconut, soil-plant nutrient dynamics, physico-chemical properties

Gas Exchange and Morphological Responses of Miniature Dendrobium Hybrids to Heat Stress

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ABSTRACT:
Ongoing climate change has led to a sustained increase in global temperatures, posing serious constraints on plant growth and productivity. This study investigated heat stress responses in miniature *Dendrobium* hybrids, an economically important potted orchid, through the evaluation of gas exchange parameters and morphological characteristics under elevated temperature conditions. Plants were exposed to three day/night temperature regimes: 30/25 °C (control), 35/30 °C, and 40/35 °C for 16 days. Physiological parameters, including CO_2 exchange rate (CER), stomatal conductance (g_s), transpiration rate (E), water use efficiency (WUE), and leaf greenness, were monitored. Temperature significantly affected CER. Plants grown at 30/25 °C maintained positive CER values (0.45–0.77 μmol m^{-2} s^{-1}), whereas those exposed to 35/30 °C and 40/35 °C exhibited negative CER values, indicating a shift from net carbon gain to net carbon loss. Stomatal conductance was significantly reduced under both elevated temperature regimes compared with the control. Although plants at 35/30 °C showed the lowest transpiration rate at 4 days after treatment, no significant differences were detected among treatments at 8 and 16 days. Morphological observations revealed severe and irreversible deterioration in plants exposed to 40/35 °C, characterized by extensive leaf browning, tissue desiccation, and leaf abscission. In contrast, plants subjected to 35/30 °C exhibited only a slight reduction in leaf greenness without visible structural damage. These findings indicate that extreme high temperature (40/35 °C) exceeds the physiological tolerance threshold of miniature *Dendrobium* hybrids, resulting in functional disruption and irreversible decline.

Keywords: Photosynthetic inhibition, Thermal injury, Stomal conductance, Orchid

Growth and Maintenance Respiration in Relation to Leaf Development in Robusta Coffee under Low-Light Environments

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ABSTRACT:
In low-light agroforestry systems, the balance between growth and maintenance respiration strongly influences carbon-use efficiency and leaf development in coffee plants. However, developmental respiratory dynamics in Robusta coffee remain insufficiently characterized. This study investigated the relationship between respiration components and leaf expansion in two widely cultivated Thai Robusta cultivars, Chumphon 2 (CH2) and a local variety (LO), under shaded conditions.

One-year-old plants were grown under 80% shade in a greenhouse. Newly unfolded leaves (4–7 cm) were tagged at day 0, and daily measurements of single-leaf area and dark respiration rate were conducted using an LI-6400 system until full expansion (n = 10 plants/cultivar).

Leaf expansion followed a typical sigmoid pattern in both cultivars. CH2 expanded more rapidly, reaching full expansion at day 19 with a larger final leaf area (106 cm²) compared to LO (day 21, 93 cm²). Respiration rate declined logarithmically with leaf age, and the relative growth rate of leaf area showed a strong positive linear relationship with Rd in both cultivars.

Two-component respiration modeling revealed no significant difference in growth respiration coefficients between cultivars. However, LO exhibited slightly higher baseline maintenance respiration. Despite its greater final leaf biomass, CH2 maintained lower maintenance respiration, indicating a modest advantage in carbon-use efficiency during leaf expansion.

These results demonstrate that under shaded conditions, both cultivars exhibit sigmoid leaf development and tight coupling between respiration and growth. Nonetheless, CH2 shows a subtle advantage in carbon allocation efficiency, providing useful physiological insights for cultivar selection and management in shaded agroforestry systems.

Keywords: Relative growth rate, Leaf expansion, Growth respiration, Maintenance respiration, Shade adaptation, *Coffea canephora*

Evaluation of Soil Fertility in Sugarcane Production Areas of Central Thailand

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ABSTRACT:
This study evaluated the soil fertility of major sugarcane production areas in Central and Northern Thailand, specifically targeting lands classified as moderately suitable (S2) according to the Agri-Map database. Soil samples were collected from 15 plots each in Nakhon Sawan, Lopburi, Kanchanaburi, and Suphan Buri provinces between October 2024 and March 2025 to assess fertility levels and identify soil constraints. The results revealed that 81.6% of the total surveyed area contained very high levels of exchangeable potassium (K_2O). Organic matter (OM) was predominantly at a medium level (43.4%), while (P_2O_5) was very high in 40% of the samples. Among the studied provinces, Lopburi exhibited the highest soil fertility, with 100% of the samples reaching high to very high levels of both OM and available P. Suphan Buri followed as a high-potential area, with very high levels of available P and exchangeable K (86–93%) and high to very high OM (66.7%). In Nakhon Sawan, while most nutrient were high, 16.7% of the area still showed low phosphorus levels, identifying P as a primary limiting factor. Conversely, in Kanchanaburi, despite having high to very high available P and exchangeable K in over 70% of the area, 53.3% of the soil samples were characterized by low to very low organic matter. Consequently, low overall soil fertility due to organic matter depletion remains the significant constraint for sugarcane production in Kanchanaburi.

Keywords: Soil Fertility, Sugarcane, Agri-Map, Soil Constraints, Nutrient Management

Technology for Producing Particle Boards from Rice Production Residues to Support Green Economy Development.

ABSTRACT:
The utilization of rice straw and rice husk—agricultural by-products from the rice production process—to manufacture particle boards using modern technology enables these materials to serve as substitutes for natural wood products. This approach maximizes the value of agricultural residues, helps reduce air pollution (particularly PM2.5) caused by the burning of rice straw and husks, and adds economic value to these waste materials. Consequently, it can also generate additional income for farmers.

Based on experimental tests on the production of particle boards from rice straw and rice husk using an automatic hydraulic pressing system, the performance of the boards was evaluated according to the Thai Industrial Standard for Flat-Pressed Particleboard (TIS 867-2565). The tested parameters included:

1. Density
2. Moisture content
3. Thickness swelling
4. Modulus of Elasticity (MOE)
5. Modulus of Rupture (MOR)
6. Internal Bond strength (IB)

The results indicated that producing one particle board panel with dimensions of 40 × 40 cm requires 1.5 kg of rice straw and rice husk, combined with isocyanate adhesive at 100, 120, or 140 grams, in order to meet the quality requirements of the standard. However, when using 140 grams of adhesive, a longer time is required for the adhesive spraying process.

Keywords: Rice Straw, Rice Husk, Particle Board, Agricultural Waste Valorization, PM2.5 Air Pollution Reduction, Isocyanate Adhesive, Wood Substitute Materials

Effect of Packaging and Temperature on Short-Term Storage of RD43 Rice Seeds

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ABSTRACT:
Currently, the deterioration of rice seeds before the planting season is a critical issue that affects seed quality. Proper seed storage is considered a potential approach to mitigate this problem. This research aims to study the effects of packaging types and storage temperature on storability of RD43 rice seeds. The experimental design was split-split plot in CRD with 4 replications. The RD43 rice seeds were packed in 3 types of packaging: paper bags, sealed and vacuum-sealed aluminum foil bags, and stored at five storage conditions, consisting of ambient temperature, 25°C, and low temperatures (15°C, 5°C, -15°C) for 24 months. The percentage of germination and germination index (GI) were recorded monthly. The results showed that both packaging and temperature significantly affected rice seed quality. Rice seeds stored at low temperatures in three types of packaging exhibited the highest seed germination percentages and seed vigor, followed by rice seeds stored in sealed aluminum foil bags at 25°C and rice seeds stored in paper bags at ambient temperature, respectively. The findings suggested that appropriate packaging and temperature can effectively prolong seed viability. This information can be applied by rice breeders and farmers to improve seed storage strategies and ensure the availability of high-quality seeds for further cultivation.

Keywords: rice, seed, seed storage, germination

Intercropping in Rice Paddies: A Sustainable Choice to Increase Yield, Reduce Costs, and Mitigate Greenhouse Gas Emissions in the Area

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ABSTRACT:
This study aims to test the intercropping system with rice as the main crop in Chai Nat Province during the years 2023–2025. It compares the continuous rice cultivation system (rice-rice) with the intercropping system of rice with other plants (rice-green bean), focusing on greenhouse gas emissions using the Closed Chamber Technique. A chamber measuring 30x30x120 cm was used to collect gas samples at intervals of 0, 6, 12, 20, and 30 minutes, along with an economic return assessment.

The results indicated that the rice-green bean intercropping system had a greenhouse gas emission rate of 1,562 kg CO_2e/season/rai, which is lower than the rice-rice system, which emitted 1,910 kg CO_2e/season/rai, representing an 18% reduction. In terms of yield, the rice-green bean system showed an increase of approximately 106 kg/rai, or 17%, while the continuous rice cultivation resulted in stable or slightly reduced yields. Additionally, the rice-green bean system reduced production costs to 6,527 baht/rai compared to 7,847 baht/rai for the rice-rice system. However, in terms of economic returns, the rice-rice system yielded a higher net profit of 4,663 baht/rai, while the rice-green bean system had a net profit of 2,883 baht/rai.

In conclusion, intercropping with green beans presents a sustainable option for increasing yields, reducing pollution, and lowering production costs. However, effective price and market management is necessary to enhance net profit efficiency in the future.

Keywords: Intercropping, Rice Paddy, Greenhouse Gas, Mungbean, Chai Nat Province

Optimized Callus Induction Protocol for Gnetum gnemon L. Using Plant Growth Regulators, Leaf Size and Explant Type

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ABSTRACT:
Gnetum gnemon L. is an underutilized tropical plant with significant potential for nutritional and biotechnological applications; however, efficient in vitro propagation protocols remain limited. Callus culture is a fundamental technique in plant biotechnology, enabling applications such as micropropagation, germplasm conservation, and secondary metabolite production. This study aimed to optimize callus induction by evaluating the effects of plant growth regulators, leaf size, and explant type in G. gnemon.

A factorial experiment arranged in a completely randomized design was conducted using Murashige and Skoog (MS) medium supplemented with different combinations of plant growth regulators. After 8 weeks of culture, MS medium containing 0.5 mg L^{-1} 2,4-dichlorophenoxyacetic acid (2,4-D) combined with 0.5 mg L^{-1} 6-benzyladenine (BA) produced the highest callus induction rate (100%), followed by MS medium supplemented with 0.5 mg L^{-1} naphthaleneacetic acid (NAA) and 0.5 mg L^{-1} BA (96.30%), while the control treatment showed the lowest response (18.52%).

Among leaf sizes, large leaves exhibited the highest callus induction (85.18%), followed by medium (66.67%) and small leaves (62.96%). Leaf explants showed the highest induction rate (40.73%), compared with stem (31.48%) and nodal explants (16.66%). Morphologically, calli obtained from 2,4-D + BA and NAA + BA treatments were compact and white, indicating good quality and suitability for further applications.

These findings establish an optimized and reliable protocol for callus induction in G. gnemon, which can serve as a platform for large-scale propagation, germplasm conservation, and future biotechnological applications.

Keywords: Callus induction, *in vitro* culture, plant biotechnology, *Gnetum gnemon*, propagation protocol

The 4th International Conference of Tropical Plants

Tropical Plants: Cultivating Climate-Smart Resilience for a Sustainable Bioeconomy

Session 2:

Physiological and Molecular Mechanisms of Stress Tolerance in Tropical Plants

PUSHING THROUGH: QTL-SEQ INSIGHT INTO ROOT PENETRATION UNDER SOIL COMPACTION IN RICE

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ABSTRACT:
Soil compaction is a major constraint in modern agricultural systems, limiting root growth and reducing crop productivity. Improving root penetration ability (RPA) is therefore an important target for developing crop varieties with enhanced adaptation to compacted soils. Restricted gas diffusion under compacted conditions leads to ethylene accumulation, which inhibits root growth through interactions with auxin and abscisic acid (ABA) signaling pathways. This study aimed to evaluate root responses under ethylene and compaction treatments and to identify genomic regions associated with root length reduction (RLR) and RPA. First, ethylene sensitivity was assessed in the roots of 220 rice accessions, revealing substantial phenotypic variation in RLR, ranging from 22.5% to 87.4%. Genome-wide association studies (GWAS) identified a significant quantitative trait locus (QTL) on chromosome 10, designated qRLR10. Three candidate genes encoding cyclin-like F-box domain-containing proteins (LOC_Os10g03620, LOC_Os10g03740, and LOC_Os10g03870) were identified, suggesting roles in protein degradation, root development, and hormone signaling. Subsequently, an F_2 population derived from a cross between Dharia and PTT1 was used for QTL-seq analysis of RPA under a compacted gel-based system. Significant QTLs were identified on chromosome 3 ($p < 0.01$). Notably, LOC_Os03g18600 (OsPYL6), an ABA receptor, and LOC_Os03g18910 (OsBC1L1), a COBRA-like protein, were identified as candidate regulators. Polymorphisms in these genes effectively distinguished F_2 and F_3 populations. Furthermore, OsPYL6 knockout mutants exhibited significantly higher RPA than the wild type, suggesting that reduced ABA sensitivity alleviates inhibition of root growth under compaction. These findings provide insights into the genetic mechanisms underlying root penetration ability and offer potential breeder-friendly markers for improving rice adaptation to compacted soils.

Keywords: rice, root, penetration ability, QTL-seq, GWAS

Single Nucleus RNA-sequencing for Understanding Secondary Cell Wall Patterning of Xylem Vessels

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ABSTRACT:
Xylem vessels are essential for plant drought adaptation since they govern long-distance water transport and influence its vulnerability to cavitation under climate stress. The VND (VASCULAR-RELATED NAC-DOMAIN) transcription factor family is a well-known master regulator of xylem vessel differentiation. Specifically, VND6 and VND7 are responsible for specifying metaxylem and protoxylem vessel differentiation, respectively. Secondary cell walls (SCWs) of these two vessel types exhibit distinct patterns, “pitted” or “reticulate” in metaxylem and “spiral” or “annular” in protoxylem, which are tightly linked to hydraulic safety, flexibility, and growth under fluctuating water availability. Despite considerable efforts to understand the genetic control of SCW patterning, the molecular mechanisms that distinguish VND6- and VND7- dependent developmental programs remain unclear. Here, we hypothesize that the characteristic SCW architectures of metaxylem and protoxylem vessels are tightly regulated by distinct downstream target genes of VND6 and VND7. To investigate this, we used inducible VND6- and VND7-inducible systems in *Arabidopsis*, in which dexamethasone treatment triggers the differentiation of metaxylem and protoxylem-like vessel cells in an ectopic manner. We performed single-nucleus RNA sequencing (snRNA-seq) to capture the transcriptomic landscape of induced xylem vessel-like cells. We identified candidate regulators of SCW patterning that are differentially associated with VND6- versus VND7-driven systems. These candidates provide a focused set of targets for functional validation and phenotypic analysis, which will confirm their role in SCW patterning and ultimately inform strategies for improving drought and climate resilience in plants.

Keywords: secondary cell wall patterning, snRNA-seq, VND6, VND7, xylem vessel.

Uncovering the Genetic Basis of Mega-Papillae Formation in Rice (*Oryza sativa* L.) Through QTL-seq and Genome-Wide Association Studies

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ABSTRACT:
Rice, one of the world's most important cereal crops, plays a crucial role in global food security. However, climate change increasingly threatens rice production, particularly by exacerbating water scarcity. Like other plants, rice relies on stomata to balance CO_2 uptake and water loss. Uniquely, rice possesses specialized epidermal protrusions on its stomatal subsidiary cells known as papillae. We identified a novel anatomical trait characterized by enlarged papillae, termed "mega-papillae," which partially cover the stomatal pore and potentially enhance water-use efficiency. The genetic mechanisms underlying mega-papillae development, however, remain unknown. To uncover the genetic basis of this trait, we conducted a QTL-seq analysis on an F_2 population derived from a cross between Pathum Thani 1 (normal papillae) and Dharia (mega-papillae). Based on the delta SNP index, we identified a major quantitative trait locus (QTL) on chromosome 5. Complementing this, a genome-wide association study (GWAS) using a rice diversity panel identified two significantly associated regions on chromosomes 2 and 5. The overlapping signals on chromosome 5 from both approaches highlighted a highly robust QTL. Haplotype analysis of the 33 annotated genes within this region pinpointed *Os05g0454200* (bgl) as the most promising candidate gene. Subsequent functional validation via gene knockout revealed a dramatic reduction in mega-papillae formation in the mutants compared to the wild type. These findings demonstrate that *Os05g0454200* plays a critical role in mega-papillae development, providing a valuable genetic target for breeding climate-resilient rice varieties in the future.

Keywords: Rice, Stomata, Mega-papillae, QTL-seq, GWAS, Climate change resilience

Effect of chitosan coating combined with 1-Methylcyclopropene on postharvest quality and storage life of MD2 pineapple under low-temperature conditions

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ABSTRACT:
MD2 pineapple is a major export cultivar of Thailand valued for its sweet flavor, golden-yellow peel, and pleasant aroma; however, its short storage life often results in water loss and postharvest decay during handling and long-distance transportation. Chitosan coatings can reduce fruit transpiration and respiration, while 1-methylcyclopropene (1-MCP) inhibits ethylene action and delays ripening. This study evaluated the combined effects of chitosan and 1-MCP on fruit quality and storage life of MD2 pineapple. Mature-green fruits were cleaned, fungicide-treated, coated with chitosan at 0.5% or 1.0%, and exposed to 1-MCP sachets (2 or 4 sachets). Five treatments were arranged in a completely randomized design and stored at 13 °C. Quality attributes, including weight loss, peel color (L*, a*, b*), firmness, total soluble solids, titratable acidity, and decay incidence, were assessed every three days. Results showed that 1.0% chitosan combined with four sachets of 1-MCP most effectively maintained firmness and minimized weight loss over 18 days ($P < 0.05$). This treatment also delayed peel yellowing and preserved green coloration for more than 12 days compared with the control. The combined application of 1.0% chitosan and 1-MCP extended shelf life by reducing water loss and suppressing ethylene-mediated ripening, demonstrating strong potential for export-oriented storage and long-distance transportation of MD2 pineapple.

Keywords: MD2 pineapple, chitosan, 1-MCP, edible coating, postharvest storage

Molecular regulation of sugar accumulation in citrus under cold stress

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ABSTRACT:
The citrus industry plays an important role in economic development in rural areas of Southern China. However, the sustainable development of citrus industry is influenced by different factors, among which cold stress is an important environmental factor restricting the growth, yield, and geographic distribution of citrus. Understanding physiological and molecular responses to cold stress is of paramount value for coming up with desirable approaches, either cultivation or breeding, to mitigate cold stress. Soluble sugars have been known to accumulate in plants exposed to cold stress, but the transcriptional mechanisms underlying this phenomenon remain largely elusive in plants, particularly in perennial woody plants like citrus. During the last decade efforts have been made to answer this question using trifoliate orange (Poncirus trifoliata), a closely related genus of citrus, that is extremely cold hardy. Cold-responsive genes were identified in trifoliate orange by Subtraction suppression hybridization or RNA-sequencing. A number of sugar metabolism-related genes, including those coding for amylase (*PtrBAM1*) and alkaline/neutral invertase (*PtrA/NINV7*), were up-regulated by cold. We showed that *PtrBAM1* and *PtrA/NINV7* function positively in cold tolerance by modulating the degradation of starch and sucrose, respectively. In addition, CBF1 was shown to regulate the expression of *PtrBAM1*, while PtrAHL14 and PtrAHL17 were confirmed as transcriptional activators of *PtrA/NINV7.* Moreover, PtrAHL14 and PtrAHL17 can interact with each other or with histone acetyltransferases, including GCN5. Consistent with the transcriptional regulation, the identified transcription factors were demonstrated to function positively in cold tolerance by orchestrating the metabolism of the soluble sugars. In addition, PtrERF110 was shown to regulate glucose transporter and sucrose synthesis in response to cold stress. These findings unravel the transcriptional regulatory networks relate d to soluble sugar accumulation in response to cold conditions, which provide novel insight into the molecular understanding of sugar metabolism under cold stress and pave the way for designing strategies to combat cold stress by modulating soluble sugar levels.

Toward Climate-Smart Rice: Integrative Genomic Approaches for Candidate Gene Discovery Under Drought-prone Environments

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ABSTRACT:
Drought has affected many regions worldwide over the past few decades and has been exacerbated by climate change. Roots, the hidden half of a plant, are of primary importance for numerous functions including absorption and translocation of water and nutrients and structural support. Plant roots exhibit highly plastic responses to drought stress and have evolved a series of adaptive strategies to enhance water acquisition. This study aimed to define a drought-adaptive root ideotype in rice and identify the underlying genetic factors associated with improved performance under water-limited environments. Phenotypic analyses revealed that steeper root growth angles, together with larger meta-xylem and low density of lateral roots, exhibited higher grain yield under drought stress suggesting that reduced root branching combined with enhanced hydraulic capacity may improve drought adaptation. Genome-wide association studies (GWAS) combined with QTL mapping were conducted using high-density genomic markers to identify genomic regions associated with these traits. Several significant loci were detected, and integrative genomic analyses highlighted a candidate region similar to the deeper-rooting locus *DRO1*, suggesting the presence of a *Dro1*-like genomic region influencing root architecture. Candidate genes within this region are likely involved in the regulation of root growth angle and vascular development. These findings provide new insights into the genetic architecture underlying drought-adaptive root traits and define a root ideotype for rice grown in drought-prone environments

Keywords: Rice, drought-prone environments, root traits, genomics

Multi-omics approach reveals the mechanisms of salt tolerance in rice

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ABSTRACT:
Salinity is a major hurdle to rice growth and yield production. Underpinning mechanisms that enhance tolerance to salt stress in rice are vital for developing salt-tolerant rice cultivars, thus maintaining food security. In this study, we employed transcriptomics and proteomics approaches to unravel the complex mechanisms underlying salt stress tolerance in rice. Pokkali, NRM17103, PSL10012, RD95, RD85, and IR29 were used for proteomics and transcriptomics analyses under salt stress. The experiments were conducted at the seedling stage by gradually increasing the NaCl concentration of the hydroponic solution from 8 dS/m to 12 dS/m within 3 days. After 0, 1, 2, 3, 4, and 7 days under salinity conditions. Changes in Pokkali's transcriptome and proteome in response to salt stress since the first day after salt stress treatment revealed several differentially expressed proteins involved in photosynthesis, reactive oxygen species (ROS) scavenging, ion homeostasis, and signal transduction pathways. Both transcriptomics and proteomics results indicated the upregulation of genes functioning in ion transport, such as OsSultr1;2, and Os12g0118400 encoding a protein similar to the inwardly rectifying potassium channel subunit

Keywords: Transcriptomics, Proteomics, Rice, Salt tolerance.

