

Joint International Conference on Sustainable Rice Cultivation & Vegetable Science and Innovation

24 October 2025
Grand Richmond Hotel,
Nonthaburi, Thailand

<https://riceveg.thailandricehub.org>



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Welcome Message

It is our great pleasure to invite you to the upcoming Joint International Conference on Sustainable Rice Cultivation and Vegetable Science & Innovation.

Rice and vegetables are two fundamental components of global food systems, particularly across Asia. In the face of climate change, resource scarcity, and population growth, there is a growing need for sustainable innovations in both rice cultivation and vegetable production. This on-site event will bring together researchers and students to exchange knowledge, share best practices, and foster strategic alliances for the advancement of sustainable agriculture.

Co-organized by the Thailand Rice Science Research Hub of Knowledge (Hub of Rice) and the Hub of Talents for Thai Vegetable Seeds (Veg-SeedHub), funded by the National Research Council of Thailand (NRCT).



Assist. Prof. Dr. Chutchamas Kanchana-Udomkan

Co-Convener

Director of Tropical Vegetable
Research Center, Kasetsart University



Assoc. Prof. Dr. Siwaret Arikitt

Co-Convener

Director of Rice Science Center,
Kasetsart University

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- Ministry of Higher Education, Science, Research and Innovation (MHESI)
- National Research Council of Thailand (NRCT)
- National Science and Technology Development Agency (NSTDA)
- Kasetsart University (KU)
- Hub of Talents for Thai Vegetable Seeds (Veg SeedHub)
- Thailand Rice Science Research Hub of Knowledge (HUB of RICE)
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- National Omics Center (NOC)
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Rice Science Center, Kasetsart University

General information

Venue

Grand Richmond Stylish Convention Hotel.
282 Rattanathibeth Rd., Bangkrasor, Muang,
Nonthaburi 11000, Thailand



Google maps

Parking

There is parking available at the venue for participants

Registration

Please have your QR code ready to scan at the counter.

You will then receive your name badge at the registration desks.