Loss and Recovery Dynamics of Mitochondria in Laticifers of the Rubber Tree During Repeated Latex Harvesting

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ABSTRACT:
Natural rubber is synthesized in the laticiferous cells of rubber trees and harvested by periodically cutting the bark to release latex. Although mitochondria are suspended in the cytoplasm and were expected to leak out with the expelled latex during tapping, earlier studies failed to detect their presence. In this study, we confirmed the presence of mitochondria and plastids in expelled latex using molecular method and confocal microscopy after staining latex, revealing a concentration of 13,850 ± 800 mitochondria per microliter. Microscopic and ultrastructural measurements of isolated laticifers indicated an average cell volume of approximately 0.008134 µL. Based on RT-qPCR and microscopic analysis, each laticifer cell released approximately 113 ± 7 mitochondria and 746 ± 35 mitochondrial genomes per tapping event, with each mitochondrion containing 6.7 ± 0.6 genome copies (mean ± SD). We further analyzed the dynamics of mitochondrial loss and replenishment in laticifers by quantifying mitochondrial concentrations at intervals during tapping cycles. The initial latex flow exhibited the highest mitochondrial concentration (18,749 ± 954/µL), which progressively decreased, dropping by 30% (13,192 ± 790/µL) within 5 minutes and ultimately declining to 40% of the initial level (7,542 ± 940/µL) by 30 minutes, likely due to dilution from water influx. Following latex vessel plugging, the mitochondrial population rebounded rapidly, reaching 1.4 times the initial concentration in 3 days. In subsequent tapping cycles (second and third), mitochondrial loss and recovery followed a similar trend, though recovery kinetics shifted from a linear (first cycle) to a logarithmic pattern. These findings suggest that tapping stimulates mitochondrial proliferation and that laticifer mitochondria lack protective mechanisms akin to those of the nucleus, leading to their expulsion with latex during harvesting.

Keywords: Rubber tree, Mitochondria, Latex, Mitochondrial staining, Janus Green B, regeneration

Regulation of Cassava Immune Response by Xpm typeIII effectors

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ABSTRACT:
Professor Yinhua Chen is a Professor, PhD Supervisor, and Position Scientist of the National Cassava Industry Technology System in China. He is also a member of the National Teaching Steering Committee, Chair of the Provincial Teaching Steering Committee for Agronomy, and Council Member of the Genetics Society of China. His research focused on cassava-microbe interactions, and disease prevention and control technologies.

Professor Chen and his team isolated and purified *Xanthomonas phaseoli* pv. *Manihotis* (*Xpm*) strains causing cassava bacterial blight, and carried out genome sequencing and comparative genomic analyses, and they further evaluated the resistance phenotypes of more than 700 cassava germplasm accessions against *Xpm*. In parallel, the team identified TAL effectors from *Xpm* and constructed corresponding mutants to investigate their roles in pathogenicity and host adaptation. By integrating pathogen genomics, host resistance evaluation, and molecular biology, Prof. Chen's group has elucidated key molecular mechanisms underlying TAL effector-cassava interactions, advancing the understanding of cassava disease susceptibility and resistance. This work provides an important theoretical and technical foundation for the development of resistant cassava germplasm and effective bacterial blight control strategies.

Professor Chen has published more than 200 papers in leading journals, authored 5 books, and obtained 30 authorized patents. Over the past five years, he has led 30 research projects, including those funded by the National Natural Science Foundation of China. He has supervised 15 PhD students, 35 master's students, and more than 100 undergraduate students.

Keywords: cassava, *Xanthomonas phaseoli* pv. Manihotis, disease resistance evaluation, TAL effectors, resistance mechanisms

Title Integrated proteomic insights into resistance mechanisms against cassava anthracnose disease (CAD) and cassava bacterial blight (CBB) in cassava (Manihot esculenta)

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ABSTRACT:
Cassava is a primary staple and industrial crop, but its productivity is severely limited by major fungal and bacterial diseases, particularly cassava anthracnose disease (CAD), caused by Colletotrichum gloeosporioides f. sp. manihotis, and cassava bacterial blight (CBB), caused by Xanthomonas axonopodis pv. manihotis. This presentation combines two proteomic investigations comparing resistant/tolerant cultivars ('Huaybong 60' (HB) for CAD and 'Rayong 72' (R72) for CBB) against the susceptible cultivar 'Hanatee' (HN). Using 2-dimensional gel electrophoresis (2-DE) and shotgun proteomics, we identified distinct host-defense strategies. Against CAD, the resistant cultivar (HB) mobilized a three-arm strategy: down-regulating carbohydrate metabolism to starve the pathogen, up-regulating photosynthesis and ATP synthase to trigger an oxidative burst, and increasing cyanogenesis (via hydroxynitrilase). In response to CBB, the tolerant cultivar (R72) exhibited a sophisticated reactive oxygen species (ROS) management system. While higher stem malondialdehyde (MDA) levels correlated with susceptibility in HN, R72 maintained tolerance through the upregulation of NAD/NADP biosynthesis (QNS), glutathione-based redox regulation (GSS), and MAPK signaling (MAPKKK18). Validation via quantitative PCR confirmed these proteins as reliable biomarkers for resistance. Together, these studies provide a molecular framework for advancing marker-assisted breeding to develop high-yield, multi-pathogen resistant cassava varieties.

Keywords: Cassava disease resistance, Proteomics, Cassava Anthracnose disease, Cassava bacterial blight

Physiological and Growth Performance Evaluation of Hybrid and Mutant Sugarcane Clones under Controlled Drought Stress Conditions

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ABSTRACT:
Sugarcane (*Saccharum officinarum* L.) is a major economic crop in tropical and subtropical regions, particularly in Thailand's sugar industry. However, increasing drought frequency and severity driven by climate change threaten productivity and sugar quality. This study aimed to evaluate the physiological responses, growth performance, and yield potential of four drought-tolerant sugarcane clones (KU58-4-176, KU58-4-108, KU58-4-83, and KU-MTB-Tr2-2) compared with the commercial cultivar Khon Kaen 3 under controlled greenhouse conditions. Two irrigation regimes were imposed during the elongation stage (5–7 months), a critical water-demand period: well-watered (40–70% available water capacity, AWC) and drought stress (<20% AWC).

KU58-4-176 exhibited superior performance across key physiological and agronomic traits, including plant height, stem number per clump, stem length, stem diameter, leaf area index, and photosynthetic rate. Under drought conditions, this clone maintained relatively stable photosynthetic activity, high water use efficiency, and effective regulation of transpiration and stomatal conductance, indicating enhanced drought adaptation mechanisms. Following re-watering, KU58-4-176 showed rapid physiological recovery and sustained biomass accumulation until harvest at 12 months, producing a total stem weight of 7,273.36 g/clump compared to 4,905.06 g/clump in Khon Kaen 3. KU58-4-108 also demonstrated strong performance (6,357.60 g/clump). CCS analysis revealed no significant differences among KU58-4-176, KU58-4-108, and Khon Kaen 3, confirming that improved drought tolerance did not compromise sugar quality. These results identify KU58-4-176 and KU58-4-108 as promising genetic resources for breeding drought-resilient sugarcane cultivars suitable for future water-limited environments.

Keywords: drought tolerant, drought adaptation, physiological responses, stress recovery

Development and Evaluation of Parthenocarpic Cucumber Production and Hybrid Seed System in Plant Factory with Artificial Lighting

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ABSTRACT:
Parthenocarpic cucumbers are well suited to protected cultivation when pollination is unreliable. Plant factories with artificial lighting (PFAL) provide fully controlled environments, yet production and seed-multiplication protocols for parthenocarpic cucumbers in PFALs remain limited. This study had two objectives: (i) to optimize photoperiod and light spectra for fruit production of a parthenocarpic cucumber cultivar (Cengel ; Dutch Greenery Co., Ltd.) in a PFAL, and (ii) to develop and evaluate a PFAL-based hybrid seed production system using Basha (Hortigenetics research (s.e.asia) Ltd.) and Smile (AGRO STAR SEEDS Co., Ltd.) as parental lines. Cengel was grown under white LED (W-LED) at three photoperiods (12, 14 and 16 h day-1). Extending photoperiod to 14-16 h increased fruit number (up to 28 fruits plant-1) and yield (up to 1.12 kg plant-1) without compromising external fruit quality, although placenta thickness increased slightly. Under the 16 h photoperiod, three spectra white led (W-LED), white-blue led (WB-LED) and white-red-blue led (WRB-LED)) were compared. WRB-LED promoted vegetative growth (greater plant height, internode length and leaf area) but reduced fruit weight and size relative to W-LED and WB-LED, whereas fruit number and marketable percentage (≈91–95%) were not affected. For hybrid seed production, reciprocal crosses (Basha x Smile and Smile x Basha) were performed under W-LED or WRB-LED. Spectrum did not affect seed number per fruit or germination, while WRB-LED slightly increased 100-seed weight. Hybrid seeds produced in PFAL showed high germination (>93%) and vigorous seedlings, with no significant spectrum x cross direction interaction. Overall, PFAL can support fruit production and reliable hybrid seed multiplication of parthenocarpic cucumbers, enabling year-round breeding and seed production under fully controlled environments.

Keywords: parthenocarpy, PFAL, photoperiod, fruit set, seed production

Changes in Physiological Responses and Yield of Promising Sugarcane Clones under Normal and Drought Conditions

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ABSTRACT:
Drought is a major limiting factor in sugarcane production. This study aimed to evaluate physiological responses and yield of promising sugarcane clones under well-watered and drought conditions. The experiment was conducted using a split-plot design in a randomized complete block design (RCBD) with three replications. The main plot consisted of the well-watered condition (WW) and drought-stress condition (DS), while the subplot comprised two clones, KU58-4-108 and KU-MTB-tr2-2, along with three check varieties. Physiological parameters were recorded before, during, and after drought treatment. Physiological parameters were not significantly different between water regimes, but genotypic differences were observed in transpiration and photosystem II activity. During the drought treatment, KU-MTB-tr2-2 exhibited the lowest leaf temperature under both WW (31.42 °C) and DS (32.92 °C). After the drought treatment, KU-MTB-tr2-2 showed strong recovery, with the highest stomatal conductance and transpiration values of 0.029 mol m^{-2} s^{-1},and 0.681 mmol m^{-2} s^{-1}, respectively. The DS condition resulted in lower yields across all parameters. Under drought conditions, KU58-4-108 showed the highest stalk length (410.50 cm). For stalk fresh weight per stool, KU-MTB-tr2-2 was not significantly different from K88-92, which was the highest (7.56 kg). KU-MTB-tr2-2 showed the highest stalk dry weight per stool (1.57 kg). Interestingly, KU-MTB-tr2-2 showed the highest CCS under both well-watered and drought conditions (13.22% and 9.28%, respectively). KU-MTB-tr2-2 was outstanding for recovery from drought stress with high yield potential.

Keywords: Sugarcane, Drought stress, Physiological traits, Yield components, Commercial cane sugar

Molecular and Metabolic Analysis of Khon Kean 3, and KU-MTB-Tr2-2 Sugarcane under Drought Conditions

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ABSTRACT:
KU-MTB-Tr2-2 is a sugarcane mutant derived from Khon Kean 3 (KK3) via Ethyl methane sulfonate (EMS) mutagenesis and subsequently selected for enhanced drought tolerance under tissue culture, greenhouse-induced drought, and field conditions. Although previous evaluations indicated that KU-MTB-Tr2-2 exhibits superior drought tolerance and yield stability compared with KK3, the genetic basis of the mutation and the mechanisms underlying its drought tolerance relative to its original cultivar remained unclear. In this study, we combined DArT sequencing, metabolomic profiling, and yield/quality assessment under two contrasting water regimes (well-watered vs drought) to elucidate these mechanisms. DArT analysis confirmed that KU-MTB-Tr2-2 is a true mutant of KK3, exhibiting approximately 25% genetic divergence. Metabolomic analysis revealed that under well-watered conditions, KU-MTB-Tr2-2 has higher levels of metabolites associated with glycolysis/TCA cycle, purine metabolism, and phenylpropanoid/flavonoid pathways than KK3, indicating a greater basal metabolic capacity. Under drought stress, both genotypes showed a general reduction in metabolite levels; however, KU-MTB-Tr2-2 maintained a higher central carbon flux and stronger phenylpropanoid/phenolic profiles, whereas KK3 exhibited more pronounced stress- and protein-degradation–related signatures. Greenhouse evaluation under controlled drought confirmed that KU-MTB-Tr2-2 consistently produced significantly higher sweetness than KK3 ($P < 0.05$). Together, these results demonstrate that KU-MTB-Tr2-2 acquires drought tolerance through a metabolically robust strategy that preserves sugar production, providing molecular and metabolic signatures useful for breeding drought-tolerant, high-sugar sugarcane.

Keywords: Mutant sugarcane, Metabolomics analysis, Drought, Sweetness

Gene Expression Signatures and Biochemical Markers Associated with Drought Tolerance in Promising Sugarcane Clones

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ABSTRACT:
Water deficit is considered one of the most important limiting factors to crop productivity and growth rates. Plants can overcome this constraint by accumulating osmoprotectants to maintain cell water balance, which enables them to grow under water stress conditions. In this study, transcriptional profiling of genes was performed to elucidate gene expression patterns associated with drought stress in promising sugarcane developed at the Nakhon Sawan Field Crops Research Center. the expression of three genes, Purple acid phosphatase (PAP), Trehalose phosphate synthase (TPS), and Sugar transporters (PST3), in sugarcane clones/varieties was investigated using qRT-PCR to better understand their drought tolerance mechanisms. The results revealed that all three genes were expressed in both stress and non-stress conditions. Moreover, the expression profiles of these genes varied across different fourteen sugarcane clones/varieties, the DOA Khon Kaen3 DOA Nakhon Sawan2 DOA Nakhon Sawan1 and 04-2-1383 demonstrated higher expression levels of these genes in dehydration compared to the control group. Physiological and biochemical changes related to oxidative stress, osmoprotectant substance accumulation, and cell destruction substances were also identified. Testing in a controlled environment, coupled with the detection of growth, physiological, and biochemical changes provided an effective approach for evaluating and selecting drought-tolerant sugarcane clones. The testing results showed that the tested sugarcane clones/varieties had low drought tolerance compared to DOA Khon Kaen3, DOA Nakhon Sawan2, DOA Nakhon Sawan1 and 04-2-1383 potentially exhibited moderate water stress tolerance, while LK92-11 were potentially water stress-sensitive. These findings have important implications for the development of new drought-tolerant sugarcane varieties.

Keywords: Sugarcane, gene expression, drought, physiological, biochemical.

Evaluation of photosynthetic light response in microgreens using minimum saturating irradiance and maximum electron transport rate

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ABSTRACT:
Understanding plant light requirements is essential for optimizing microgreen production. This study aimed to evaluate the photosynthetic light response of several microgreen species by determining two key physiological parameters: the minimum saturating irradiance (I_k) and the maximum electron transport rate (ETR_{max}). These parameters were derived from rapid light curves (RLCs), which assess photosynthetic performance under increasing light intensities and provide insights into plant light-adaptation strategies. Among the evaluated species, onion microgreen exhibited the highest I_k value (607.09 µmol $m^{-2}s^{-1}$), indicating that this species requires a higher light intensity to reach photosynthetic saturation than other microgreens. In contrast, red cabbage microgreen showed the lowest Ik value (216.14 µmol $m^{-2}s^{-1}$), suggesting that saturation occurs under considerably lower light levels. Regarding electron transport capacity, wheatgrass microgreen recorded the highest ETR_{max} value (37.92 µmol $m^{-2}s^{-1}$), indicating a superior potential for photosynthetic electron transport rate under increasing irradiance. Conversely, red cabbage microgreen exhibited the lowest ETR_{max} value (17.60 µmol $m^{-2}s^{-1}$), indicating a comparatively lower photosynthetic capacity. Overall, the relatively low I_k values observed in most of the tested microgreen species indicate that photosynthetic saturation occurs at low to moderate light intensities. This suggests that increasing irradiance beyond this level does not substantially enhance photosynthetic efficiency. These responses suggest that microgreens have photosynthetic traits that are well-suited to environments with restricted light availability. Therefore, microgreens can be considered to exhibit traits typical of shade-adapted plants.

Keywords: Chlorophyll fluorescence, Photosynthesis, Light saturation point, Rapid light curve, Sprout

Arbuscular Mycorrhizal Symbiosis Shapes Growth and Biomass Partitioning Of Maize Under Zinc And Phosphorus Limitation

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ABSTRACT:
Arbuscular mycorrhiza fungi (AMF) are a type of fungi that form symbiosis with plants. This symbiotic relationship aids plants acquire nutrients, as such, they serve as biofertilizers in the sustainable production of crops. The aim of this experiment was to observe the impact of AMF in zinc and phosphorus-deficient environment on: (i) the growth and development of maize (ii) biomass accumulation. An RCBD split plot pot experiment was conducted with 6 replications for 22 days in sand culture using SUWAN 5819 maize seeds. 5 levels of nutrient using Hoagland's solution: +Zn+P, -Zn-P, -Zn+P, Zn-P, control (DI water), and 2 levels of AMF, with and without, were used. +Zn+P and -Zn+P showed significantly higher agronomic response across all parameters. In the presence of phosphorus, AMF reduced leaf, shoot, root, and total dry weights as observed from +Zn+P and -Zn+P and only improves leaf dry weight in +Zn-P. AMF have no significant impact on leaf area across all treatments. Highest SLA was observed in the control+AMF treatment, while Zn-P showed higher SLA for non-inoculated compared to inoculated. Shoot and root mass fraction are strongly influenced by nutrient treatments but less by mycorrhiza. However, in +Zn+P, mycorrhiza caused higher shoot biomass accumulation. Presence of AMF seems to shift the allocation of biomass to the shoots as observed with +Zn+P and -Zn-P treatments. These results indicate a costly symbiosis for maize when nutrient supply is sufficient. Phosphorus seems to be a more influential nutrient in growth and development with AMF influencing biomass accumulation.

Keywords: Mycorrhiza, Hoagland, Biomass

Correlation Between Anthocyanin Content and Anthracnose Resistance in F2 Population of *Capsicum annuum* L.'CA365' × 'CA1355'

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ABSTRACT:
Chilli (*Capsicum* spp.) is an economically important crop, however, anthracnose caused by *Colletotrichum* spp. severely limits yield. Previous studies have suggested that anthocyanins function as antioxidants and may enhance plant tolerance to both biotic and abiotic stresses. This study investigated the relationship between anthocyanin accumulation and anthracnose resistance to facilitate the development of chili cultivars with combined disease resistance and high nutritional value. A population of 100 F_2 individuals was developed from a cross between *C. annuum* L. 'CA365' (female parent, green fruit, susceptible to anthracnose) and *C. annuum* 'CA1355' (male parent, purple fruit, resistant to anthracnose). Anthracnose susceptibility in the parents, F_1, and F_2 population was evaluated by inoculating mature green fruits with *Co. truncatum* '158ci' using a non-wound spray method, and disease symptoms were scored over 14 days. Anthocyanin content was quantified spectrophotometrically at 540 nm using cyanidin chloride as a standard, and its association with anthracnose resistance was analysed using Pearson's correlation coefficient (r). Anthracnose resistance in the F_2 population fit a Mendelian 3:1 segregation ratio, suggesting control by a single recessive gene ($\chi^2 = 1.33$, $p > 0.05$). In contrast, anthocyanin content showed continuous variation, ranging from 8.91 to 81.82 mg cyanidin chloride per 100 g fresh weight, with a median of approximately 20–25 mg. No significant correlation was observed between anthocyanin content and anthracnose resistance ($r = -0.12$). Although anthracnose resistance was observed in the F_2 population at the mature-green fruit stage, the results indicate that anthocyanin accumulation is not directly associated with anthracnose resistance in this population.