Open hours check-in

24 October 2024 | **07:30 – 08:30 AM**

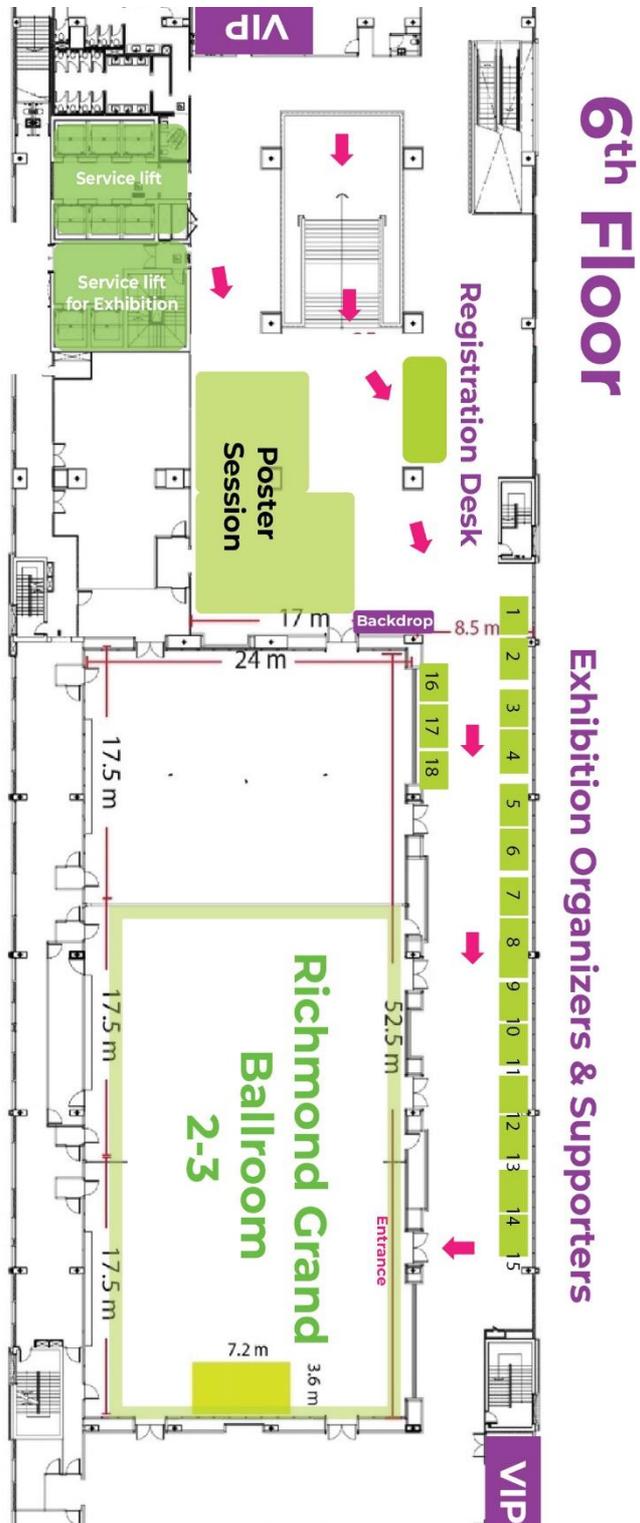
Poster presentation

Your poster board number is included in this abstract.

book. The conference organizers will provide all necessary equipment for displaying the posters, including pins and adhesive materials. Kindly remove your poster after the final poster session at 3:30 PM.

Floor Plan

Richmond Grand Ballroom 2-3



24 October 2025Richmond Grand Ballroom 2-3 | 6th Floor**07:30 - 08:30 Registration**

Please have your QR code ready for quicker check-in. (Excluding Committee members and Speakers.)

08:30 - 09:00**Welcome Speech****Prof. Dr. Kornorn Srikulnath**Assistant to the President for Research and Internationalization,
Kasetsart University (KU)**Report Speech****Assoc. Prof. Dr. Siwaret Arikit**

Director of Rice Science Center, Kasetsart University

Assist. Prof. Dr. Chutchamas Kanchana-Udomkan

Director of Tropical Vegetable Research Center, Kasetsart University

Opening Address**Dr. Wiparat De-ong**

Executive Director, National Research Council of Thailand (NRCT)

Dr. Krissanapong Kirtikara

Chairman of Kasetsart University Council

MC: Assoc. Prof. Dr. Patompong Johns Saengwilai - Mahidol University**09:00 - 09:30****THE NEXT GENERATION OF RICE: Sustainable and low-emission transformation of rice-based systems**

Dr. Yvonne Pinto - Director General of International Rice Research Institute (IRRI)

09:30 - 10:00**Vegetables for nutritious, climate-resilient and sustainable food systems**Ms. Delphine Larrousse - Director - Global Engagement Regional
Director - East and Southeast Asia (ESEA) of WorldVeg**10:00 - 11:00 Coffee Break | Photo Session | Poster Session****11:00 - 11:30****Safeguarding the Future of Food: The Importance and Role of Biodiversity in Agriculture**

Dr. Janny van Beem - Global Genebank Partnership Coordinator, Crop Trust

11:30 - 12:00**Financing the transition to climate-smart rice farming – perspectives on past challenges and future opportunities**Mr. Tobias Breunig - Advisor Agricultural Finance Thailand Agriculture & Food
Cluster - GIZ**12:00 - 13:00 – Lunch – 2nd Floor Topaz Room****13:00 – 13:30 Poster Session**

PROGRAM

24 October 2025

Richmond Grand Ballroom 6th Floor

CONCURRENT SESSION : RICE

Chair: Prof. Dr. Piyada Theerakulpisut - Khon Kaen University

Co-Chair: Assoc. Prof. Dr. Siwaret Arikrit - Rice Science Center, Kasetsart University

13:30 - 14:05

Could non-flowering rice lines revolutionize whole-crop silage cultivation?