Keywords: *Colletotrichum truncatum*, spray inoculation, non-wounded resistance, secondary metabolite

Comparative Evaluation of Coconut Coir and Peat Moss for Mitigating Salinity Stress in Water Spinach

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ABSTRACT:
Saline soil and saltwater intrusion in agricultural areas directly affect the growth and yield of water spinach. This research aimed to compare the effects of coconut coir and peat moss on the growth and physiological responses of water spinach across varying salinity levels to evaluate their potential to mitigate salinity stress. The experiment was conducted using a 2×3 factorial in a completely randomized design with two main factors: types of growing media (peat moss and coconut coir) and salinity levels (NaCl) at 3 levels (0, 0.5%, and 1.0% w/v). The results showed that increasing salinity levels had a significantly negative impact on both fresh and dry weight. Specifically, at 1.0% NaCl, plant weight decreased by 60–70% compared to the control group. However, coconut coir demonstrated superior growth support compared to peat moss across all salinity levels, maintaining higher plant height and biomass. In terms of photosynthetic efficiency, as analyzed by chlorophyll fluorescence, the plants showed slight stress, with the maximum quantum yield of PSII ranging from 0.73 to 0.75. Notably, water spinach grown in coconut coir demonstrated a more robust adaptation mechanism, characterized by significantly higher non-photochemical quenching, which dissipates excess energy as heat, thereby protecting the photosynthetic apparatus more effectively than in peat moss. Furthermore, coconut coir maintained higher levels of chlorophyll a and chlorophyll b compared to peat moss. In conclusion, coconut coir is a more effective growing medium than peat moss for mitigating salinity stress and promoting greater biomass accumulation in water spinach, even under high-salinity conditions.

Keywords: Chlorophyll fluorescence, Growing media, Ipomoea aquatica, Salt stress, Water Convolvulus

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Session 3:

Advanced Breeding and Biotechnology for Climate-Resilient Tropical Crops

QTL-seq Identifies a Wall-associated Kinase as a New Resistance Gene to Bacterial Leaf Streak in Rice

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ABSTRACT:
Bacterial leaf streak, caused by *Xanthomonas oryzae* pv. *oryzicola*, is one of the devastating bacterial diseases that impose significant annual threats to global rice production. Although the deployment of host plant resistance is the most sustainable management strategy, the characterized resistance and defense-related genes against BLS remains limited. In this study, a combination of whole-genome resequencing and QTL-seq approach were employed in a F_2 mapping population derived from a cross between two Thai rice varieties, Homcholasit (susceptible) and Niaw Dam Chaw Mai Pai 49 (resistant). Phenotypic screening was conducted using the virulent Thai Xoc isolate, 1NY2-2. The QTL-seq approach identified a major QTL (quantitative trait loci) region on chromosome 2, encompassing 16,689 single nucleotide polymorphisms (SNPs) and 1,883 annotated genes. Expression analysis was performed on SNPs within the 200 kb spanning region of the peak SNP and *OsWAK16* has most significant and highest expression fold change between two parental lines. Marker trait association analysis also showed that *OsWAK16* is responsible for BLS resistance in this population. To validate the function of this candidate, CRISPR/Cas9- mediated knockout was performed. Two independent *oswak16* mutant lines exhibited significantly enhanced susceptibility and more severe disease symptoms upon *Xoc* inoculation compared to wild type. Collectively, this study demonstrates that *OsWAK16* is a novel resistance gene providing a valuable genetic resource for molecular breeding programs aimed at improving rice resilience against BLS.

Keywords: Bacterial leaf streak (BLS), *Xanthomonas oryzae* pv. *oryzicola* (Xoc), resistant genes, Quantitative trait loci (QTL), single nucleotide polymorphism (SNPs)

NKI17196-102-2-1-1-1-SKN-1: A Promising Photoperiod Insensitive Glutinous Rice Line with Blast and Bacterial Blight Resistance for Irrigated Lowland Area in Northeastern Thailand

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ABSTRACT:
Glutinous rice is an important stable food for people in the northeastern Thailand. The most popular variety for irrigated lowland in dry season is RD22 which is a certified variety from the Rice Department. However, it has gradually lost its resistance to blast since the variety was first released in 2016. Thus, 9 rice research centers in northeastern Thailand have jointly conducted a breeding program of photoperiod-insensitive glutinous rice with the objective to develop a new variety with high yield and resistance to blast and other major diseases for irrigated lowland in northeastern Thailand. The project resulted in a promising rice line, designated as NKI17196-102-2-1-1-1-SKN-1 which had a better resistance to blast and bacterial blight and a higher average yield than RD22. The highest potential yield was 1,092 kilograms/rai or 6,825 kilograms/hectare. The average yields from 3 cropping seasons under farmer field conditions from wet season 2024 to wet season 2025 was 754 kilograms/rai or 4,712 kilograms/hectare which was 11 percent higher than RD22 that yielded 679 kilograms/rai or 4,244 kilograms/hectare. It had the harvesting age about 131 days, which was the same as RD22. The average height was 118 centimeters. In term of physical and chemical property, it was considered a long-grain glutinous rice that meets the market demand with a slender shape and a length-to-width ratio of 3.07±13. Cooking temperature was low. When rice is cooked, the texture is soft. This promising line could be an alternative for farmers to cope with blast in upper northeastern Thailand.

Keywords: glutinous rice, photoperiod insensitive rice, blast, blast resistance

Carotenoid Accumulation and Regulation of Carotenogenic Gene Expression During Ripening of Red-Fleshed 'Siam Red Ruby' Pumelo (*Citrus grandis*)

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ABSTRACT:
The 'Siam Red Ruby' (*Citrus grandis*) is a newly developed lycopene-accumulating pumelo cultivar cultivated exclusively in the Pakpanang area of Nakhon Si Thammarat Province, Thailand. In this study, 'Siam Red Ruby' fruits were harvested at five ripening stages to investigate changes in carotenoid accumulation and the expression of carotenogenic genes in the pulp. During fruit ripening, the contents of phytoene, ζ-carotene, lycopene, β-carotene, β-cryptoxanthin, and all-trans-violaxanthin gradually increased, whereas the levels of α-carotene and lutein decreased in the pulp. In mature fruit, lycopene accumulated at a remarkably high level, accounting for more than 93.26% of the total carotenoid content. This massive accumulation of lycopene contributed to the distinctive red coloration of the pulp in 'Siam Red Ruby'. Furthermore, gene expression analysis revealed that the upregulation of upstream carotenogenic genes (*CitPSY*, *CitPDS*, *CitZDS*, *CitZISO*, and *CitCRTISO*), together with the downregulation of downstream genes (*CitLCYb1*, *CitLCYb2*, *CitLCYe*, *CitHYb*, and *CitHYe*), represents the primary molecular mechanism responsible for lycopene accumulation in the pulp of 'Siam Red Ruby' pumelo.

Keywords: carotenoid accumulation, gene expression, lycopene, 'Siam Red Ruby' pumelo.

Reconceptualizing Cassava: Regional Approaches to Breeding, Processing, and Market Integration

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ABSTRACT:
The East and Southern Africa Cassava Breeding Network (ESACB-Net) was established to address challenges in cassava breeding through a participatory approach involving local stakeholders and national agricultural research systems. This initiative aims to align breeding priorities with regional needs, particularly for the 'White Cassava for Processing' market segment. High-Quality Cassava Flour (HQCF) and starch are essential processed cassava products due to their shelf life, versatility, and consumer preference. The 'White Cassava for Processing' breeding pipeline combines modern and conventional methods to develop varieties with critical traits like high dry matter content, elevated starch yield, low HCN levels, and stable fresh root yields under disease pressures. Despite these advancements, processors face challenges such as inconsistent supply of quality cassava, low extraction efficiency, increased processing costs, and reduced profitability. These issues have broader economic, social, and environmental implications, including limited rural employment, constrained farmer margins, and restricted market linkages.

This study analyses the genetic diversity, errors, and variances in the ESACB-Net breeding pipelines using historical trial data from the past decade. It examines both early- and late-stage breeding materials to quantify genetic and error variances across breeding programs for market segments MS01069 and MS00892. Product profiles, including Cassava EAF TPP00449 (East Africa) and Cassava SAF TPP00610 (South Africa), are examined to confirm that the varieties meet processing-grade standards. The findings provide insights into the genetic diversity of critical processing traits, enabling the optimisation of breeding strategies for the region. A comprehensive regional testing program established by this research lays the foundation for developing and disseminating high-yielding cassava varieties that meet the needs of farmers, processors, and consumers. This ultimately aims to enhance food security, improve rural livelihoods, and stimulate economic growth in East and Southern Africa, positioning cassava as a key component of sustainable agricultural transformation.

Keywords: Cassava breeding, ESACB-Net, white cassava for processing, HQCF, starch, dry matter content, CBSD, CMD, genetic diversity, regional testing program.

Multi-omics Decipher the Metabolic Basis of Flavor and Nutritional Quality of Tropical Fruits

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ABSTRACT:
Litchi, durian, and waxapple are economically significant tropical fruit trees that efficiently exploit tropical environmental resources to yield fruits with distinct flavors and high nutritional value. However, advancements in the genetic improvement of complex traits, such as fruit quality, are constrained by insufficient genomic and genetic resource knowledge. This study has generated comprehensive genome maps and pan-genome variation maps for these three tropical fruit species, elucidating, for the first time, the evolutionary relationships among their cultivated varieties. Concurrently, employing re-sequencing, metabolomics, and ionomics techniques, the study analyzed flavor and nutritional compounds at the population level and investigated the biosynthetic pathways of key metabolites, identifying crucial genes and breeding markers. A relevant database was established as part of this research. This work provides a critical foundation for fundamental research and the breeding of these vital tropical fruit trees.

Keywords: Litchi; Duian; Waxapple; Genome; Metabolites

Driving Genome Innovation: Complete T2T Genomes and Multi-Omics Solutions

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ABSTRACT:
ONT sequencing offers a versatile platform for multi-omics data generation. Here, we present ONT-only workflows from our lab for genome assembly and integrated multi-omics studies. Optimized DNA extraction allows routinely obtaining ultra-long reads with N50>150 kb from challenging samples like fibrous plants and small invertebrates, producing highly contiguous, gap-free assemblies that resolve complex repeats. Leveraging this genomic foundation, we extended ONT workflows to full-length transcriptome sequencing and epigenomic profiling, including SMAC-seq for single-molecule analysis of transcript boundaries, isoforms, chromatin accessibility, and DNA methylation. These approaches provide practical solutions for exploring genome structure and multi-omics regulation across diverse biological systems.

Keywords: long read sequencing; T2T genome; multi-omics integration

Development of DOA Nakhon Sawan 2: A High-Yielding Sugarcane Variety for Thailand

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ABSTRACT:
Sugarcane production in Thailand is currently dominated by a single commercial variety, DOA Khon Kaen 3 (DOA KK3), which occupies more than 96% of the national cultivation area. This heavy reliance on monoculture increases vulnerability to pests, diseases, and yield instability. To enhance varietal diversity and productivity, the Nakhon Sawan Field Crops Research Center's sugarcane breeding program was conducted to develop high-yield and high-sugar varieties adapted to loam to clay soils.

DOA Nakhon Sawan 2 was developed from a cross between Q85 and DOA U-Thong 8 in 2013. Selection and evaluation were conducted through multi-stage trials, including preliminary (2017–2019), standard (2020–2022), and farm trials (2023–2025) across plant cane, first ratoon, and second ratoon crops. DOA KK3 and LK92-11 were used as check varieties.

Across trials, DOA Nakhon Sawan 2 demonstrated an average cane yield of 112.5 tons ha^{-1}, exceeding DOA KK3 and LK92-11 by 14% and 26%, respectively. The average sugar yield was 15.7 tons CCS ha^{-1}, representing increases of 13% and 28% over the check varieties, while CCS values (14.1) were comparable. The variety also showed moderate resistance to red rot and wilt diseases and had loosely attached leaf sheaths, supporting both manual and mechanical harvesting.
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These results indicate that DOA Nakhon Sawan 2 is a promising alternative sugarcane variety that improves yield performance, enhances genetic diversity, reduces the risks associated with monoculture, and supports sustainable sugarcane production in Thailand, particularly in loam to clay soils of the central and northern regions.

Keywords: sugarcane breeding, high yield, sugar yield, CCS, varietal diversification

Development of cassava mosaic disease resistant cassava adapted to Thailand using field evaluation and molecular markers

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ABSTRACT:
Cassava mosaic disease (CMD) has emerged as a major constraint to cassava production in Thailand since 2018, resulting in yield losses and increased reliance on costly clean planting materials. Genetic resistance represents a sustainable strategy for managing CMD in cassava-based production systems. In this study, segregating populations were developed by crossing the CMD-susceptible Thai cultivar Huay Bong 80 (HB80) with the CMD-resistant IITA parent IITA-TMS-IBA980581, generating 76 progenies. Field evaluations were conducted in single-row trials using an augmented randomized complete block design with three replications and parental checks. Fresh root yield did not differ significantly ($p > 0.05$) between the progenies and the susceptible parent HB80, indicating no evidence of a yield penalty associated with CMD resistance under the conditions of this study. Broad-sense heritability (H^2) for CMD resistance was moderate (46.91%), suggesting a substantial genetic component underlying phenotypic variation. At a 10% selection intensity, eight progenies were identified that combined CMD resistance with favorable agronomic performance. In addition, the SNP marker S12_7926132 exhibited high prediction accuracy (0.83) for CMD resistance, supporting its utility in marker-assisted selection. These findings demonstrate that combining field-based phenotypic selection with molecular markers can accelerate the development of CMD resistant cassava cultivars adapted to Thai growing environments.

Keywords: CMD-resistant cassava, SNP marker, S12_7926132, CMD2

Genome-wide association study identifies candidate genes for hull and pericarp coloration in rice (*Oryza sativa* L.)

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ABSTRACT:
The pigmentation of rice hulls and pericarps represents an agronomically and nutritionally important trait, contributing to varietal differentiation, market value, and bioactive compound enrichment. In this study, a diversity panel of 306 rice accessions, including glutinous and non-glutinous types, was evaluated for hull and pericarp coloration using two phenotyping methods: presence/absence scoring and degree of coloration scales. Whole-genome resequencing and genome-wide association study (GWAS) using 1,021,144 high-quality SNPs identified a total of 19 quantitative trait loci (QTLs) across chromosomes 3, 4, 7, 8, 9, and 12. Key candidate genes included *Os03g0421800* (X8 domain-containing protein), *Os03g0425800* (SANT domain protein), and *Os07g0211500* (Rc, a bHLH transcription factor), all strongly associated with hull and pericarp pigmentation. Notably, *Os03g0421800* was consistently detected across both traits, suggesting shared genetic regulation. Linkage disequilibrium analysis indicated an average genome-wide LD decay of ~200 kb, supporting resolution for QTL mapping. These findings reveal novel insights into the genetic control of rice pigmentation and provide valuable resources for molecular breeding to develop nutritionally enriched and commercially distinct colored rice varieties.

Keywords: Rice hull color, Pericarp pigmentation, GWAS, QTL, Anthocyanin biosynthesis

Evaluating CMD resistance in cassava progenies from crosses between resistant and Thai commercial varieties

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ABSTRACT:
The integration of Cassava Mosaic Disease (CMD) resistance into high-yielding, high-starch varieties is the most sustainable strategy for curbing disease transmission and reversing production declines. Marker-assisted selection (MAS) targeting the CMD2 locus via the S12_7926132 SNP marker has proven highly effective for early-stage screening.This study evaluated 605 genotypes derived from crosses between Thai commercial cultivars and resistant germplasm from the International Center for Tropical Agriculture (CIAT). Initial selection based on yield potential and harvest index (HI) identified 148 genotypes for single-row trials, which were further validated through genotypic analysis. Subsequently, 16 superior genotypes underwent preliminary yield trials. Advanced yield trials were conducted on six final candidates to assess root yield, starch content, HI, and disease severity (scored 1–5) at 3, 6, and 9 months after planting (MAP). Results highlighted four elite genotypes—MKUC62-83-51, MKUC62-88-85, MKUC62-98-112, and MKUC62-98-118 which achieved yields ranging from 20.11 to 25.42 t ha^{-1}. These yields were statistically comparable to check varieties TMEB419, IITA-TMS-IBA980581, HB90, and HB100. Furthermore, these lines exhibited high starch content (22.90%–24.90%) and favorable HI (0.54–0.63). Notably, all four genotypes maintained 0% disease incidence and a severity score of 1, confirming the presence of CMD2 resistance alleles. These promising lines will proceed to regional trials to evaluate yield stability and environmental adaptability.

Keywords: CMD resistance, Cassava, SNPs, *CMD2*

Induction of Haploid or Doubled Haploid Plantlets through Ovary Culture in Parthenocarpic Cucumber

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ABSTRACT:
Parthenocarpic cucumbers, which can bear fruit without pollination, produce seedless fruits that are highly desired by consumers, agricultural producers, and breeders. However, the seedless nature of these cucumbers poses challenges for breeding improvements and often requiring extended periods. Unpollinated ovule culture, a plant tissue culture technique, can expedite the production of inbred lines. This research aims to investigate the factors influencing ovules and ovaries culture in parthenocarpic cucumbers by examining the influence of three factors: genotype (Hom Bai Toey, Smile, Basimah and Cengel), incubation temperature (25°C and 33°C), and TDZ concentration (0.00, 0.04, 0.06 and 0.08 mg/L). The results showed that Smile with 0.06 mg/L TDZ induced the highest percentage of ELS at 90.0%, which was not significantly different from Smile with 0.08 mg/L TDZ and Cengel with 0.08 mg/L TDZ (83.3% and 70.0%, respectively). These cultures were then transferred to Murashige and Skoog (MS) medium without hormones to induce callus or ELS development into plants, resulting in the induction of five plants. Flow cytometer analyses confirmed that 40% of the plants were double haploids and 60% were mixoploids. However, molecular markers are required to distinguish true doubled haploids from diploids derived from somatic tissues.

Keywords: *Cucumis sativus* L., Parthenocarpic, Ovary culture, Thidiazuron, ELS

Marker-Assistant Selection for Bitterness Trait in Parthenocarpic Cucumber

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ABSTRACT:
Cucumber bitterness in leaves and fruits, a significant trait affecting consumer preference and marketability, is primarily due to cucurbitacins, which are triterpenoid metabolites. These accumulate when the oxidosqualene cyclase (OSC) pathway is activated, a process controlled by the Bitter (*Bi*) locus. The recessive *bi* allele suppresses cucurbitacin biosynthesis, effectively conferring a non-bitter phenotype. Although environmental stresses like high temperatures and increased pest or pathogen pressure can trigger cucurbitacin accumulation in susceptible plants, certain cucumber cultivars consistently remain non-bitter, emphasizing the genetic control over bitterness. In this study, we employed a SNP marker within a Modified Mass Selection (MMS) method, which involves selecting plants based on genetic markers linked to non-bitter traits, to accelerate the breeding to non-bitter cucumber varieties. We conducted the study using an M3 improved population from multiple parent lines. The population was divided into two groups of 150 lines each: one group consisted of short-fruit parthenocarpic cucumbers, and the other group included short-fruit parthenocarpic cucumbers crossed with commercial cultivars. The C393Y position is predicted to cause a cysteine-to-tyrosine substitution, potentially altering the structure of oxidosqualene cyclase affecting the formation of cucurbitadienol, an early precursor in cucurbitacin biosynthesis. Cucurbitadienol is an early precursor in cucurbitacin biosynthesis. We identified a C393Y variant in the cucumber Bi gene and developed a SNP marker (*Bi*-C393Y) for bitterness screening. Using a KASP assay on a Flex Real-Time PCR platform, rhich allows for precise allele discrimination, allele calls were obtained from standard allele-discrimination plots. Genotype calls matched the tasting-based bitterness scores: T/T genotype plants were consistently non-bitter, while the presence of the C allele (C/T or C/C) indicated bitterness. This pattern is consistent with dominant action of the C allele and recessive inheritance of T for the non-bitter phenotype. All eight parents used for population group 1 were T/T; in group 2, seven parents were T/T and one was C/C. In group 2 progenies, 112 were T/T, 37 were C/T, and 1 was C/C. The foliage bitterness evaluation results consistently matched the SNP marker, underscoring *Bi*_C393Y as a crucial tool for significantly enhancing the accuracy and efficiency of cucumber breeding programs, with potential application in developing consumer-preferred, non-bitter cucumber varieties.

Keywords: The *Bi* gene, Fruit bitterness, cucumber, parthenocarpy, SNP marker

Identification of Candidate Genes Associated with Anthracnose Resistance in Chilli (*Capsicum annuum* L.) Using RNA-Seq

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ABSTRACT:
Anthracnose, caused by *Colletotrichum* spp., is a devastating disease that results in significant yield losses in chilli production worldwide. This study aimed to identify candidate genes associated with anthracnose resistance in two *Capsicum annuum* L. accessions: CA365 (susceptible) and CA1191 (resistant). Chilli fruits at the mature green stage were inoculated with a spore suspension of Colletotrichum truncatum '158ci' using a spray inoculation method. Genome-wide gene expression levels were subsequently analyzed using RNA sequencing (RNA-seq) at 0 and 4 days after inoculation (DAI) to identify transcriptomic responses. Differentially expressed genes (DEGs) analysis revealed that the susceptible accession exhibited 2,624 genes specifically expressed at 4 DAI, whereas the resistant accession showed 1,499 specifically expressed genes. Comparative transcriptome analysis further identified 962 genes that were uniquely up-regulated in the resistantnaccession at 4 DAI, representing potential candidate genes associated with anthracnose resistance. These genes are mainly involved in plant defence responses and secondary metabolic pathways. In conclusion, RNA-Seq analysis identified 962 candidate genes associated with the resistance in CA1191. These findings provide a valuable genomic resource for the development of molecular markers to accelerate chilli breeding programs for anthracnose resistance.