Prof. Dr. Takeshi Izawa - University of Tokyo

14:05 - 14:30

From a Conspiracy Theory to Innovation: Medicinal Rainbow Rice

Prof. Dr. Apichart Vanavichit - Rice Science Center, Kasetsart University

14:30 - 14:55

Sustainable Rice Straw Management: Solutions Beyond Open Burning

Prof. Dr. Chanakan Prom-u-thai - Lanna Rice Research Center, Chiang Mai University

14:55 - 15:15 Coffee Break & Poster Session

Chair: Assoc. Prof. Dr. Sutkhet Nakasathien - Kasetsart University

Co-Chair: Dr. Jonaliza Siangliw - NSTDA

15:15 - 15:50

Sustainable rice and Low carbon Innovations

Mr. Jens Soth -The Sustainable Rice Platform (SRP)

15:50 - 16:15

Monitoring And Reporting of GHG Emissions From Rice: Available Tools and Latest Research Advances

Dr. Bjoern Ole Sander- IRRI

16:15 - 16:40

Assessment of GHGs Emission and Low Carbon Rice Production in Thai Rice Systems

Dr. Chitnucha Buddhaboorn - Rice Department

16:40 Closing Remarks

Prof. Dr. Peerasak Srinives - Representative from NRCT and KU



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RICE

PROGRAM

24 October 2025

Richmond Grand Ballroom 6th Floor

Joint International
Conference on Sustainable
Rice Cultivation &
Vegetable Science
and Innovation



CONCURRENT SESSION : VEGETABLE

Chair: Ms. Kunaporn Phuntunil - The Asia and Pacific Seed Alliance (APSA)

Co-Chair: Dr. Salit Supakitthanakorn - Kasetsart University

13:30 - 14:00

Vegetable innovations in the Asia and Pacific region

Dr. Le Dong - Food and Agriculture Organization of the United Nations (FAO)

14:00 - 14:30

Advance Analytics for Vegetable Seeds

Mr. Johan Van Asbrouck - Rhino Research Co. Ltd

14:30 - 14:50

Diversity to discovery, developing a pan-genome for marker development in vegetable breeding

Dr. Ya-ping Lin - WorldVeg

14:50 - 15:15 Coffee Break & Poster Session

Chair: Dr. Jukkrapong Pinyo - Kasetsart University

Co-Chair: Assist. Prof. Dr. Patcharaporn Tinchan - Kasetsart University

15:15 - 16:00

Innovation in postharvest technology to maintain quality, extend shelf-life, and increase market value of fresh vegetables

Prof. Dr. Giancarlo Colelli - University of Foggia

16:00 - 16:20

From Nitrogen to Stress Responses: Building Plant Resilience

Assist. Prof. Dr. Kulaporn Boonyaves - Mahidol University

16:20 - 16:40

Ensuring Seed Purity through Database Integration and DNA Marker Innovation

Dr. Jeremy Ross Shearman - BIOTEC

16:40 Closing Remarks

Prof. Dr. Peerasak Srinives - Representative from NRCT and KU

VEG



Yvonne Pinto

International Rice Research Institute (IRRI)

Short bio: Dr. Yvonne Pinto serves as the Director General of the International Rice Research Institute (IRRI). She has over 30 years of experience in technology, innovation, and international development. With a background in agricultural research, she spent 15 years in philanthropy investing in agriculture, enterprise, and education across Africa. She's worked with governments, UN agencies, and foundations, focusing on evidence-based solutions and the intersection of big data, science, and sustainability.

THE NEXT GENERATION OF RICE: SUSTAINABLE AND LOW-EMISSION TRANSFORMATION OF RICE-BASED SYSTEMS

Yvonne Pinto

Director General of International Rice Research Institute (IRRI)
Y.Pinto@cgiar.org

Abstract:

As climate change, economic shocks, and conflict intensify global food insecurity, cultivating rice, a staple for over half the world's population, must undergo a transformation. IRRI is driving the next generation of rice systems that are climate-resilient, low-emission, and economically viable, especially for smallholder farmers.