Keywords: *Colletotrichum truncatum*, spray inoculation, non-wounded resistance, Differentially expressed genes

FNBLS#140, a Barley Promising Line

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ABSTRACT:
Consumption of barley in Thailand has significantly increased in recent years, with annual imports exceeding 1.3 million tons. Since the climate in Thailand is not suitable for most barley varieties grown worldwide, a new variety has been developed to adapt to the northern climate and meet the requirements of the brewing industry. The varietal development process included the introduction of genetic resources from the International Maize and Wheat Improvement Center (CIMMYT) in Mexico, followed by evaluations for yield, brown spot disease resistance, and other agronomic characteristics conducted between 1988 and 2025. In addition, grain and malt quality evaluations were conducted to ensure they meet industrial standards. An outstanding line, FNBLS#140, was selected from these evaluation processes. FNBLS#140 takes approximately 84 days to mature, with an average plant height of 102 cm. The average yield is 373 kg/rai, with a potential yield of up to 524 kg/rai. The grain is brown with a length of 12.49 mm, a protein content of 11.1%, and a beta-glucan content of 2.0%. The malting yield is 85% with a saccharification time of less than 10 minutes, which represents optimal quality for beer production. This variety is suitable for planting in the upper northern regions of Thailand. However, the optimal planting period is between mid-December and early January, and waterlogging must be avoided during the seedling stage.

Keywords: barley (*Hordeum vulgare* L.), varietal improvement, malt quality, beer, upper northern

Integrative Analysis of Gene Expression Signatures Related to Sucrose Synthesis in Promising Sugarcane Clones

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ABSTRACT:
Sucrose biosynthesis represents a fundamental metabolic process governing carbon partitioning, sugar accumulation, and productivity in sugarcane (*Saccharum officinarum*). However, the molecular regulatory mechanisms coordinating sucrose metabolism during plant development remain insufficiently characterized. In this study, transcriptional profiling of sucrose related genes was conducted to elucidate molecular expression signatures associated with sucrose biosynthesis in promising sugarcane clones developed at the Nakhon Sawan Field Crops Research Center. Quantitative real-time PCR (qRT-PCR) analysis was performed to quantify the transcript abundance of three candidate genes implicated in sucrose metabolic pathways, including Calreticulin (*MIE8*), Glucose-6-phosphate isomerase (*KIE18*), and a Loricrin-like protein (*TPIE105*), across developmental stages. Significant genotype dependent variation in transcriptional activity was detected, indicating differential molecular regulation among sugarcane clones. At 8 months of growth, DOA Khon Kaen3, DOA Nakhon Sawan2, Q85, NSUT13-154, and DOA Nakhon Sawan1 showed elevated transcript accumulation relative to other genotypes. During maturation (12 months), transcriptional activation was further enhanced, particularly in NSUT13-106, DOA Khon Kaen3, DOA U Thong 10, DOA Nakhon Sawan2, NSUT13-289, Q85, NSUT13-154, and DOA Nakhon Sawan1, suggesting dynamic developmental regulation of sucrose metabolism associated genes. The coordinated upregulation of these genes during maturation indicates a tightly regulated transcriptional network contributing to sucrose accumulation in sugarcane stems. Collectively, these findings provide molecular level insights into the transcriptional control of sucrose biosynthesis and identify high expression clones as valuable genetic resources for molecular breeding aimed at improving sucrose yield and crop productivity.

Keywords: Sugarcane, gene expression, sucrose.

Artificial Pollination Improves Fruit Set and Yield of Greenhouse Cherry Tomato under Heat Stress

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ABSTRACT:
Summer greenhouse production of cherry tomatoes is challenged by low fruit set, as high temperature impair pollen viability and stigma receptivity, compounding the lack of natural pollination. This study therefore aimed to evaluate the effectiveness of artificial pollination on the yield and quality of greenhouse-grown cherry tomatoes under these high-temperature conditions. Three pollination methods (natural, water, and stem vibration) were applied in two cherry tomato cultivars (‘Dang Komen’ and ‘Red Cherry 603’). Results indicated that even with temperatures exceeding 40 °C, the stem vibration pollination was the most effective method for increasing yield. Compared to natural pollination, it significantly increased fruit set and total yield by 2.60 and 2.64 times in ‘Dang Komen’ and by 2.19 and 2.20 times in ‘Red Cherry 603’, respectively. In addition, tomato fruits gained from the stem vibration technique showed a higher fruit weight and tended to increase fruit width and length compared to the other pollination methods in 'Red Cherry 603'. Regarding fruit quality, the pollination methods did not negatively impact key attributes such as fruit firmness, total soluble solids, and fruit color. Interestingly, ascorbic acid content in tomato fruits from the stem vibration tended to increase compared to other pollination methods. In conclusion, stem vibration pollination is a highly effective artificial pollination technique to mitigate the negative effects of high summer temperatures, significantly improving cherry tomato yield in greenhouse production without compromising quality. It is a recommended strategy for maintaining productivity during challenging growing seasons.

Keywords: Artificial pollination, Cherry tomato, Heat stress, Net house

CMR59-55-202: High Starch Yield Elite Cassava Variety

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ABSTRACT:
The elite variety CMR59-55-202 is a new developed cassava variety by Rayong Field Crops Research Center. It was high yield and starch yield, was derived from cross-pollination between CMR5-73-6, a high yield cultivar and DOA Rayong 11, a high starch content cultivar. It was developed since 2016 after seedling selection, clonal selection and the evaluation of yield in preliminary trial, standard trial regional trial, and farmer trial in 14 provinces amount 26 experimental fields. The CMR59-55-202 variety had the average starch yield of CMR59-55-202 was 1,409 kg rai^{-1}, which was 26, 10 and 13% higher than DOA Rayong 5, DOA Rayong 11 and DOA Rayong 72, respectively. Also has the average fresh root yield of 5,791 kg rai^{-1}, which was 17 and 19% higher than DOA Rayong 5 and DOA Rayong 11, respectively. Average starch content 24.0%, which was 10 and 15% higher than DOA Rayong 5 and DOA Rayong 72, respectively. CMR59-55-202 is under consideration for cassava cultivar namely “CASSAVA DOA RAYONG 17”.

Keywords: cassava, breeding, starch yield, fresh root yield

Integrating volatile metabolomics, sensory science and candidate gene identification for flavor-targeted breeding of holy basil (*Ocimum tenuiflorum* L.) for the food industry

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ABSTRACT:
Holy basil (*Ocimum tenuiflorum* L.) is an important medicinal and aromatic herb in Southeast Asia, valued primarily for its unique clove-like, spicy, and piquant flavor that strongly influences consumer acceptance and market value. Despite its importance, germplasm selection and breeding practices are mainly based on agronomic performance, while aroma and flavor-related quality evaluation remains subjective and poorly understood. In addition, most existing studies focus on essential oil composition, with limited integration of sensory perception and gene expression regulation.

This study aims to characterize aroma and flavor diversity in holy basil by integrating sensory science, volatile metabolomics, and candidate gene expression analysis, thereby providing a scientific foundation for flavor-targeted breeding. Holy basil breeding lines will be tested under field conditions. Aroma-related compounds will be analyzed using headspace solid-phase microextraction coupled with gas chromatography-mass spectrometry (HS-SPME GC-MS), a widely applied approach for volatile profiling. Sensory attributes and consumer preferences will be assessed using quantitative descriptive analysis. Key aroma-active compounds contributing to perceived flavor will be identified through odor activity value, and the candidate genes involved in flavor biosynthesis will be investigated and linked to variation in volatile composition and sensory traits.

The expected outcome includes the identification of distinct aroma and flavor profiles among holy basil breeding lines, driven by a limited number of key aroma-active volatiles. These compounds are expected to be associated with specific biosynthetic genes linking sensory traits with volatile profile and gene expression. Overall, these findings will provide a robust framework for flavor-oriented breeding and the development of holy basil cultivars with consistent, industry-preferred aroma.

Keywords: volatile metabolomics, sensory perception, flavor diversity, aroma-active compounds

Resistance to Anthracnose Assessed by Non-wound Inoculation in an F_2 Chilli (*Capsicum annuum* L.) Population Derived from 'CA365' × 'CA1191'

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ABSTRACT:
Breeding for anthracnose resistance is a critical strategy for sustainable chili improvement. This study evaluated non-wounded anthracnose resistance in an F_2 population (n=171) derived from a cross between the susceptible parent 'CA365' and the resistant parent 'CA1191' (*Capsicum annuum* L.), sourced from the Tropical Vegetable Research Center, Department of Horticulture, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University. The objective was to characterize resistance phenotypes to facilitate future gene identification. Fruits were inoculated with *Colletotrichum truncatum* '158ci' using a non-wound method at both mature green and ripe red stages. Disease severity was assessed on a 0–9 scale at 5, 7, 10, and 14 days after inoculation (DAI). The results showed significant segregation of resistance within the population. At the mature green stage, 84 samples remained symptom-free (score 0) throughout the 14-day observation period, while 16 samples reached the maximum disease severity (score 9). At the ripe red stage, the number of symptom-free samples were 34, whereas 20 samples reached the maximum severity by 14 DAI. These findings demonstrate substantial phenotypic variation for anthracnose resistance within the F_2 population, providing a robust foundation for the molecular identification and mapping of resistance-associated genes in future chilli breeding programmes.

Keywords: *Colletotrichum truncatum*, mature green resistance, ripe red fruit resistance

Investigation of Aroma Traits Using Molecular Markers to Monitor the F_3 Rice Population

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ABSTRACT:
Developing rice varieties using marker-assisted selection (MAS) is important for selecting traits associated with the physiological characteristics of rice and requires the breeder's expertise. Sometimes, the selected rice varieties may lack certain characteristics or may not meet the intended objectives. This research aims to use molecular markers to monitor rice quality traits such as aroma and low amylose content. Screening was conducted on a photoperiod-sensitive F_3 population, comprising 1,965 lines from the Phrae, Phitsanulok, Chai Nat, Lopburi, and Ratchaburi Rice Research Centres. The next step involved DNA extraction and screening using target markers, including the aroma marker (*badh2*), the waxy marker (Wx^b) and the selection of homozygous genotypes carrying all or some of the targeted genes. Promising lines were chosen for amylose content and yield trial evaluation. Four groups of promising lines were selected: (1) 632 lines (32%) carrying both *badh2* and Wx^b; (2) 244 lines (12%) carrying *badh2* and intermediate-high amylose content; (3) 283 non-aromatic lines (14%) with low amylose content; and (4) 421 non-aromatic lines (21%) with intermediate-high amylose content. Using molecular markers for detection makes the development of rice varieties in each generation of the selection process more efficient and accurate. Breeders can reduce the population size in subsequent generations, resulting in decreased workload and labour in the experimental field. Therefore, selection becomes more effective.

Keywords: molecular marker, aroma, low amylose, intermediate to high amylose

Evaluation of High Temperature Wheat Germplasm from International Maize and Wheat Improvement Center (CIMMYT)

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ABSTRACT:
Wheat can be grown in the upper northern region of Thailand. However, high temperatures accelerate flowering and shorten the harvest period. Insufficient vegetative growth often results in lower yields and poor grain quality. The objective of this study was to evaluate high temperature tolerant wheat germplasm from the International Maize and Wheat Improvement Center (CIMMYT). A total of 49 bread wheat varieties were compared with a local check variety (Fang 60) at the Mae Hong Son Rice Research Center during the 2024/2025 growing season. The average yield ranged from 285 to 606 kg/rai. Among them, 45 varieties produced higher yields than Fang 60. The highest yield was observed in variety MHSBWS24049, which produced 606 kg/rai, representing a 74% increase compared with Fang 60 (347 kg/rai). Grain quality analysis showed that protein content ranged from 10.83% to 14.26%, with 30 varieties having a protein content higher than 12%. The highest protein content was observed in variety MHSBWS24014, with a protein percentage of 14.26%.

Keywords: Wheat, High Temperature

CNT16008-38-2-1-2-1: A High-Yielding Photoperiod-Insensitive Non-Glutinous Rice Elite Line

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ABSTRACT:
To serve the need for high-yielding rice varieties in irrigated rice farming areas in the Central and Lower Northern Regions, the rice line CNT16008-38-2-1-2-1 was developed. It was a photoperiod-insensitive rice line, which was obtained from a cross between PSL09082-CNT-140-2-3-1-1-2-1 and PSL14190-MAS(6)-CNT-8-11. The line has the mean yield of 4.01 t ha^{-1}, which is 3 and 6 percents higher than RD41 (3.87 t ha^{-1}) and RD57 (3.78 t ha^{-1}), respectively. The line had the highest recorded yield of 6.26 t ha^{-1} in 2024 wet season in Sao Hai district, Saraburi province. Its yield was stable across different environmental conditions. The yield was responsive to nitrogen fertilizer application at a rate higher than 150 kg ha^{-1}. The plant has an erect stature with an erect flag leaf. Its culms are very strong. The plant height was 112 cm. The maturity period was 117 days, when transplanted. Its brown rice is slender in shape with a dimension of 8.08 mm × 2.12 mm × 1.87 mm. Its milling quality is very good, having the head rice recovery rate of 45.74 percent. The rice has a high amylose content (27.96 %), soft gel consistency (53.80 mm gel length), low gelatinization temperature (7.0 alkali spreading value), and normal elongation when cooked (1.47 times). It should also be noted that the line is moderately susceptible to brown planthopper, white-backed planthopper, blast and bacterial blight diseases.

Keywords: plant breeding, rice line, high-yielding rice

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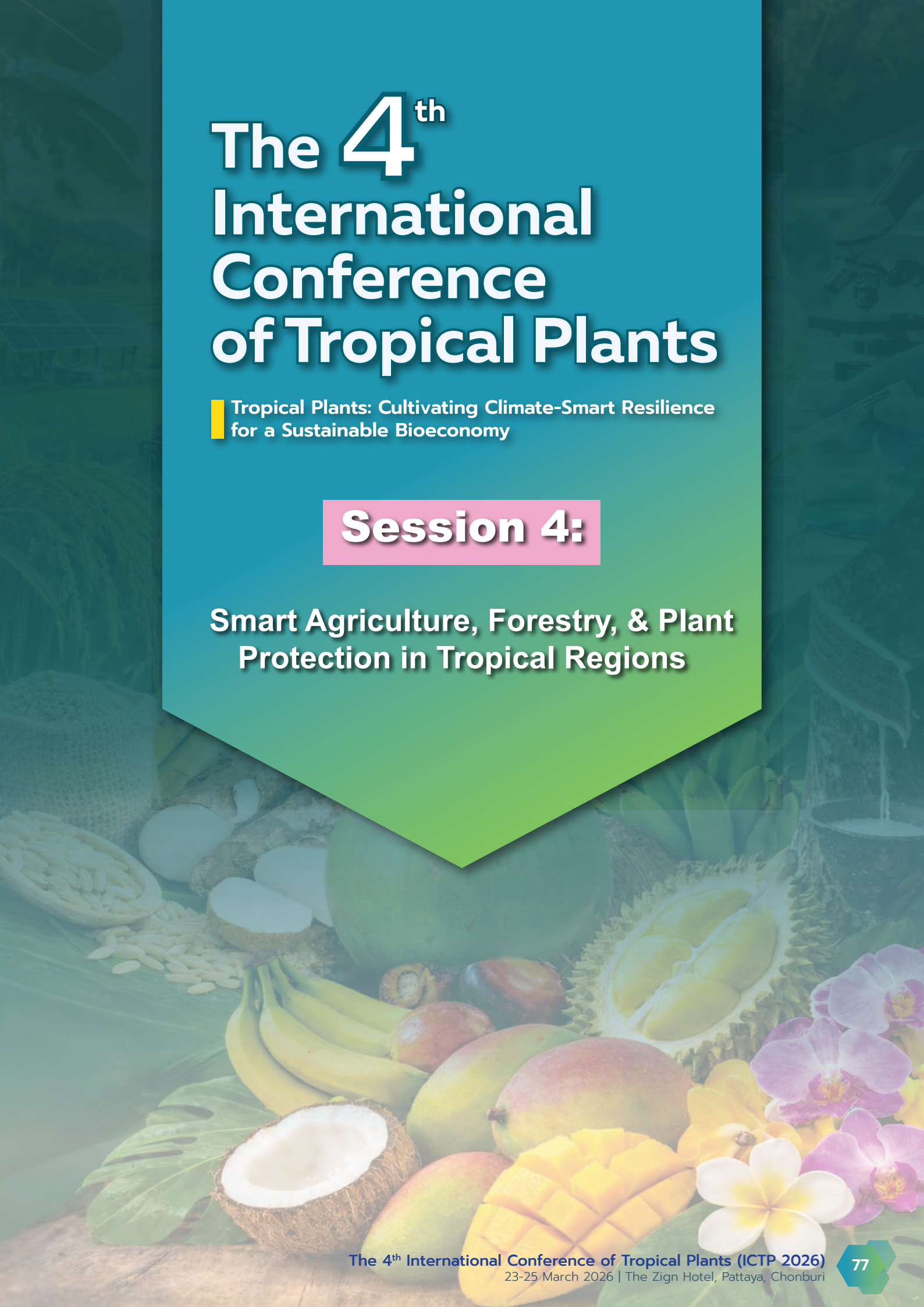

Regenerative Design for Agriculture Service Providers in Thailand: A Structured Analytical Review of Ecological, Economic, Organizational, Social, and Governance Transitions

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ABSTRACT:
Agriculture service providers (ASPs) play a pivotal role in service-based agricultural systems, particularly in smallholder-dominated economies where mechanized services mediate daily farming operations. Despite the growing prominence of regenerative agriculture, existing research remains largely farm-centric and offers limited understanding of how regenerative principles are operationalized through service systems. This article addresses this gap through a structured analytical review that integrates insights from ecology, service management, organizational studies, behavioral science, and governance research. Rather than adopting a systematic review protocol, the analysis focuses on conceptual integration across five dimensions: ecological foundations, economic logics, organizational capabilities, social dynamics, and governance arrangements. The synthesis demonstrates that regenerative outcomes depend on alignment across these dimensions, as ecological principles alone are insufficient without compatible service design, incentive structures, capabilities, and trust-based relationships. Building on this synthesis, the article advances theoretical propositions and develops a Regenerative Service–Ecosystem Framework that repositions ASPs as ecosystem enablers. The study concludes by outlining a multi-level research agenda to guide future empirical inquiry.

Keywords: Regenerative agriculture, Agriculture service providers, Service ecosystem, Sustainability transitions

Enhancing Tea Oil Yield of *Camellia oleifera* Through Optimized Root Zone Soil Management

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ABSTRACT:
Low tea oil yield in northern Thailand has been associated with degraded soil conditions and poor root zone functionality despite continuous chemical fertilizer application. This study aimed to improve tea oil (Camellia oleifera) productivity through optimized root zone soil management by enhancing soil microbial activity and nutrient availability. The experiment was conducted during 2019–2021 at Ban Pang Mahan, Mae Fah Luang District, Chiang Rai Province, on low-yield plantations growing on soils derived from metamorphic rock. Soils were acidic (pH 5.3–6.5) with high organic matter (3.7–9.3%) and excessive available phosphorus (148–903 mg kg-1). Micromorphological observations indicated poorly decomposed organic residues and limited biological activity, suggesting soil degradation.

Four treatments were evaluated: (1) water (control), (2) banana shoot fermented extract with Super LDD 2, (3) chili fermented extract with Super LDD 7, and (4) combined banana shoot and chili fermented extracts, each applied at 600 mL per week. Results showed that organic liquid treatments significantly increased soil microbial populations compared with the control. The combined treatment (Treatment 4) produced the highest fresh fruit yield (852 kg rai^{-1}), representing a 72% increase over the control (496 kg rai^{-1}), followed by Treatment 2 (682 kg rai^{-1}) and Treatment 3 (550 kg rai^{-1}).

The findings demonstrate that improving root zone biological activity through organic liquid amendments can enhance nutrient utilization efficiency and substantially increase tea oil yield under degraded soil conditions. Root zone soil management is therefore a practical and sustainable strategy for improving Camellia oleifera productivity in northern Thailand.

Keywords: Root zone soil management, Camellia oleifera, Soil microbial activity, Yield improvement

Association Between Canopy Size from RGB Images and Destructively Measured Biomass for Growth Assessment in Holy Basil

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ABSTRACT:
The yield of holy basil (*Ocimum tenuiflorum* L.) consists of stems and leaves, which are closely associated with plant growth at all developmental stages. However, information on this relationship is limited. Biomass assessment using the harvest method directly reflects yield but requires destructive sampling, preventing continuous monitoring. In contrast, canopy projected area derived from RGB images provides a non-destructive, high-throughput approach for tracking plant growth over time. This study aimed to investigate the association between biomass obtained from the harvest method and canopy size (top and side projected areas) derived from RGB images, at plant ages of 32, 41, 50, and 65 days in three holy basil varieties including OS100 (short plants with small leaves), OS108 (tall plants with large leaves), and their F_1 hybrid, with the aim of developing an appropriate approach for monitoring growth in holy basil populations. Results showed that total dry mass (Md total) differed significantly among varieties from 41 days onward, whereas canopy size (top and side views) showed significant differences as early as 32 days. Linear regression analysis between total dry mass and canopy size at each growth stage revealed that top and side projected areas could explain variations in above-ground dry mass, with R^2 values ranging from 0.56–0.68 and 0.95–0.96, respectively. These findings indicate that side-projected canopy area from RGB images is a robust, non-destructive indicator for monitoring holy basil growth across developmental stages.