This presentation highlights IRRI's integrated approach across three areas: in-field innovations, off-field tools, and the development of climate-smart rice varieties. Proven techniques like Alternate Wetting and Drying (AWD), Direct-Seeded Rice (DSR), laser land leveling, and deep fertilizer placement are significantly reducing water use and methane emissions, while increasing yields and boosting farmer incomes. AI and drone technologies are enhancing precision, safety, and efficiency in seed planting, nutrient delivery, and pest management.

Post-harvest, circular solutions such as microbial composting and biofertilizers turn rice straw from waste into value, contributing to soil health and climate goals. Meanwhile, off-field innovations like Rice Crop Manager and PathoTracer deliver real-time, data-driven advice to farmers and researchers. In parallel, accelerated breeding powered by genomics and machine learning is fast-tracking the release of rice varieties that are high-yielding, nutritious, and resilient to stresses. Successful models like Vietnam's 1-million-hectare low-emission rice program offer a replicable blueprint for other countries.

Transforming rice systems is possible, but it will require cross-sector collaboration, enabling policies, and targeted investment to scale innovation where it's needed most.

Keywords: Low-emission rice systems, Climate resilience, Sustainable intensification, AI-driven innovation, Smallholder livelihoods



Delphine Larrousse

World Vegetable Center, Thailand

Short bio: Delphine Larrousse is Director for Global Engagement and Regional Director for East and Southeast Asia at the World Vegetable Center (WorldVeg), based in Bangkok, Thailand, and a member of its Executive Management Team.

She began her career in 2004 working with indigenous farming communities in Latin America, urban populations in India, and founded her own NGO in Ecuador. She held roles with UNESCO, UNICEF, and local organizations before joining Canada's International Development Research Centre (IDRC) in 2009. As Senior Program Officer for Agriculture and Food Security, she co-designed and managed global R4D programs, partnering with governments, UN agencies, NGOs, and researchers worldwide. She also led the communications and engagement strategy for the Canadian International Food Security Research Fund, supporting research uptake and policy relevance.

In 2019, she joined WorldVeg, driven by a strong belief in the role of vegetable research in building more nutritious and resilient food systems. Delphine has lived in ten countries and worked across regions, bringing strengths in strategic leadership, external engagement, and cross-sector partnerships, alongside a deep understanding of global food systems. She is fluent in five languages and experienced in bridging research with policy and practice, facilitating collaboration across disciplines.

She holds an International MBA from Kedge Business School (France) and Hochschule Bremen (Germany), a Postgraduate Diploma in Public Policy from FLACSO (Ecuador), and a Master's in Intercultural Communication from Anglia Ruskin University (UK).

VEGETABLES FOR NUTRITIOUS, CLIMATE-RESILIENT AND SUSTAINABLE FOOD SYSTEMS

Delphine Larrousse

World Vegetable Center, Thailand
delphine.larrousse@worldveg.org

Abstract:

Vegetables are nutritional powerhouses—rich in vitamins, minerals, fiber, protein, and phytonutrients. Beyond their health benefits, vegetables offer significant income opportunities, particularly for women, youth, and others with limited access to land or capital. They can be cultivated in small spaces and harvested frequently, making them well-suited for diverse farming systems. They fill a wide range of market niches—both fresh and processed—and contribute to resilient and sustainable food systems.

Despite their immense potential, vegetables remain underutilized in global food systems. Consumption falls far below the World Health Organization's recommended intake, and malnutrition persists in every country. On the supply side, constraints include poorly adapted varieties, weak seed systems, low productivity, inefficient or excessive use of external inputs, and high postharvest losses. On the demand side, barriers include food safety concerns, limited affordability, lack of access, and an unsupportive food environment. These challenges are further intensified by policy frameworks that often overlook the importance of local, safe vegetable production and consumption.