Keywords: *Ocimum tenuiflorum* L., harvest method, non-destructive method

Synergistic Effects of Pre-harvest UV-A Supplementation and CO_2 Enrichment on Physiological Traits and Phytonutrient Profiles of Kale

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ABSTRACT:
A plant factory with artificial lighting (PFAL) offers a unique opportunity to enhance crop quality through precise environmental control. This study investigated the physiological and nutritional responses of kale (*Brassica oleracea* var. *sabellica*) to optimized abiotic factors, specifically ultraviolet-A (UV-A) supplementation and carbon dioxide (CO_2) enrichment. Our findings demonstrate that pre-harvest UV-A exposure at 10 W/m² for five days significantly enhanced shoot fresh weight by over 47% and increased phytonutrient accumulation, including vitamin C (2.6-fold increase) and total phenolics (56.7% increase), while effectively reducing nitrate content by over 2.1 times. Concurrently, optimizing CO_2 concentrations revealed a critical balance between yield and quality; while elevated CO_2 at 1200 µmol/mol maximized biomass, it negatively affected vitamin C levels. In contrast, moderate enrichment to 800 µmol/mol proved optimal, boosting protein content and reducing nitrate accumulation. Collectively, these results highlight that integrating specific UV-A supplementation with controlled CO_2 levels is essential for overcoming the trade-off between yield and nutritional value. This research provides an optimized cultivation protocol for PFAL systems to produce premium kale that is both high-yielding and rich in health-promoting compounds.

Keywords: *Brassica oleracea*, Controlled environment agriculture, Phytonutrients, Plant Factory with Artificial Lighting, Ultraviolet-A

A Smart and Sustainable Biocontrol Strategy Integrating *Streptomyces* Metabolites and Low-Concentration Ethanol for the Management of Durian Stem Rot

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ABSTRACT:
Durian (*Durio zibethinus* L.) production in tropical regions is severely constrained by root and stem rot caused by *Phytophthora palmivora*. This aggressive oomycete pathogen is commonly managed through intensive fungicide use. To promote smart and sustainable plant protection, this study evaluated an integrated biocontrol strategy combining microbial metabolites with a low concentration of ethanol to enhance pathogen suppression and host defense activation. The synergistic effects of cell-free culture filtrate (CF) produced by *Streptomyces* sp. and ethanol (5%, v/v) were investigated using *in vitro* assays and detached leaf tests. The combined treatment significantly inhibited mycelial growth of *P. palmivora* (approximately 75%), induced colony lysis, caused hyphal deformation, and disrupted sporangial development. *P. palmivora* pre-treated with CF and ethanol exhibited markedly reduced infection ability on durian leaves, resulting in significantly smaller necrotic lesions compared with untreated controls. Beyond direct pathogen inhibition, durian leaves inoculated with CF + ethanol-treated *P. palmivora* showed significantly enhanced activities of defense-related enzymes, including peroxidase and polyphenol oxidase, indicating the activation of host defense responses. These results suggest that the combined treatment functions through a dual mechanism involving direct suppression of pathogen viability and indirect stimulation of plant defense. Overall, this study highlights a smart and environmentally friendly disease management approach that integrates microbial-based biocontrol with a simple, low-impact enhancer. The strategy offers strong potential to reduce chemical fungicide dependency and support sustainable plant protection practices in tropical agricultural systems.

Keywords: Smart agriculture; Sustainable plant protection; Biological control; *Streptomyces* metabolites; Durian; Tropical crops

Indigenous *Trichoderma asperelloides* as a Dual-Function Agent for Plant Growth Promotion and Biological Control of Phytopathogenic Fungi

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ABSTRACT:
An indigenous fungal strain, TSUxPT3.5, isolated from organic rhizosphere soil in southern Thailand, was identified as *Trichoderma asperelloides* based on multilocus sequence analysis of the ITS, tef1, and rpb2 genes together with phylogenetic analysis. The strain was evaluated for its plant growth–promoting and biocontrol potential against several economically important phytopathogenic fungi. Indole-3-acetic acid (IAA) production was detected in this strain, indicating its potential role in direct plant growth promotion. In dual culture assays, the strain exhibited antagonistic activity against *Colletotrichum gloeosporioides, Colletotrichum capsici, Fusarium oxysporum, Rhizoctonia solani, Sclerotium rolfsii, Fusarium moniliforme* and *Pyricularia grisea*. Further characterization revealed positive activity of cell wall–degrading enzymes, particularly chitinase, as well as the emission of volatile organic compounds (VOCs) with antifungal properties. In addition, the efficacy of *T. asperelloides* TSUxPT3.5 in controlling anthracnose disease caused by *Colletotrichum* was evaluated using Chaiburi White chilli fruits (*Capsicum frutescens*). The strain reduced anthracnose lesion development with an average inhibition rate of 38.56%. These results suggest that *Trichoderma asperelloides* TSUxPT3.5 should be applied before disease occurrence, as it is more effective for disease prevention than for disease treatment.

Keywords: Biological control, *Capsicum frutescens*, Plant growth promotion, *Trichoderma*, Thailand

Monitoring of disease occurrence in torch ginger intercropped with rubber trees.

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ABSTRACT:
Torch ginger (Etlingera elatior) is an ornamental and medicinal plant widely cultivated in tropical Southeast Asia, particularly in southern Thailand. A comparative field survey was conducted in two production systems: torch ginger intercropped with rubber trees in Srinagarindra District, Phatthalung Province, and monoculture torch ginger plantations in Sikao District, Trang Province. Abnormal symptoms were observed in both locations, including necrotic lesions on floral organs and stem blight symptoms. Based on symptomatology and pathogen identification, the disease was classified as anthracnose caused by Colletotrichum atlanticum, which has recently emerged as a major constraint on commercial torch ginger production, causing severe damage to flowers and significantly reducing market value.

This study investigated the biocontrol efficacy of Trichoderma sp. strain Z2-02 against C. atlanticum using in vitro, in vivo, and field evaluations. Dual culture and sealed plate assays demonstrated that strain Z2-02 markedly inhibited pathogen growth, with inhibition rates of 74.44% and 84.26%, respectively. The suppression was attributed to competitive interactions and the production of volatile organic compounds (VOCs).

Keywords: Torch ginger (Etlingera elatior), *Colletotrichum atlanticum*, *Trichoderma* sp. strain Z2-02

Development of an Agricultural Service Provider Model for Organic Cassava Production in Northeastern Thailand: Evidence from Ubon Ratchathani Province

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ABSTRACT:
Organic cassava production has become an important strategy for promoting sustainable agriculture, environmental conservation, and rural economic development in Thailand, particularly in the northeastern region. However, organic cassava production remains constrained by labor shortages, limited access to mechanization, insufficient technical knowledge, and weak integration of agricultural services. This study aims to develop an appropriate Agricultural Service Provider (ASP) model to enhance organic cassava production efficiency, with a specific focus on Ubon Ratchathani Province. The study employs a comprehensive literature synthesis to examine sustainable agriculture practices, agricultural mechanization services, digital agriculture technologies, and value chain development frameworks. The proposed conceptual framework identifies production service quality, technology support, certification support, market linkage services, and institutional support as key determinants influencing farmers' adoption of organic cassava practices, which subsequently affects production efficiency, economic performance, and sustainability outcomes. The findings indicate that an integrated ASP model that combines mechanization services, digital advisory systems, certification support, and value chain integration can significantly improve productivity, reduce production costs, and enhance market competitiveness. Furthermore, institutional collaboration, technology adoption, and farmer capacity development are critical factors for successful implementation. The study contributes to the literature by proposing a comprehensive ASP model for organic cassava production and provides policy implications for agricultural modernization, sustainable farming systems, and rural development in Thailand.

Keywords: agricultural service provider, organic cassava, sustainable agriculture, technology adoption, Thailand, Ubon Ratchathani

Economic Feasibility of Agricultural Service Provider Utilization and Cassava Production Efficiency in Ubon Ratchathani, Thailand

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ABSTRACT:
Cassava is a major economic crop in Thailand, particularly in the northeastern region, where it plays a significant role in rural livelihoods and agro-industrial development. However, cassava farmers increasingly face challenges such as rising production costs, labor shortages, and price volatility, which affect farm productivity and profitability. Agricultural Service Providers (ASPs) have emerged as an important institutional mechanism to address these constraints by offering mechanization and farm operation services that improve operational efficiency and reduce production risks. This study aims to examine the economic feasibility of ASP utilization and its effects on cassava production efficiency in Ubon Ratchathani Province, Thailand. The study integrates economic feasibility analysis and production efficiency concepts based on Transaction Cost Economics and Diffusion of Innovation Theory. Economic evaluation methods, including cost–benefit analysis and investment appraisal approaches, are used to assess the financial viability of ASP utilization, while production efficiency is examined in terms of operational timeliness, input utilization, and yield performance. The findings suggest that ASP utilization improves farm efficiency by reducing labor dependency, optimizing input use, enhancing crop management practices, and increasing yield per unit area, leading to improved economic returns and financial sustainability. The study contributes to the literature by providing an integrated framework linking ASP utilization, economic feasibility, and production efficiency in cassava farming. The results offer important policy implications for promoting agricultural mechanization services and improving sustainable agricultural development in Thailand.

Keywords: agricultural service providers, economic feasibility, production efficiency, cassava production, mechanization, Thailand, Ubon Ratchathani

Study of The Interaction of Tapioca and *Sri Lankan cassava mosaic* virus on Phytohormones Production

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ABSTRACT:
Cassava production in Southeast Asia has been severely affected by *Sri Lankan cassava mosaic virus* (SLCMV), a whitefly-transmitted begomovirus causing cassava mosaic disease. Salicylic acid (SA) is a key phytohormone involved in antiviral defense and Systemic Acquired Resistance (SAR). This study aimed to elucidate the role of the whitefly *Bemisia tabaci* in modulating SA accumulation during SLCMV infection in cassava cultivars with contrasting resistance levels: resistant C33, tolerant Kasetsart 50 (KU50), and susceptible Rayong 11 (R11).

Phytohormone analysis revealed that SA was the only hormone significantly induced following SLCMV inoculation via whitefly infestation, whereas jasmonic acid (JA) and abscisic acid (ABA) remained unchanged. SA accumulation peaked earlier in KU50 (2 days after inoculation, dai) and slightly later in C33 (3 dai), indicating a rapid defense response in tolerant and resistant genotypes. In contrast, R11 exhibited no significant SA induction. Expression analysis demonstrated that PR9e, PR7f5, HSP90, Hsf8, SPS1, and SYP121 were upregulated in association with SA accumulation, supporting their involvement in SAR activation.

These findings highlight the central role of SA-mediated signaling in cassava defense against SLCMV, particularly in resistant genotypes, and provide insights into hormone-associated mechanisms that could be exploited for breeding CMD-resistant cultivars and improving sustainable cassava production.

Keywords: Salicylic acid (SA), *Sri Lankan cassava mosaic virus* (SLCMV), *Bemisia tabaci*, Systemic Acquired Resistance (SAR), Cassava mosaic disease (CMD)

Digital Agricultural Innovation, Agricultural Service Provider Utilization, Production Efficiency, and Economic Feasibility in Cassava Farming: A Conceptual Framework

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ABSTRACT:
This study develops a conceptual structural model to examine the relationships among digital agricultural innovation, agricultural service provider (ASP) utilization, production efficiency, and economic feasibility in cassava farming in Northeastern Thailand. The framework integrates perspectives from precision agriculture, technology adoption theory, and agricultural productivity theory. The study proposes a set of research propositions to explain the causal relationships among latent variables. The model suggests that digital agricultural innovation enhances ASP utilization and production efficiency, which subsequently improves economic feasibility and environmental sustainability. The conceptual model contributes to the literature on digital agriculture and service-based agricultural production and provides a foundation for future empirical testing using structural equation modeling.

Keywords: Digital Agriculture, Agricultural Service Providers, Production Efficiency, Economic Feasibility, Structural Equation Modeling, Cassava Farming

Integrated Multiplication–Distribution, Technology Transfer and Logistics Assessment for Edible Cassava (Pirun 4) Value-Chain Upgrading in Nakhon Ratchasima, Thailand

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ABSTRACT:

This study developed and evaluated an integrated system for edible cassava production upgrading in Nakhon Ratchasima Province, Thailand, covering knowledge and technology transfer, demonstration-based field management, stem cutting multiplication and distribution, logistics time assessment, and multi-stakeholder network building. The study integrated five components: (1) establishment of demonstration plots, (2) training and technology transfer on edible cassava production and GAP-aligned field practices, (3) multiplication plots to produce high-quality planting materials for farmer distribution, (4) logistics time analysis from harvest to factory entry, and (5) development of collaborative networks among farmers, government/community actors, and industry. The program targeted 400 farmers but reached 650 participants. Demonstration plots achieved average fresh root yields of 6.9 and 5.2 t rai-1 with production costs of 10,400–17,200 THB rai^{-1}, comparable to conventional industrial cassava cultivation. Scientific field management reduced pest and disease losses and increased net profit by approximately 30–65% relative to typical farmer practices. Stem multiplication and distribution covered 1,147 rai (47 rai multiplication and 1,100 rai distribution), with a cutting survival rate of 90–100% and an average net-income increase of ~10% among participating farmers. A logistics survey of 300 farmers indicated that the main delays occurred during harvesting and aggregation due to labor, equipment, and weather constraints, while community-level transport planning remained limited. Overall, the integrated approach demonstrates a scalable research-to-extension model to strengthen raw material security for high-value edible cassava supply chains and improve farmer livelihoods.

Keywords: Pirun 4 edible cassava, Stem cutting multiplication, Clean planting material distribution, Smallholder profitability, Agricultural extension model

Relationship Between Age and Height of Coconut Trees to Assess Underplanting or Replacement Areas in Prachuap Khiri Khan Province

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ABSTRACT:
The objective of this study was to classify coconut plantation areas in Prachuap Khiri Khan Province into two categories: 1) underplanting areas, defined as areas with coconut trees aged between 45–55 years and heights of 15–18 meters. And 2) Replacement areas: Defined as areas with coconut trees older than 55 years and heights exceeding 18 meters, which are characterized by low yields and harvesting difficulties. The study was conducted by measuring the height of coconut trees with known planting years at the Chumphon Horticultural Research Center to calculate the average height and age based on planting records. Correlation analysis was performed by designating age as the independent variable (x) and height as the dependent variable (y). The results of the analysis revealed a statistically significant correlation between age and height ($r^2 = 0.91$). This relationship is non-linear, as represented by the following equation: $y = 0.89x-0.133X^2+ 0.00008x^3-3.607$. The accuracy of this equation was tested by randomly measuring the height of coconut trees in farmers' plots in Prachuap Khiri Khan Province and correlating them with age data from the farmers' registration database; the results were consistent with the established equation. Based on 2020 coconut plantation data for the total provincial area of 406,687 rai, the findings are as follows: Using age as the criterion, 72,291 rai require underplanting, and 60,508 rai require replacement. Using height as the criterion (via the relationship equation): 81,391 rai requires underplanting, and 63,098 rai requires replacement.

Keywords: Coconut Tree, Coconut plantation areas, Underplanting, Replacement, Prachuap Khiri Khan Province

Effect of Salicylic Acid on Systemic Acquired Resistance in *Sri Lankan Cassava Mosaic Virus*–Infected Cassava

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ABSTRACT:
Cassava mosaic disease (CMD), caused by *Sri Lankan cassava mosaic virus* (SLCMV), severely affects cassava production in Thailand. Symptoms include mosaic and distorted leaves, stunted and yield losses of approximately 40-80%. The SLCMV widespread rapidly through the whitefly (*Bemisia tabaci)* vector and unsanitary propagative stems. This study aimed to investigate the efficacy of salicylic acid (SA) in inducing Systemic Acquired Resistance (SAR) in SLCMV-infected cassava cultivar Kasetsart 50. Plants were treated with foliar sprays of SA at concentrations of 100 and 200 mg/mL. The results revealed no statistically significant differences in disease severity compared to the control group; however, newly emerging leaves on SA-treated plants showed no visible symptoms. Real-time PCR analysis demonstrated that SA application significantly reduced viral titers at 1 and 2 weeks post-treatment, after which viral levels increased again at weeks 3 and 4, corresponding to the reappearance of disease symptoms. These findings suggest that SA can effectively activate SAR in SLCMV-infected cassava, leading to reduced viral accumulation. SA can induce plant resistance through the SAR process, which enhances plant resistance to infectious agents. Therefore, SA holds potential for field-level application as a strategy to manage CMD outbreaks in cassava cultivation.

Keywords: Cassava mosaic disease, *Sri Lankan cassava mosaic virus* (SLCMV), salicylic acid (SA), Systemic acquired resistance (SAR), plant immune response

Comparative Proteomic Analysis Reveals Defense-Related Proteins Associated with Cassava Mosaic Disease Resistance Against *Sri Lankan cassava mosaic virus*

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ABSTRACT:
Cassava mosaic disease (CMD), caused by *Sri Lankan cassava mosaic virus*, is a major constraint to cassava production in Southeast Asia. Understanding host responses to viral infection is essential for developing effective disease management and resistance strategies. This study investigated temporal protein expression profiles in cassava cultivars exhibiting different resistance phenotypes at 0, 21, 32, and 67 days after inoculation (dpi) using liquid chromatography–tandem mass spectrometry (LC–MS/MS). Graft inoculation was performed using infected rootstocks and three scion cultivars: TMEB419 (resistant), KU50 (tolerant), and R11 (susceptible). Viral infection was confirmed in all cultivars at 21 dpi. At 67 dpi, TMEB419 exhibited mild symptoms (severity score 2), whereas KU50 and R11 showed more severe symptoms (scores >3).

Proteomic analysis identified 541 differentially expressed proteins across cultivars and time points. In TMEB419, defense- and metabolism-related proteins, including RuBisCO activase, fructose-bisphosphate aldolase (FBA), AP2/ERF, MYB, TCP transcription factors, peroxidase, and protein kinases, were upregulated at 21 and 32 dpi. At 67 dpi, FBA, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), TCP, and leucine-rich repeat (LRR) proteins remained elevated. KU50 showed increased expression of CW-type proteins, bZIP transcription factors, glutathione hydrolase, peroxidase, thioredoxin, ubiquitin-specific protease (USP), and U-box proteins. In contrast, R11 exhibited upregulation of photosynthesis-related proteins, including oxygen-evolving enhancer protein 1 (OEE1), PSI-G, chlorophyll(ide) b reductase, and PSI-F.

RT-qPCR analysis supported the proteomic data, with strong induction of defense-related genes, including receptor-like serine/threonine kinase (RSTK), protein kinases, and LRR genes in TMEB419. These findings provide molecular insights into CMD resistance mechanisms and identify potential protein biomarkers for breeding CMD-resistant cassava cultivars.

Keywords: Cassava mosaic disease, *Sri Lankan cassava mosaic virus* (SLCMV), proteomics, and gene expression

Differential Responses of Two Kale Cultivars to Elevated CO2 on Growth, Photosynthesis, and Phytonutrient Profiles in a Plant Factory with Artificial Lighting

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ABSTRACT:
Enrichment of carbon dioxide (CO_2) is known to enhance the growth and biomass of vegetables in the Brassicaceae family. This study aimed to investigate the impact of CO_2 concentration on the growth, biomass, and phytonutrient production of kale grown in a plant factory with artificial lighting (PFAL) in two kale cultivars ('Curly Kale' and 'Red Ursa'). Plants were grown under three CO_2 concentrations: 400 (ambient CO_2), 800, and 1200 µmol mol^{-1}, using a completely randomized design with four replications/treatment. The results revealed that increasing CO_2 concentration to 1200 µmol mol^{-1} significantly increased the growth and biomass in both kale cultivars compared to other CO_2 concentrations. The average height of 'Curly Kale' and 'Red Ursa' increased to 48.73 cm and 45.00 cm, respectively. The highest average shoot fresh weight was 176.87 g/plant for 'Curly Kale' and 113.75 g/plant for 'Red Ursa'. Increasing CO_2 concentration to 1200 µmol mol^{-1} also significantly enhanced net photosynthesis rate and stomatal conductance. Conversely, the intermediate concentration of 800 µmol mol^{-1} CO_2 was most effective at increasing total vitamin C, soluble protein, and total phenolic contents in both kale cultivars. Notably, 1200 µmol mol^{-1} CO_2 treatment caused a significant reduction in vitamin C content. Furthermore, both elevated CO_2 levels (800 and 1200 µmol mol^{-1}) successfully decreased nitrate accumulation in both kale cultivars. In conclusion, cultivating kale in a PFAL at 1200 µmol mol^{-1} CO_2 optimizes for growth, biomass, and photosynthesis, while at 800 µmol mol^{-1} CO_2 is superior for enhancing phytonutrient quality.