The World Vegetable Center (WorldVeg) is the only international non-profit organization with a global mandate for vegetables. With more than 50 years of experience, the Center has become a global leader in advancing vegetable science and innovation, supported by world-class expertise, infrastructure, and a broad network of trusted partners worldwide. WorldVeg contributes to healthier, more resilient food systems by advancing research and innovation across the entire vegetable value chain—from breeding and seed systems to sustainable production, postharvest management, nutrition-sensitive interventions, and enabling policy environments.

This presentation will highlight selected examples of WorldVeg's research and innovations that contribute to more nutritious, resilient, and sustainable food systems.

Keywords: Vegetables, food systems, resilience, nutrition, agriculture



Janny van Beem

Crop Trust

Short bio: Janny van Beem is the Global Genebank Partnership Coordinator at the Crop Trust, an organization dedicated to securing the world's crop diversity to ensure global food security and resilience against climate change and other challenges. She holds a doctorate in

Plant Breeding and Genetics from Cornell University. Her previous experience includes breeding wheat and beans at CIMMYT, Mexico and CIAT in Colombia. She also managed the ISO accreditation at the genebank in CIP, Peru, and collaborated with national commissions to protect and ensure the equitable sharing of plant genetic resources and their traditional knowledge within Peru.

She currently manages the implementation of quality and risk management systems in national genebanks across 20 countries. The service aims to support the adoption of higher standards in crop conservation and strengthen the global network of genebanks to ensure the world's food supply is resilient and secure.

SAFEGUARDING THE FUTURE OF FOOD: THE IMPORTANCE AND ROLE OF BIODIVERSITY IN AGRICULTURE

Janny van Beem

Global Crop Diversity Trust, Platz der Vereinten Nationen 7, 53113 Bonn, Germany
janny.vanbeem@croptrust.org

Abstract:

The Global Crop Diversity Trust (Crop Trust) works to conserve and provide access to the world's crop diversity, ensuring global food and nutrition security. It supports international genebanks, the Svalbard Global Seed Vault, and develops sustainable funding mechanisms for long-term conservation. Guided by its *2030 Strategic Plan: Food Forever*, the Crop Trust envisions a future where crop diversity is preserved and used to build resilient, sustainable, and healthy food systems. Central to this mission is a global network of genebanks that safeguard millions of accessions, promote their exchange, and ensure their availability to researchers, breeders, and farmers.

The Crop Trust supports international genebanks recognized under Article 15 of the International Plant Treaty through its Crop Diversity Endowment Fund, which covers essential operational costs. Long-term partnerships and grants help sustain these genebanks while improving digital tools like GRIN-Global Community Edition and Genesys to improve data management and access.

Complementary initiatives further enhance its impact. The BOLD Project supports national genebanks and farmers, Seeds for Resilience strengthens African genebanks, the Power of Diversity promotes underutilized crops in Africa, Asia, and Latin America, and Global Crop Conservation Strategies align conservation priorities worldwide.

The Crop Trust's broader goals are to ensure access to crop diversity, strengthen the global genebank system, raise public and political awareness of its significance, and promote international collaboration in plant genetic resources. These efforts collectively position the Crop Trust as a key player in enhancing the resilience of the global food system.

Keywords: Crop diversity, Genebanks, Conservation, Food security



Tobias Breunig

Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ)

Short bio: Tobias Breunig is a Financial Advisor at the GIZ Agriculture and Food Cluster in Thailand, and overseeing the GCF Thai Rice project component on Carbon Markets. He is an Economist with a background in development and environmental economics and has previously worked with GIZ in Uganda, and was seconded to the European Commission and the German Development Ministry BMZ.

FINANCING THE TRANSITION TO CLIMATE-SMART RICE FARMING – PERSPECTIVES ON PAST CHALLENGES AND FUTURE OPPORTUNITIES

Tobias Breunig

GIZ Thailand
Tobias.breunig@giz.de

Abstract:

Smallholder rice farming—predominantly in Asia and Africa—is a major source of GHG emissions, especially methane. In many rice-producing countries, rice is a significant source of national emissions in greenhouse gas inventories.