Keywords: *Brassica*, carbon fixation, elevated CO_2, phytonutrients, photosynthesis

Induction of Multiple Shoots for Mass Propagation of True-to-Type Makapuno Coconut Seedlings under Aseptic Conditions

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ABSTRACT:
This study aimed to develop tissue culture techniques for inducing multiple shoots to increase the number of true-to-type Makapuno coconut plantlets under aseptic conditions. The experiment was divided into two steps. Step 1 compared culture media for embryo germination and seedling development. Results showed that MS medium supplemented with 2,4-D at 4.52 µM achieved the highest germination rate (93.8%) and produced seedlings with an average height of 19.3 cm, outperforming Y3 medium (72.9% germination and 16.3 cm height). Step 2 investigated media formulations for multiple shoot induction by culturing incise seedlings in Y3 medium supplemented with TDZ and CPPU. The treatment with CPPU at 10 µM produced the highest increase in secondary meristem clump weight (2.27-fold) compared to TDZ treatments. These findings indicate that CPPU and TDZ play crucial roles in shoot induction and can be applied to mass production of true-to-type Makapuno coconut plantlets under aseptic conditions, providing a promising approach for commercial propagation and genetic conservation.

Keywords: True-to-Type Makapuno coconut, Embryo culture, Multiple shoot induction, germination, meristem clump

Influence of Biochar Produced from Sugarcane Leaves on Soil Quality, Plant Growth Performance, and Yield of Vegetable Crops in Sandy Clay Soil.

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ABSTRACT:
This study aimed to investigate the effects of sugarcane leaf-derived biochar on improving sandy clay soil for vegetable production under an organic farming system. The experiment was conducted at Wang Din Niao Village, Wang Din Niao Subdistrict, Noen Maprang District, Phitsanulok Province, Thailand. A Randomized Complete Block Design (RCBD) with four replications was employed. The treatments were as follows: (1) no biochar application (control), (2) cow manure at 3 tons per rai, (3) sugarcane leaf biochar at 2 tons per rai, and (4) cow manure at 1 ton per rai combined with sugarcane leaf biochar at 1 ton per rai. The experiment was carried out using flowering Chinese cabbage (*Brassica rapa* var. *parachinensis*) and radish (*Raphanus sativus*). The results showed that the application of sugarcane leaf biochar significantly improved soil physical properties. The sandy clay soil amended with biochar exhibited greater friability, higher total porosity, and enhanced water-holding capacity compared to other treatments. Additionally, biochar application resulted in higher nutrient availability. When tested with vegetable crops, both sole biochar application and the combined application of cow manure and biochar significantly enhanced growth and yield of flowering Chinese cabbage and radish. Moreover, continuous cropping was possible without additional soil fertilizer inputs, indicating the potential of sugarcane leaf biochar as a sustainable soil amendment for organic vegetable production.

Keywords: sugarcane leaf biochar; soil amendment; organic vegetable production

Weathered basalt dust improves plant nutrient availability in acidic paddy soils: Insights from Calcium K-edge XANES technique

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ABSTRACT:
Basalt is a mafic igneous rock composed of abundant magnesium- and iron-rich aluminosilicate minerals. It contains essential plant nutrients, such as calcium, which are crucial for plant growth. In agricultural systems, basalt dust wastes have been widely proposed as suitable soil amendments to increase fertility and promote the release of plant nutrients. Herein, we conducted a detailed characterization of the mineralogical and physicochemical properties of basalt wastes from mining activities. We also measured the availability of plant nutrients in soil systems to evaluate the potential of basalt rock powder (BRP) as a soil amendment. BRP was applied to acidic paddy soils at rates of 4.0, 8.1, and 16.0 tons ha^{-1}. The results demonstrated that the characteristics of BRP are nearly identical to those of calcite and dolomite minerals (60% and 40%, respectively). The highest BRP application rate increased the soil solution pH by 4.3% and significantly ($p < 0.05$) enhanced dissolved Ca and Mg contents ($\tilde{x}$ = 652 and 149 mg L^{-1}, respectively). Soluble Si was a dominant component released from BRP ($\tilde{x}$ = 8.9–9.2 mg L^{-1}), with the initial release observed after 30 days. Furthermore, BRP improved soil fertility by promoting macronutrient release through the optimization of soil pH and redox potential (E_h). Additionally, the recommend rates (8.1 tons ha^{-1}) was conducted to assess the impact of BRP on rice growth and yield. At 60 days of cultivation, the BRP treatments resulted in a statistically significant increase in both root length and yield compared with the control. Our findings provide crucial information and establish optimal application rates for BRP in agricultural systems. Ultimately, applying BRP as a soil amendment is an effective strategy for improving overall soil health.

Keywords: Clay Mineral, Macronutrient, Solubility, Minning Waste, Soil Amendment

Effects of Synthetic Zeolite Derived from Kaolin on Methane (CH4) Emissions and Rice Yield Performance.

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ABSTRACT:

This study aimed to evaluate the optimal application rate of synthetic zeolite derived from kaolin for reducing methane (CH_4) emissions and improving rice productivity. Zeolite was synthesized from kaolin obtained from Lampang Province using a hydrothermal method with an alkaline solution. The synthesized material was identified as zeolite A with a cubic crystal structure. The cation exchange capacity (CEC) of the synthesized zeolite was 341 cmol kg^{-1}, which was approximately 26 times higher than that of the original kaolin. A pot experiment was conducted to investigate the effects of synthetic zeolite on methane emissions and rice yield. The experiment consisted of five treatments: T1 (control), T2 (chemical fertilizer), and T3, T4, and T5 (chemical fertilizer combined with synthetic zeolite at rates of 500, 1,000, and 1,500 kg rai^{-1}, respectively). The results showed that methane emissions in all treatments peaked at the fourth week after planting. Methane emissions were significantly negatively correlated with soil redox potential (Eh) ($r = -0.552$) and soil pH ($r = -0.278$). Among the treatments, the application of synthetic zeolite at 1,500 kg rai^{-1} (T5) showed the highest efficiency in mitigating cumulative methane emissions, with a value of 55.5 mg CH_4 m^{-2} day^{-1} compared with the treatment receiving chemical fertilizer alone (T2; 63.0 mg CH_4 m^{-2} day^{-1}). Regarding rice yield, the combined application of chemical fertilizer and synthetic zeolite significantly increased grain yield ($P < 0.05$). The highest yield was observed in T5, reaching 124.6 g pot^{-1}. In conclusion, the application of synthetic zeolite derived from kaolin at a rate of 1,500 kg rai^{-1} has strong potential to enhance rice productivity while simultaneously mitigating greenhouse gas emissions in rice paddy systems.

Keywords: Synthetic zeolite, Kaolin, Methane emission, Rice yield.

Expanding the Production of Short-Grain Rice for the Niche Market in the Central Region.

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ABSTRACT:
The expansion of short-grain rice production for niche rice markets in the Central region aims to enhance farmers' income by linking markets between farmer groups and entrepreneurs for the trading of short-grain rice. The project was implemented through model Community Rice Centers in eight provinces of Central Thailand (Chachoengsao, Pathum Thani, Suphan Buri, Ayutthaya, Prachinburi, Ang Thong, Phetchaburi and Phetchabun). Seed production fields and expansion fields for short-grain paddy were established in accordance with GAP (Good Agricultural Practices) standards. Research results from seed production fields during the 2024/25 crop year showed that short-grain rice varieties produced an average yield of 250–870 kilograms per rai. In the expansion fields covering 524 rai, with the participation of 49 farmers, short-grain rice production yielded on average 4.79–10.81% higher than other rice varieties commonly cultivated by farmers. As a result, farmers' income increased by 0.69–29.84%. This improvement was largely attributed to the market linkage for short-grain paddy between producers and entrepreneurs, enabling farmers to access specialized market networks. Such connections provide farmers with opportunities to negotiate directly with entrepreneurs, in a market where purchase prices are relatively stable. Short-grain paddy with 14% moisture content is purchased at 8–11 baht per kilogram, which is higher than the current market price of ordinary paddy.

Keywords: short-grain rice, niche rice markets, central region

Increase the Rice Production Potential of Community Rice Centers in the Central Region by Using Modern Agricultural Technology to Produce Rice in an Environmentally Friendly Manner.

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ABSTRACT:
This research aimed to examine approaches for applying modern agricultural technologies to produce high-quality, environmentally friendly rice in Community Rice Centers and to evaluate the economic and environmental outcomes of technology adoption, particularly cost reduction, yield improvement, and increased farmers' income. The study was conducted in prototype Community Rice Centers in seven Central provinces: Chachoengsao, Prachin Buri, Phra Nakhon Si Ayutthaya, Pathum Thani, Suphan Buri, Phetchabun, and Saraburi. Demonstration plots were established to implement modern technologies for environmentally friendly rice production, including laser land leveling, drone-based seed broadcasting, alternate wetting and drying water management, and fertilizer application based on soil analysis. Lessons learned from the implementation were synthesized to develop capacity-building processes for Community Rice Centers. The results showed that in irrigated ecosystems during the 2024/25 dry season and the 2025/26 wet season, average production costs per rai decreased by 1.3–35.7% and 3.1–20.0%, respectively. Farmers' income increased by 0.9–50.6% and 7.2–97.7%, while profits rose by 10.6–1,195.2% and 147.9–629.9%. In rainfed ecosystems during the 2025/26 wet season, production costs decreased by 13.8–22.1%, income increased by 6.9–9.0%, and profits increased by 32.7–43.6%. In deep-water ecosystems, production costs decreased by 1.3–10.7%, income increased by 15.0–22.3%, and profits increased by 28.6–99.8% compared with non-adopting farmers. The lesson-learned process also enhanced the knowledge and skills of farmer groups in Community Rice Centers, enabling effective application of modern technologies and supporting environmentally sustainable rice production.

Keywords: modern agriculture, rice production, Community Rice Centers

Analysis, Monitoring, and Surveillance of Pesticide Residues Used in Rice Pest Management in Central of Thailand

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ABSTRACT:
Rice is a staple food and one of the most important agricultural export commodities of Thailand. However, intensive pest management practices may lead to pesticide residue in rice, which can pose concerns for food safety and international trade. Therefore, monitoring pesticide residues in rice is essential to ensure consumer safety and compliance with maximum residue limits (MRLs). This study aimed to determine pesticide residues in rice samples collected from the major rice-producing areas in central Thailand. During 2024-2025, a total of 259 rice samples were collected in both wet and dry seasons from Suphan Buri, Kanchanaburi, Chainat, Phra Nakhon Si Ayutthaya, and Pathum Thani provinces. Samples were extracted using the QuEChERS method according to AOAC Official Method 2007.01, and the pesticide residues were analyzed using LC-MS/MS and GC-MS/MS with a limit of quantification (LOQ) of 0.01 mg kg^{-1}. The results showed that 89 samples (34%) contained detectable residues of eleven pesticides, including acephate, ethiprole, cypermethrin, dimethoate, profenofos, triazophos, carbendazim, propiconazole, pyraclostrobin, tebuconazole, and tricyclazole. Propiconazole was the most frequently detected pesticide, commonly used to control fungal diseases in rice. These findings were consistent with field monitoring data indicating that farmers frequently applied these fungicides during the rice maturation stage. All 89 samples complied with the maximum residue limits established by the National Bureau of Agricultural Commodity and Food Standards (ACFS); however, only 15 samples exceeded the European Commission maximum residue limits (EU MRLs). These results highlight the importance of continued monitoring and surveillance of pesticide residues in rice production areas, which should be further expanded to other rice-growing regions of Thailand.

Keywords: pesticide residue, rice production, MRLs

Effectiveness of New Insecticides for Controlling the Brown Planthopper (*Nilaparvata lugens* (Stål)) in Phra Nakhon Si Ayutthaya Province

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ABSTRACT:
Recent climatic variability has affected the behavior of brown planthoppers (*Nilaparvata lugens* (Stål)), resulting in more frequent and severe outbreaks in rice-growing areas. This study aimed to evaluate the effectiveness of novel insecticide groups with different modes of action against the brown planthopper. The field experiment was conducted in farmers' rice fields in Phra Nakhon Si Ayutthaya Province during the 2025 dry season using the rice variety RD61. A randomized complete block design with three replications was employed, and insecticides were applied when brown planthopper populations reached the economic threshold. Three novel insecticide groups, including sulfoxaflor 50% WG, pymetrozine 50% WG, and flonicamid 50% WG, were evaluated. These were compared with conventional insecticides, including ethiprole 10% SC, etofenprox 20% EC, dinotefuran 20% SG, dinotefuran 20% + etofenprox 15% WP, acetamiprid 20% SP and buprofezin 5% + isoprocarb 20% WP, and an untreated control. Throughout the trial period, all insecticides were applied twice at the recommended label rates using a motorized knapsack mist blower. After the final application, the results showed that the novel insecticide groups showed high efficacy, achieving over 93% control of brown planthoppers, whereas conventional insecticides showed 80–85% efficacy. Therefore, to enhance control effectiveness and reduce the risk of resistance development in brown planthopper populations, the use of novel insecticide groups in rotation with other insecticides based on their modes of action is recommended during brown planthopper outbreaks.

Keywords: brown planthopper, *Nilaparvata lugens* (Stål), novel insecticide, rice, insecticide resistance

Effects of Pesticide Application Methods on the Diversity of Natural Enemies in Rice Fields at Phra Nakhon Si Ayutthaya Province

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ABSTRACT:
Unmanned Aerial Vehicles (UAVs) or agricultural drones play an important role in addressing labor shortages and improving crop production efficiency. This research aimed to investigate the effects of pesticide application methods on the diversity of natural enemies in rice fields on farmers' plots in Phra Nakhon Si Ayutthaya Province during the 2025 dry season. Rice cultivar RD41 was grown using the wet broadcasting method. The study was arranged as a 5×2+1 factorial experiment in a randomized complete block design (RCBD), consisting of 11 treatments with three replications and a control. At the seedling stage, insecticides (carbaryl 85% WP and thiamethoxam 25% WG) and a post-emergence herbicide (fenoxaprop-P-ethyl 6.9% EW) were applied both individually and as mixtures at recommended rates. Applications were performed using an EASY 3C agricultural drone and a motorized knapsack mist blower. Insect were sampled using D-vac suction device one day before application and 3, 7, and 14 days after application. Natural enemies were identified and counted under a stereomicroscope. Before pesticide application, natural enemies belonging to the orders Hymenoptera, Hemiptera, Odonata, Diptera and Coleoptera were recorded. After application, members of the order Araneae were additionally observed, while Hemiptera showed the greatest increase in abundance. Following both application methods, the Shannon-Wiener Diversity Index decreased. Most treatments appeared to be non-hazardous to natural enemies, except for the application of fenoxaprop-P-ethyl 6.9% EW by drone, which showed slight harmful effects. However, the application of herbicide mixtures and individual herbicide formulas using UAVs caused moderate to severe phytotoxicity in rice plants.

Keywords: rice, Unmanned Aerial Vehicles (UAVs), insecticides, herbicides, natural enemies, diversity

Application of Drone-Based NDVI for Enhancing Yield Prediction Efficiency of RD85 Rice Variety.

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ABSTRACT:
Climate change poses significant challenges to rice production systems and reduces the reliability of yield forecasting, which is crucial for national food security and export planning. This study aimed to develop an accurate rice yield prediction model by integrating geospatial technology with the normalized difference vegetation index (NDVI) derived from unmanned aerial vehicle (UAV) imagery and field-based physiological measurements, including chlorophyll content and leaf area index (LAI), using the Thai rice cultivar RD85 as a case study. Data were collected at three key growth stages: tillering (45 days after planting), panicle initiation (60 days after planting), and flowering (90 days after planting). These datasets were used to train and compare four machine learning regression models, including Random Forest (RF), Gradient Boosting Regressor (GBR), Extreme Gradient Boosting Regressor (XGBR), and Multiple Linear Regression (MLR). Model performance was evaluated using statistical indicators, including the coefficient of determination (R^2) and root mean square error (RMSE).The results indicated that the XGBR model consistently outperformed the other models across all growth stages. The best prediction accuracy was obtained at the flowering stage, with the highest R^2 value of 0.86 and the lowest RMSE of 56.40 kg/rai. This was followed by the tillering stage (R^2 = 0.81; RMSE = 65.41 kg/rai) and the panicle initiation stage (R^2 = 0.80; RMSE = 67.72 kg/rai). In contrast, the RF and MLR models showed moderate performance, whereas the GBR model produced the highest prediction errors in this study. These findings demonstrate that integrating UAV-derived NDVI with the XGBR algorithm provides a robust and reliable framework for early rice yield prediction. The proposed approach can support precision agriculture applications and enhance decision-making in rice production management and agricultural policy planning.

Keywords: Rice yield prediction, RD 85 rice, machine learning, NDVI, UAV

Enhancing rice production potential in southern Thailand by integrating crops into modern agricultural systems under the BCG Model

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ABSTRACT:
Rice production is currently facing challenges such as labor shortages and high production costs. To tackle these issues, farmers are adopting innovative agricultural machinery in the production process. This new technology is being used to enhance production efficiency and reduce costs in rice cultivation. Therefore, in this research, agricultural machinery, namely an 8-row of dry rice seeder attached to the rear of the tractor, was used for planting tests in a rubber and oil palm intercropping field. Compared to the traditional farming method, which is dry rice broadcasting, in Phatthalung province. Conducted in the wet seasons 2024/25 and 2025/26, comparing the averages using a t-test on 10 plots, using the Niaw Dam Mor 37, block glutinous rice. The results found that in the 2024/25 wet season, the rice yield from the test plots using an 8-row of dry rice seeder attached to the rear of the tractor had a significantly higher rice yield than the general farmer plots, with a statistically significant difference. The average yields were 207 and 196 kilograms per rai, respectively. For the 2025/26 wet season, the rice yield from the test plots using an 8-row of dry rice seeder attached to the rear of the tractor was higher than that of general farmers' plots but not statistically different, with average yields of 276 and 250 kilograms per rai, respectively.

However, there is a tendency that the use of modern agricultural machinery, such as an 8-row of dry rice seeder attached to the rear of the tractor, yields higher productivity and is accepted by farmers because it can reduce the amount of seed used, lower costs, and increase rice production.

Keywords: planting machinery, rice production technology, rubber plantation, rice

Effects of Solar Spectral Conversion Films on the Growth and Photosynthetic Efficiency of Cabbage Microgreens

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ABSTRACT:
Microgreens are increasingly in high demand among modern consumers due to their exceptional nutritional value, which is 5 to 40 times higher than that of mature vegetables, and their abundance of health-promoting antioxidants. Currently, production in plant factories typically relies on LED lighting to control light quality. However, such high electricity consumption increases production costs and contributes to carbon dioxide emissions, a primary cause of global warming. To address these challenges, this research project developed an innovative spectral conversion film based on quantum dots, designed to convert solar UV radiation into red or blue light wavelengths that are essential for plant development. The objective of this study was to evaluate the effects of these solar spectral conversion films on cabbage microgreen production. Both green and purple cabbage varieties were cultivated for 10 days under 4 different film conditions: no film, clear film, UV-to-red conversion film, and UV-to-blue conversion film. The study utilized a 2 x 4 factorial in a completely randomized design with four replications. The findings revealed that both cabbage species grown under the UV-to-red conversion film achieved the highest hypocotyl length and fresh weight/plant among the 3 types of film. Furthermore, this treatment enhanced photosynthetic efficiency, as evidenced by the highest maximal quantum yield of PSII, significantly outperforming the other film treatments. These results suggest that the solar spectral conversion films can effectively optimize the quality of solar light for sustainable microgreen production.

Keywords: Chlorophyll fluorescence, Spectral conversion film, Sprout, Quantum dot, UV conversion film

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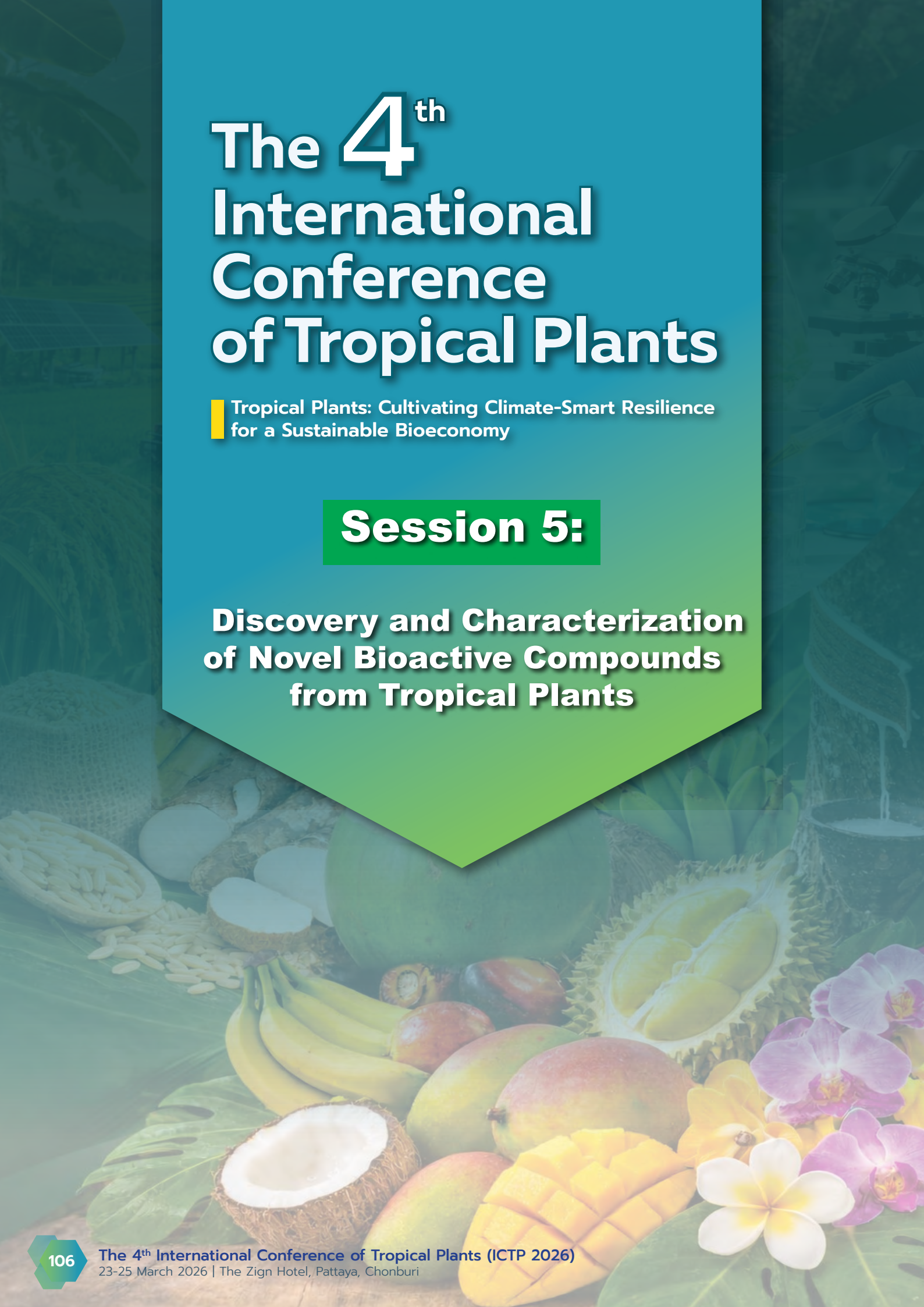

Effect of CPPU and Boric Acid on Flower Induction of Off-season Lychee

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ABSTRACT:
Studies on a flowering induction of lychee, using of Forchlorfenuron (CPPU) mixed with Boric acid combination, for the whole canopy at the Pomology Division Farm, San Sai District, Chiang Mai Province, Thailand (300 m. above sea level). The study was divided into 2 experiments as follows. The first experiment to study the concentration of 10, 15, and 20 mg/L CPPU mixed with 1,000, 1,500, and 2,000 mg/L Boric acid on flowering inductions compared with water (control) in combination with the 2 cultivars of lychee, including 'Samphao Kaew', and 'Nakhon Phanom'. They were divided into 8 Treatments. It was found that at 20 mg/L CPPU mixed with 2,000 mg/L Boric acid, there was an interaction with the cultivar. They were affected to induced the highest percentages of flowering as 95%, with 23.52% of inflorescence length and 90% of fruit setting of 'Nakhon Phanom' cultivar, which was not statistically with 20 mg/L CPPU and 2,000 mg/L Boric acid of 'Samphao Kaew' cultivar 92.00% of flowering, with 20.96 cm of inflorescence length, but low percentage of fruit setting as 22.50% respectively, they were highly significantly with other treatments. It also flowered in all directions across the canopy after CPPU and Boric acid treatment. In addition, it was found to stimulate flowering along the trunk and branches as well.

The second experiment studied the optimal concentration of the 20 mg/L CPPU combined with 2,000 mg/L. Boric acid, compared with water (control), affects flowering induction, fruit setting, and fruit quality. via spray the leaves of seven lychee cultivars, including 'Hong Huay', 'Chakraphat' (Emperor Lychee), 'Samphao Kaew', 'Sa-Raek Thong', ' Khom', 'Jeen', and Phan Thip. followed by four times to applications every week. The results showed that CPPU mixed with boric acid affected flowering and fruit setting in 5 cultivars, such as 'Chakraphat', 'Samphao Kaew', 'Khom', 'Jeen', and 'Phan Thip', they were high significant difference from the control. The 20 mg/L. CPPU mixed with 2,000 mg/L boric acid had no effected to 'Hong Huay' and 'Sa- Raek Thong' with no flowers.

Both the experiments had an effected to flowering induction and fruiting during in-season and off-season. However, the 'Jeen' and 'Chakraphat' cultivars promote the flowers and fruit setting in both in-season and off-season. In particular, the 'Jeen' Cultivar has the potential to induce the flower and fruit setting in off-season. The 'Chakraphat' cultivar, with high yield requiring low temperatures to stimulate flowering, is suitable for fruit production in low-lying areas at an altitude of 300 meters above sea level.

In conclusion, CPPU used in combination with Boric acid effectively stimulates flowering, inflorescence length, and fruit setting in all directions of the canopy of 'Samphao Kaew' and 'Nakhon Phanom', 'Chakraphat', 'Sarakthong', 'Kom', and Phantip' lychee, and flowers can develop on the shoots and along the branches in-season and off-season of Lychee

Keywords: PGR on flower induction, Off-season flowers

From Aroma to Preference: Linking Volatile Profiles and Consumer Acceptance in Landrace Chilli (*Capsicum* spp.)

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ABSTRACT:
Landrace chilli (*Capsicum* spp.) is economically important and a key ingredient in Thai cuisine, valued for its distinctive spiciness and aroma. However, chilli aroma is a complex trait determined by multiple volatile compounds, and its sensory characteristics remain insufficiently defined. In addition, limited information is available regarding consumer preferences for chilli aroma and their relationship with chemical composition. This study aimed to analyse and compare the sensory attributes and chemical profiles of green chilli fruits from three cultivars—Khee Noo Suan, Karen, and Jinda—and to examine the relationship between volatile compounds and consumer preferences. Consumer preference was evaluated through consumer testing (n = 170), while aroma descriptors were defined by trained experts (n = 9). Volatile compounds were analysed using GC–MS and GC– O. Key metabolites, including capsaicin (CAP), nordihydrocapsaicin (NOR), dihydrocapsaicin (DI), antioxidant capacity (DPPH and ABTS), vitamin C (Vit C), flavonoids (FLA), and total phenolics (PHE), were also quantified. Correlation analysis was performed to determine relationships between volatile compounds and sensory preference. Floral aroma showed a strong positive correlation with consumer preference (r = 0.752). The compounds 4-methylpentyl 2-methylpropanoate and fumaric acid, cis-hex-3-enyl pentyl ester were significantly correlated with floral aroma (r = 0.858 and 0.872, respectively), consistent with the key aroma notes identified by experts. Floral aroma intensity was highest in Khee Noo Suan and Karen and significantly different from Jinda (p = 0.002). Khee Noo Suan received the highest consumer preference, being preferred by 50% of participants. Karen exhibited the highest levels of CAP, DI, DPPH, ABTS, Vit C, and PHE (p < 0.01). These findings indicate that specific volatile compounds may serve as indicators of aroma preference and could support aromafocused chilli breeding for consumer-oriented cultivars.

Keywords: sensory analysis, aroma-active compounds, secondary metabolites

Sustainable Utilization of Betel Petiole Byproducts: Total Phenolics, Flavonoids, and Radical Scavenging Potential

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ABSTRACT:
Phatthalung province, home to Thaksin University, is a leading producer of betel leaves (Piper betle L.) in Thailand, exporting to Taiwan, Bangladesh, and Sri Lanka; farms yield 1–2 tonnes monthly, generating 3–5% petiole waste during packing that remains underutilized. This study aimed to investigate the potential bioactive compounds present in betel petioles, which are typically discarded during cultivation, and to promote sustainable agricultural practices by finding alternative uses for discarded plant parts. The study valorized betel petiole residues by preparing 70% methanolic crude extracts via maceration, followed by liquid-liquid partitioning to yield ethyl acetate and butanol fractions. Total phenolic content (TPC) was quantified using the Folin-Ciocalteu method, with absorbance at 765 nm calibrated against gallic acid standards and expressed as mg GAE/L. Total flavonoid content (TFC) employed the Jurd-Geissmann colorimetric assay, measuring absorbance at 415 nm against quercetin standards (mg QE/L). Antioxidant activity was assessed via DPPH radical scavenging assay: serial dilutions of extracts (0.01–2 mg/mL) were incubated with 0.1 mM DPPH for 30 min in darkness, absorbance was read at 517 nm, and EC50 values were derived from dose-response curves (% scavenging vs. log [concentration]. Ascorbic acid served as a positive control. Ethyl acetate exhibited superior potency (EC50: 0.0106 ± 0.00004 mg/mL), outperforming butanol (0.0851 ± 0.0004 mg/mL) and methanol (0.9958 ± 0.001 mg/mL) extracts relative to control (0.004 mg/mL), indicating robust hydrogen-donating capacity. It is suggested that these polyphenolic-rich extracts from betel petioles may potentially be used in antiinflammatory delivery, supporting circular agricultural economies.

Keywords: betel petioles, extraction, bioactive compounds, zero waste, circular agricultural economies

"Hom Mue Lo (Cham Pa Kor)" High Nutrition Local Rice Variety of Yala Province, Thailand

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ABSTRACT:
"Hom Mue Lo (Cham Pa Kor)" is a local rice variety cultivated on approximately 300 rais in Raman district, Yala province, Thailand. This variety is distinguished by its jasmine and frangipani like aroma and a red seed coat, which contributes to its high nutritional values. This research aimed to evaluate the grain characteristics and nutritional properties of three lines of Hom Mue Lo (Cham Pa Kor) rice, which were PTNC18001, PTNC20001, and PTNC20002, collected by the Pattani Rice Research Center. The results showed that all three lines of Hom Mue Lo had medium-sized grains with a length-to-width ratio of 2.5 to 2.7. The amylose contents were 21.4 to 22.8%, resulting in cooked rice with a relatively soft and slightly sticky texture, and their viscosity ranged from 2,490 - 2,686 cP. The protein and carbohydrate contents were between 9.9 - 10.3% and 71.5 - 71.7%, respectively. In addition, magnesium and zinc varied from 2,226 - 2,322 and 26.2 - 30.3 $\mu g \cdot g^{-1}$, respectively. Furthermore, high levels of phenolic compounds, flavonoids, and antioxidant activity were observed, ranging from 2,587 to 2,748 $mg \cdot kg^{-1}$, 2,554 to 2,645 $mg \cdot kg^{-1}$, and 2,989 to 3,018 $mg \cdot kg^{-1}$, respectively. These values were higher than those found in the Sang Yod Phatthalung rice variety, which showed lower levels of bioactive compounds at 1,233, 1,582, and 702 $mg \cdot kg^{-1}$, respectively. These findings indicated that Hom Mue Lo (Cham Pa Kor) rice is a nutritionally valuable rice variety and a promising local genetic resource with potential for further value-added development.

Keywords: Hom Mue Lo, high nutrition, local rice, Yala province

Effect of Physical Modification Processes on Resistant Starch of Rice

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ABSTRACT:
Resistant starch (RS) constitutes a starch fraction that demonstrates resistance to digestion within the human small intestine and undergoes fermentation by the gut microbiota in the large intestine. It there by serves as a prebiotic agent, promoting intestinal microbial balance and contributing to the reduction in the risk of metabolic-related chronic diseases. This investigation aimed to augment the RS content in rice through physical modification of its starch component. The experimental design adhered to a randomized complete block arrangement, incorporating four treatments and five replications. Four distinct rice varieties, sourced from the Phitsanulok Rice Research Center (2023 dry season) namely Phitsanulok 2, RD41, RD61, and RD95 were employed. These varieties exhibited amylose contents of 28.64, 27.15, 26.82, and 29.78 percent, respectively. Native rice starch isolated from all varieties demonstrated comparable RS contents, ranging from 7.18 to 7.54 g/100g. Enzymatic debranching, utilizing pullulanase (30 PUN/gram of starch) with the objective of promoting starch retrogradation, statistically significantly augmented RS levels ($p<0.05$). The highest RS content was recorded for RD95 (25.84 g/100g). The prebiotic potential of the resultant RS was assessed employing *Lactobacillus casei* TISTR 1463 and *Lactobacillus acidophilus* TISTR 2365. The strains exhibited maximal growth of 8.67 log CFU/mL at 12 hours and 8.03 log CFU/mL at 24 hours, respectively. These findings collectively indicate that the production of resistant starch from rice can facilitate the development of functional foods and contribute to the enhancement of the value of rice-based products.

Keywords: Resistant starch, Physical modification starch, Prebiotic, Rice

Effects of Plant Growth Regulators, Leaf Size, and Explant Type on Callus Induction of Large-Leaf *Gnetum gnemon* L.

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ABSTRACT:
Callus culture is an essential technique in plant tissue culture with applications in plant propagation, protoplast production, secondary metabolite synthesis, and germplasm conservation. The success of callus induction depends on several factors, including plant growth regulators, explant type, and culture conditions. This study aimed to evaluate the effects of plant growth regulators, leaf size, and explant type on callus induction of large-leaf *Gnetum gnemon* L. A factorial experiment arranged in a completely randomized design was conducted using Murashige and Skoog (MS) medium supplemented with different combinations of plant growth regulators. After 8 weeks of culture, MS medium containing 0.5 mg L^{-1} 2,4-dichlorophenoxyacetic acid (2,4-D) combined with 0.5 mg L^{-1} 6-benzyladenine (BA) produced the highest callus induction rate (100%). This was followed by MS medium supplemented with 0.5 mg L^{-1} naphthaleneacetic acid (NAA) and 0.5 mg L^{-1} BA (96.30%), while the control treatment without plant growth regulators showed the lowest response (18.52%). Among leaf sizes, large leaves showed the highest callus induction (85.18%), followed by medium leaves (66.67%) and small leaves (62.96%). In the explant experiment, leaf explants exhibited the highest callus induction (40.73%), followed by stem (31.48%) and nodal explants (16.66%). Morphological observations revealed that calli cultured on MS medium supplemented with either 2,4-D + BA or NAA + BA were compact and white. These findings suggest that MS medium supplemented with 2,4-D and BA is the most effective combination for callus induction in *G. gnemon*, providing a useful protocol for future propagation and biotechnological applications.

Keywords: Callus induction, plant tissue culture, plant growth regulators, *Gnetum gnemon* L., micropropagation

Seed Priming and Foliar Application of Fish Amino Acids Improve Germination and Early Seedling Growth of Sang Yod Rice

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ABSTRACT:
Uniform seed germination and vigorous early seedling growth are critical for improving crop establishment and productivity in rice cultivation. Fish amino acids (FAA), a natural biostimulant derived from fermented fish, contain readily available amino acids and nitrogenous compounds that can stimulate plant metabolic activity. This study evaluated the effects of FAA applied through seed priming and foliar spraying on germination and early seedling growth of Sang Yod rice (*Oryza sativa* L.), a traditional rice variety from southern Thailand. A factorial experiment arranged in a completely randomized design was conducted using FAA concentrations of 0.10–0.20% (v/v) for seed priming and foliar application. Germination percentage, seed vigor, leaf area, chlorophyll content, and root growth were measured during the seedling stage. FAA treatments significantly enhanced germination and seedling performance compared with untreated seeds. Seed priming with FAA at 0.10% resulted in the highest germination percentage (61%) and improved seed vigor. Furthermore, the combined application of seed priming and foliar spraying with FAA at 0.15% significantly increased leaf area, chlorophyll content, and root fresh weight. These improvements suggest enhanced photosynthetic capacity and root development, likely associated with amino acid–mediated stimulation of plant metabolic processes. Overall, FAA acts as an effective biostimulant that promotes germination and early seedling growth of Sang Yod rice, offering a practical approach to improve crop establishment in sustainable rice production systems.

Keywords: Seed priming, fish amino acids, biostimulant, rice seedlings, Oryza sativa

Efficiency of Some Thai Traditional Medicinal Plant on Tyrosinase Inhibition: Case of an Ethanolic Extracts from *Zygostelma benthamii* Bail Root Natives of Wang Dong District, Kanchanaburi Province, Thailand

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ABSTRACT:
Thai traditional medicinal plants, the well-known biological resources, have played an important role in Thai people's lives for a long time. The vining plant *Zygostelma benthamii* Bail (Pha Ya Rarkhorm or Obchei Tao or Kamyarn Tuapoo, in Thai) is a member of the Apocynaceae family, which has been known for its biological and pharmaceutical properties. Root of *Z. benthamii* Bail was used as a food ingredient, such as Kai Palo curry, etc. For traditional medicine, Thai people used the root of this plant as an ingredient of aromatic powder. The compound 2-hydroxy-4-methoxybenzaldehyde is one type of important chemical constituent in the root of this plant. The Soxhlet-ethanolic technique was used to prepare extracts of Z. benthamii Bail root, collected from Wang Dong district, Kanchanaburi province, Thailand. The HPLC analysis results showed a 0.048 µg/µL concentration of 2-hydroxy-4-methoxybenzaldehyde in the root extracts or 0.139 mg/g of root dry weight. Tyrosinase inhibition efficiency was measured by the mushroom tyrosinase and L-DOPA in a DPPH radical scavenging assay. The results of the DPPH assay showed that the IC_{50} value of its root extracts inhibited the tyrosinase enzyme activity at 45.79±0.54 mg/mL concentration. The test showed lower efficiency compared to standard synthetic agents (Butylated hydroxytoluene and Kojic acid). Tyrosinase is a member of the enzyme polyphenol oxidase (PPO) group that can be destroyed by a phenolic acid compound, including 2-hydroxy-4-methoxybenzaldehyde. The activities of tyrosinase was inhibited at the melanocyte biosynthetic pathways. This property of 2-hydroxy-4-methoxybenzaldehyde is very important for use as a natural cosmetic ingredient, which is needed as a skin whitening agent.

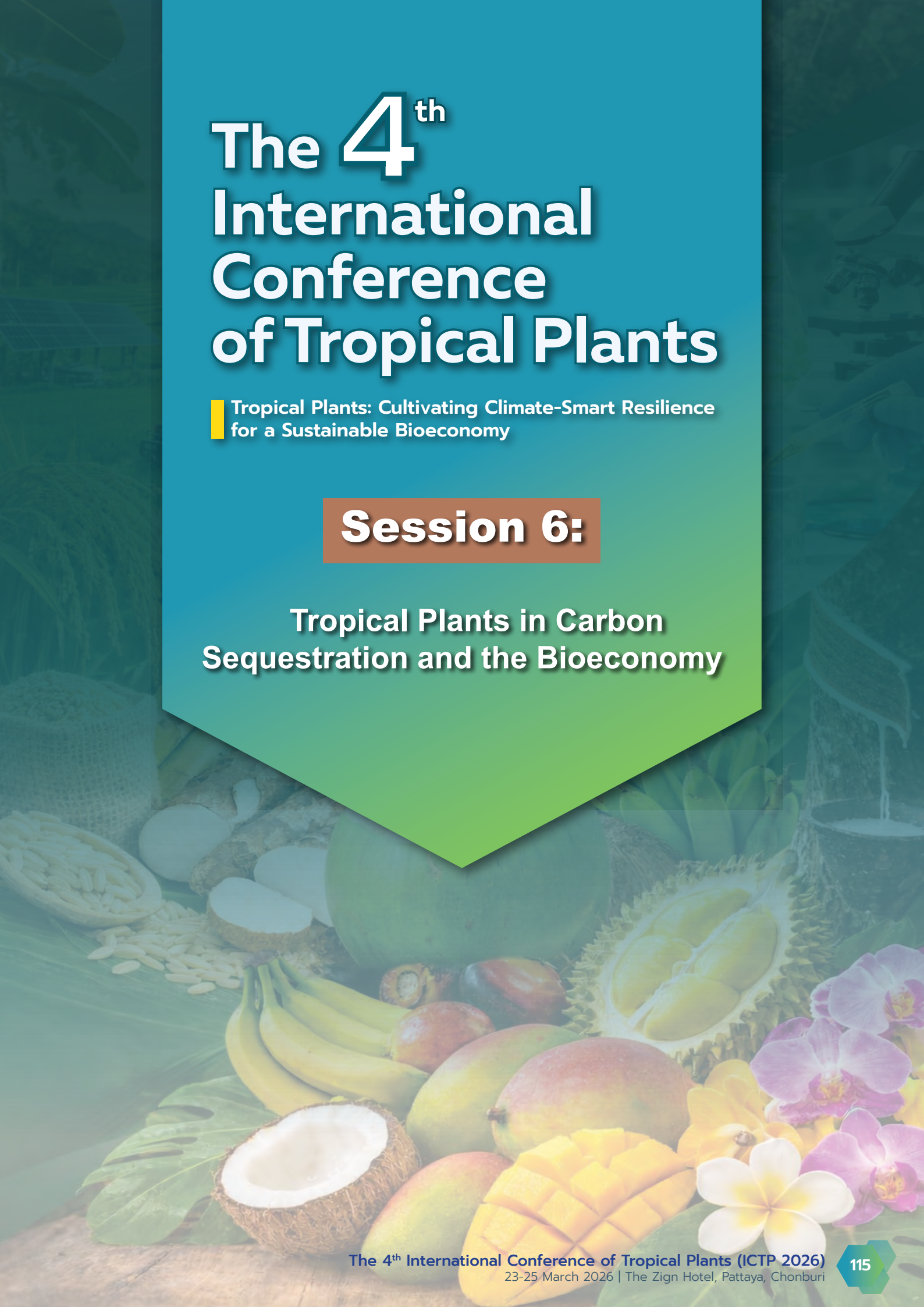
Keywords: *Zygostelma benthamii* Bail, 2-hydroxy-4-methoxybenzaldehyde, tyrosinase, skin whitening, medicinal plants

The 4th International Conference of Tropical Plants

Tropical Plants: Cultivating Climate-Smart Resilience for a Sustainable Bioeconomy

Session 6:

Tropical Plants in Carbon Sequestration and the Bioeconomy



An Extension-Driven Model for Scaling Edible Cassava to Enhance Farmer Income in Thailand's Northeastern Economic Corridor (NeEC)

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ABSTRACT:
Edible cassava (*Manihot esculenta* Crantz) was evaluated as an income-oriented alternative crop to support poverty reduction and inclusive bioeconomy transition in Thailand's Northeastern Economic Corridor (NeEC). The study focused on value-chain upgrading rather than controlled plot experimentation, integrating Good Agricultural Practices (GAP), contract farming coordination, and structured farmer network management under a Social Integrated Enterprise (SIE) framework supported by a Multi-Level Marketing (MLM) cluster model.

Field implementation with >400 farmers indicated that improved edible cassava varieties (Pirun 2 and Pirun 4) value-chain system achieved a mean yield of 6,000 kg/rai, compared with 3,414 kg/rai under the conventional industrial cassava system. Economic analysis indicated that net profit increased from 1,482.22 THB/rai to 9,057.82 THB/rai, reflecting an absolute gain of 7,575.60 THB/rai. Farm-gate prices increased from an average of 2.50 THB/kg to 2.80–3.00 THB/kg through standardized grading and organized procurement mechanisms.

Under the conventional system, farmers operated independently with fragmented marketing channels. In contrast, the SIE–MLM model integrated production standardization, coordinated aggregation, and processor linkage, strengthening supply consistency and income stability. As the dataset derived from extension implementation records, statistical dispersion metrics were not included.

These findings demonstrate that edible cassava can function as a scalable tropical bioeconomy crop when supported by structured extension networks, coordinated market mechanisms and community-based enterprise integration.

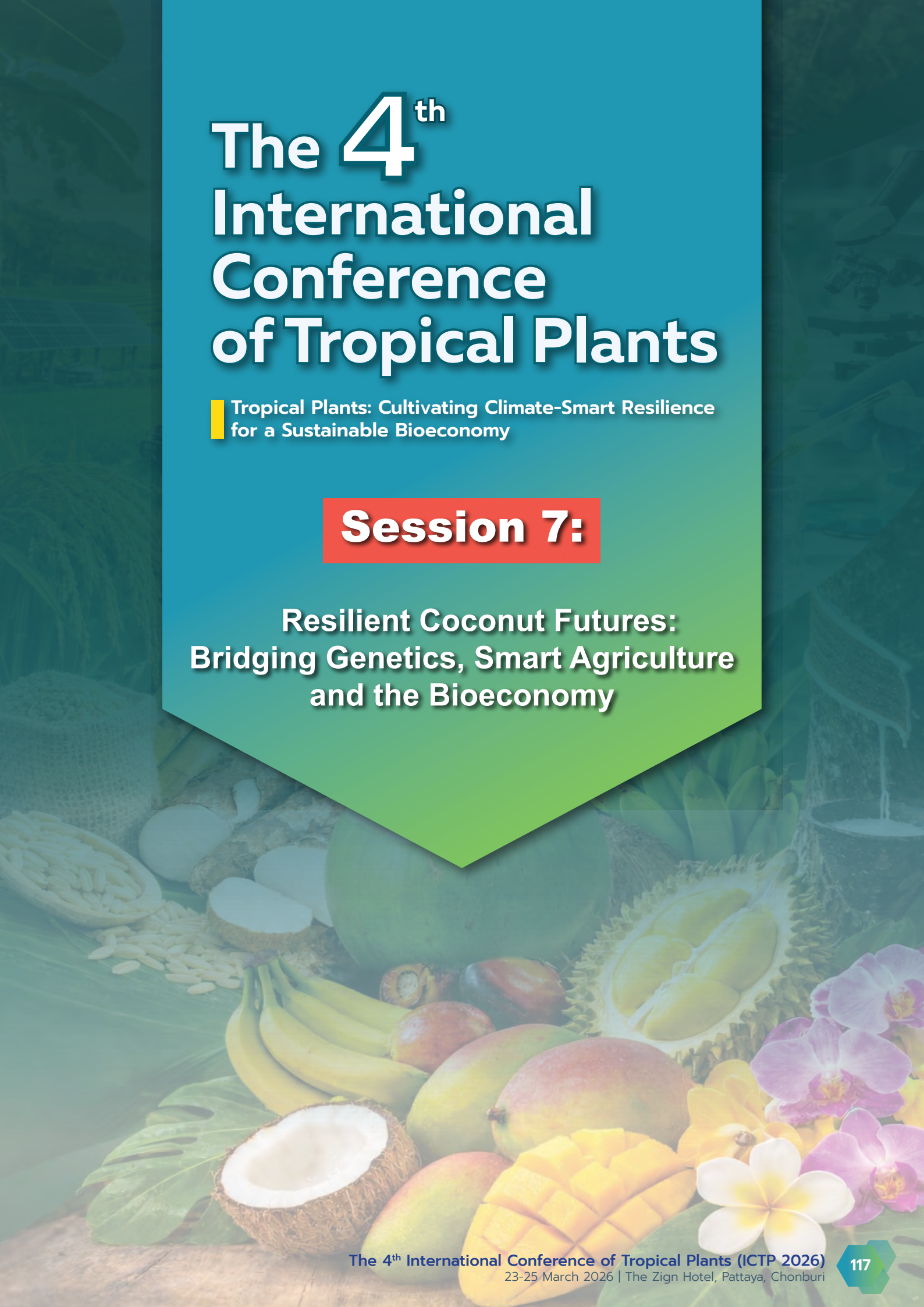
Keywords: Agricultural extension, Edible cassava, Poverty reduction, Soil restoration, Bioeconomy

The 4th International Conference of Tropical Plants

Tropical Plants: Cultivating Climate-Smart Resilience for a Sustainable Bioeconomy

Session 7:

Resilient Coconut Futures: Bridging Genetics, Smart Agriculture and the Bioeconomy



Advancing Coconut Improvement through Genomics and Molecular Breeding

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ABSTRACT:
Coconut (*Cocos nucifera* L.) is an important tropical crop that supports food security, rural livelihoods, and diverse agro-industries in many regions worldwide. Rising global demand for high-quality coconut products, especially aromatic and specialty coconuts, has created new challenges and opportunities for coconut breeding programs. However, conventional coconut breeding remains slow due to the crop's long generation cycle, high heterozygosity, and limited historical genetic resources. Recent advances in genomic technologies have greatly improved the prospects for accelerating coconut improvement. The development of high-quality reference genomes, large-scale resequencing datasets, and genome-wide molecular markers has enabled a deeper understanding of genetic diversity and population structure in coconut germplasm. Genomic approaches such as genome-wide association studies (GWAS) and quantitative trait locus (QTL) mapping are increasingly used to identify genomic regions associated with important agronomic traits, including fruit quality, aroma, sweetness, and yield potential. Molecular breeding strategies, including marker-assisted selection and genomics-assisted breeding, provide powerful tools for accelerating the development of improved coconut cultivars. By integrating genomic information with phenotypic evaluation of diverse coconut populations, breeders can identify candidate genes and molecular markers that enable earlier and more precise selection. Recent progress in coconut genomics and the application of molecular breeding approaches for coconut improvement in Thailand are highlighted. The integration of genomic resources with modern breeding strategies will play a crucial role in developing superior coconut varieties that meet future agricultural, industrial, and market demands.

Keywords: Coconut, aroma, molecular breeding, genome, GWAS

Coconut Germplasm Resources & Breeding for market competitiveness

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ABSTRACT:
Germplasm resources are the pivotal to crop breeding. Emerging global challenges, necessitates sustainable utilization of crop genetic resources to enhance market competitiveness, with focus on higher input use efficiency, climate resilience and biotic stress tolerance.

Coconut breeding efforts have resulted in development of varieties with high productivity, climate resilience, and suitable for product diversification. However, due to the long juvenile phase, the time period from pre-breeding to variety release takes nearly two decades. Speed breeding approaches to reduce crop life cycle, through manipulation of environmental factors to achieve faster growth and crop maturity, enabling more crop cycles in lesser time period, is difficult in coconut owing to large canopy size and customized infrastructure requirements. In oil palm, researchers have claimed reduction in breeding cycle, from 19 years to 6 years through genomic selection. In coconut, use of genomic resources coupled with bioinformatics tools and genome-wide association studies (GWAS), has resulted in identification of genes for economically important traits, to facilitate marker-assisted selection (MAS) and aid trait-specific breeding. Modern breeding approaches, combining technological advancements with traditional methods, are required to overcome challenges in varietal development of coconut viz., long juvenile phase, long evaluation period, genetic complexity of desirable agronomic traits, inbreeding depression and large area/resource requirements.

This presentation takes stock of the status of research in coconut improvement and the scope of new research findings, along with molecular resources in better utilization of the genetic diversity available in the crop, and modifying the conventional breeding strategies, to hasten varietal development.

Key words: Genetic resources, MAS, GWAS, molecular breeding, varietal development

Coconut Tissue Culture: Present Developments and Future Opportunities

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ABSTRACT:
The development of diverse, reproducible, and efficient tissue culture technologies for coconut serves several important purposes.

First, these technologies help address the increasing global demand for elite coconut planting material. Conventional propagation mainly relies on seeds, which leads to high genetic variability and slow multiplication rates. To overcome these limitations, somatic embryogenic cultures have been developed from different tissues, including plumules, immature inflorescences, and ovaries. Although these techniques were first reported in 1989, large-scale industrial applications have not yet been widely implemented. Recently, a novel axillary shoot multiplication protocol, known as the COAXIM method, has been established. This approach starts from in vitro seedlings and shows promising potential for more efficient coconut micropropagation.

Second, tissue culture technologies facilitate the safe international exchange of coconut germplasm. The transfer of plant material in the form of in vitro cultures helps reduce the risk of spreading pests and diseases across regions. For this purpose, excised zygotic embryos or in vitro shoots can be used effectively.

Third, advanced in vitro techniques such as cryopreservation provide tools for the long-term conservation of valuable coconut germplasm. Currently, most coconut genetic resources are maintained in field genebanks, which are vulnerable to environmental threats and disease outbreaks. Successful cryopreservation protocols have been reported for zygotic embryos, plumules, and meristem cultures, offering a more secure alternative for germplasm preservation.

Finally, tissue culture systems are essential for applying advanced breeding technologies such as genetic transformation and gene editing, which require transformation-competent tissues like embryogenic cell suspensions. Overall, tissue culture plays a key role in improving coconut propagation, conservation, and genetic improvement..

Keywords: in vitro culture, shoot culture, somatic embryogenesis, cryopreservation

Coconut agronomy and the evolving landscape of international trade

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ABSTRACT:
Coconut (Cocos nucifera L.) is one of the most versatile and economically significant plantation crops, cultivated across 93 countries spanning approximately 12.23 million hectares globally. As the world's top four producers namely Indonesia, Philippines, India, and Sri Lanka — collectively account for around 80% of global output, agronomic management of coconut systems has become increasingly critical to sustaining supply chains that underpin a rapidly expanding international market. Global coconut products market, valued at USD 14.18 billion in 2025, is projected to reach USD 37.11 billion by 2035 at a CAGR of 10.1%, driven by surging demand for coconut oil, desiccated coconut, coconut water, and other value-added derivatives in the US, European Union, and emerging Asian markets. These trade dynamics are reshaping agronomic priorities and shifting focus from traditional subsistence and bulk copra production toward high-quality, certified, and traceable produce aligned with clean-label and organic market standards. However, this trade growth is constrained by agronomic bottlenecks including climate variability, aging palm populations, declining yield per hectare, and limited adoption of precision agriculture technologies. Bridging the gap between agronomic productivity and international trade requirements demands coordinated interventions in variety improvement, soil health management, integrated pest management, and digital agronomy tools such as UAV-based monitoring and AI-driven advisory systems. This paper examines the intersection of coconut agronomy and international trade, highlighting how evidence-based agronomic practices and technological innovations can strengthen the resilience and competitiveness of coconut-exporting nations in the evolving global marketplace.

Keywords: Coconut agronomy, International trade, Value-added products, Precision agriculture, Global market

Genomic Selection: Principles and Example Application in Oil Palm

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ABSTRACT:
Plant breeding is a key driver of sustainable, productive, and resilient agriculture. Perennial crops play a major economic and social role, but their genetic improvement faces significant challenges: long life cycles, delayed entry into production, and extended evaluation periods. These characteristics significantly slow down the development of new varieties. Paradoxically, it is also these species that stand to benefit most from recent scientific and technological advances: next-generation sequencing and high-throughput multi-omic data acquisition, high-throughput phenotyping, the development of high-performance computing infrastructure, big data analysis methods and artificial intelligence, etc.

Genomic selection is an approach based on the large-scale use of genomic data to predict the genetic performance of plant material that has not been evaluated in the field. Already widely applied in animal breeding, it is gradually transforming plant breeding strategies. This presentation will first address the context of marker-assisted selection, before detailing the principles of genomic selection and the parameters affecting its efficiency. Next, a case study of genomic hybrid breeding in oil palm will be presented. Finally, current trends in genomic selection will be discussed.

Keywords: Genomic selection, oil palm, breeding, perennial crops

Navigating molecular diagnostics to strengthen pest surveillance for resilient trade and shared prosperity

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ABSTRACT:
Tropical coconut pests present significant biosecurity challenges due to high phenotypic plasticity, which frequently confounds traditional morphological diagnostics. While reports on inflorescence-infesting moths, including *Tirathaba* spp., remain limited, the presence of numerous similarly-looking caterpillar species across the Philippines complicates field monitoring. Resolving the status of these re-emerging populations requires an integrative taxonomic approach that combine multivariate morphometrics, aedeagal characterization, and sequencing. For instance, while Asiatic Palm Weevils (*Rhynchophorus* spp.) exhibit polymorphism in body and genitalia structure, *mitochondrial cytochrome oxidase I (mtCOI)* data suggest these variants can be conspecific. Meanwhile, high haplotype diversity within single locations indicates a complex phylogeographic history driven by multiple introductions via germplasm movement.

Although mtCOI remains a vital diagnostic tool, recent evidence from Coconut Rhinoceros Beetle (*Oryctes rhinoceros*) demonstrates that full mitogenome analysis provides the superior resolution needed to track invasion biology. Mitogenome mapping revealed that the Guam "CRB-G" population is distinct, and unrelated to recent Pacific outbreaks, correcting previous misidentifications based on partial sequences. By identifying precise hitchhiking pathways between native and introduced ranges, high-resolution mapping enables accurate nomenclature and prevents the misidentification of pest provenance.

Transitioning from ambiguous field observations to precision surveillance is critical for safeguarding international trade. Accurate identification is especially vital for polyphagous pests to establish baselines for resistance breeding and quarantine screening of imported plants. By resolving taxonomic uncertainty and moving toward full genomic resolution, we enable the deployment of species-specific management and establish robust diagnostic protocols that safeguard international trade.

Keywords: Coconut Biosecurity, *Rhynchophorus*, *Oryctes rhinoceros*, Pest Surveillance, Phytosanitation

Sustainable Production and Dissemination of Three-Way Cross Hybrid Coconuts for Farmers

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ABSTRACT:
This study aimed to develop high-yielding coconut hybrids to address climate variability and provide sustainable alternatives for industrial farming. Since 1975, the Chumphon Horticultural Research Centre has conducted extensive breeding programs. A longitudinal study from 1990 to 2018 (28 years) focused on evaluating four elite three-way hybrid combinations: (1) (RNT x WAT) x THT, (2) (MYD x WAT) x THT, (3) (MYD x THT) x THT, and (4) (MRD x RNT) x THT. The research identified two superior hybrids officially certified by the Department of Agriculture (DOA) in 2018. Three way cross Hybrid Chumphon no.1 [(RNT x WAT) x THT] exhibited a mean yield of 102 nuts/tree/year (14,075 nuts/ha/year) with 61% oil content. Three way cross Hybrid Chumphon no.2 [(MYD x WAT) x THT] demonstrated higher productivity with 108 nuts/tree/year (14,285 nuts/ha/year) and 62% oil content. Since 2021, the distribution of 95,514 seedlings across 695 ha. has generated over 3.1 million THB, benefiting more than 1,000 farmers. The development of three-way hybrids represents a significant advancement in coconut breeding, offering high-yield potential and economic resilience for the Thai coconut industry

Keywords: Coconut Hybridization, Three-Way Cross hybrid, Yield Improvement, Coconut seedlings

Innovation-Driven and Sustainable Development of Thai Coconut Products

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ABSTRACT:
Coconut is rapidly becoming a strategic crop for climate-smart agriculture and Thailand's emerging bio-circular-green economy. Thailand's coconut sector has evolved from traditional products such as coconut milk, coconut water, and nam hom water—each enhanced through diverse preservation technologies—to a new generation of high-value innovations that reflect modern lifestyles, health consciousness, and sustainability.

A major breakthrough has been the rise of coconut flower–based products. These include a spectrum of natural sweeteners with varying viscosities, colors, and flavor profiles, as well as innovative nectar powders. Coconut flower derivatives have expanded into fermented and infused products such as coconut vinegar blended with turmeric or ginger, concentrated wellness tonics, and sparkling coconut cider beverages. Culinary applications have also grown, with coconut-based cooking sauces such as coconut amino, coconut amino teriyaki, and coconut amino marinades offering clean-label alternatives to traditional condiments. Beverage innovation continues with coconut blossom water produced through both retort and high-pressure processing technologies.

Beyond food, coconut flower resources have inspired new cosmetic applications, including facial essences, cleansing gels, and serums derived from coconut flower dewdrops—demonstrating Thailand's capacity to translate agricultural materials into high-value beauty and wellness products.

Driven by the global growth of the coconut water industry, Thailand is also advancing circular innovations. Young coconut shells and fibers are now utilized for biomass electricity generation, organic fertilizers, biochar, and wood pellets. Young coconut meat is transformed into freeze-dried fruit ice cream snacks, while young coconut water is incorporated into konjac-potassium beverages and functional blends with herbs, fruits, and vegetables.

Mature coconut development remains active as well, with innovations such as MCT coconut oil tablets and coconut yogurt contributing to Thailand's expanding portfolio of value-added products.

Together, these advancements illustrate Thailand's dynamic role in shaping the future of coconut-based food, wellness, and sustainable materials, reinforcing the country's position as a leader in climate-smart coconut innovation.

Developing and Extension with Certification and Traceability System for True-to-type Aromatic Coconut Mother Blocks using SNP Markers in the Central Region

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ABSTRACT:
This research aims to develop and scale up the certification system for aromatic coconut mother palm plots, expanding from the prototype area in Ratchaburi Province to Nakhon Pathom and Samut Sakhon—the primary production hubs of Thailand. The methodology integrates morphological evaluation with rhAmp SNP Genotyping molecular marker technology to confirm the homozygous aromatic genotype (Genotype C/C), effectively addressing the issue of varietal contamination within the production system.

Conducted between 2024 and 2025, the project initially established certification criteria and protocols in Ratchaburi before adapting them to the specific local contexts of Nakhon Pathom and Samut Sakhon. The findings demonstrate a 100% accuracy rate in identifying genetic purity, with several prototype plots achieving total homozygous aromaticity across all palms.

Economic analysis indicates that the expansion of this certification system increased the value of certified seedlings by 106,666 THB per rai annually, totaling 5.27 million THB per year, while farmers' net income rose by an average of 19.7%. Furthermore, the study produced Standard Operating Procedures (SOPs) and a traceability database system to facilitate the concrete implementation of the certification system in other regions. This research underscores that scaling technology from prototype areas to production networks significantly enhances the credibility of aromatic coconut products and fosters sustainable area-based agricultural development.

Keywords: Aromatic Coconut, Mother Palm Plot, Certification, SNP Marker, Traceability

Study and Selection of Morphological trait of Nam Hom Coconut for Selection Criteria of Mother Palm Plot

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ABSTRACT:
Studying coconut morphology data is 1 of 3 research activities. There were 3 activities consisting of morphology examination, genetic examination and aromatic scent examination in the project. In order to select mother palms, documented database for each palm and specified criteria for selection Nam Hom coconut mother palm plot. Morphology data such as leaf, trunk, inflorescence and fruit morphology included fruit composition were collected from 3 different farm standards in Ratchaburi Province during June 2022 to May 2023. Along with leaf samples were collected from 3 farm plots to analyzed aromatic gene and young tender nuts were collected for aroma substance 2-Acetyl-1-pyrroline (2-AP) determination. In addition, the mother palms were selected based on the criteria of the Department of Agriculture. While some morphological data showed dwarf type of selected palms (detected homozygous aromatic gene and detected 2-AP) were analyzed for correlation. It was found that farm plots no.1 (Coconut GI Ratchaburi plot), no. 2 (none certified plot), and no. 3 (GAP certified plot) with 165, 166, and 209 palms passed all selection criteria. And the morphology data of selected coconut palms were obtained for database creation. While studying correlation of these population of 3 farms found that there is correlation between coconut palm bole and short trunk, correlation between short trunk and short inflorescence, correlation between short inflorescence and peduncle. Hence, aside from homozygous aromatic gene, those mentioned criteria must found in Nam Hom mother palm. However, 6.7 % of selected mother palms have excess number of setting criteria. While the aroma determination by using GC-MS has found error with 34.4%. For the sweetness of coconut water which set at least 7 brix was found error at 18.4%. Thus, initial selection criteria of mother palms will use the presence of detected homozygous aromatic gene and detected 2-AP) and short trunk and short inflorescence basic criteria.

Keywords: Nam Hom coconut, coconut morphology, aromatic genes

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