At the same time, rice is critical for global food security. Climate change, in particular increased volatility in weather patterns and temperature extremes are projected to negatively impact rice yields in the future in the absence of adaptive measures.

Technical interventions like regenerative agriculture and climate smart rice farming have the potential to significantly reduce GHG emissions from rice, as well as increase the resilience of farmers towards climate change impacts. For example, interventions like improved water management in rice through alternative wetting and drying (AWD) and increased nutrient input management can significantly reduce emissions in rice while also benefitting farmers financially, for example through reduced costs.

While interventions are technically feasible and demonstrated, global investment into climate smart rice remains limited. In SEA, the sector is characterized by smallholder farmers, an ageing population and a high exposure to climate change and other economic risks. This talk will explore past challenges and success stories, including the example of the “GCF Thai Rice” project, one of the largest global initiatives on low-emission rice to show future opportunities for investments into climate-smart rice.

Keywords: Climate change, Rice, Carbon markets, Climate finance, Climate change adaptation, Methane



Takeshi Izawa

University of Tokyo

Ph.D. Doctoral degree by dissertation April 1994

Graduate School of Science, University of Tokyo

M.S. Graduate School of Science, University of Tokyo (March 1988)

Supervised by Prof. Yoshiki Hotta

B.A. Faculty of Physics, University of Tokyo (March 1986)

PROFESSIONAL EXPERIENCE

4/2016–present	Professor, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan
10/2001–3/2016	Chief (and then Senior) Researcher, National Institute of Agrobiological Sciences, Japan
4/1994–9/2001	Assistant Professor, Nara Institute of Advanced Science and Technology, Japan
4/1990–3/1992	Guest Investigator, The Rockefeller University, USA, (cf. Prof. Nam-Hai Chua)
4/1988–3/1994	Researcher, Plantech Research Institute, Ltd., Japan

COULD NON-FLOWERING RICE LINES REVOLUTIONIZE WHOLE-CROP SILAGE CULTIVATION?

Takeshi Izawa

Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan
takeshizawa@g.ecc.u-tokyo.ac.jp

Abstract:

Flowering time in rice, one of the world's most important staple crops and a model plant for studying short-day flowering, is mainly regulated by photoperiod, ambient temperature, and light quality. In this regulatory network, blue light promotes flowering while red light suppresses it, with both light signals being precisely gated by the circadian clock. In my presentation, I will summarize recent advances in understanding the molecular mechanisms underlying photoperiodic flowering in rice. This includes transcriptome analyses of non-flowering rice plants that carry double mutations in the florigen genes *Hd3a* and *RFT1*, and the identification of cis-regulatory DNA elements that control the key floral repressor gene *Ghd7* (Sun et al., 2025; Ogo et al., 2025). Following updated Japanese government guidelines on gene-edited materials, we have recently started cultivating these non-flowering rice lines in field conditions to evaluate their agricultural traits. Interestingly, these lines produced more than twice the dry weight of normal rice plants when harvested at the usual timing, and they also accumulated about twice as much soluble sugar. These findings suggest that non-flowering rice lines, which continue vegetative growth without transitioning to the reproductive stage, may offer novel opportunities for developing high-biomass crops. I will discuss their potential applications as high-yield whole-crop silage cultivars in rice, linking basic flowering research to agricultural innovation.

Keywords: Rice, Photoperiodic flowering, Florigen genes, Whole-Crop silage



Apichart Vanavichit

Rice Science Center, Kasetsart University

Apichart Vanavichit, the Professor of Plant Breeding and Genomics, has devoted himself to being a pioneer in molecular rice breeding. He gained his Ph.D. in Crop Science from Oregon State University, USA, and established Kasetsart University's Rice Gene Discovery and Rice Science Center. He led a group of Thai scientists to join an international consortium of nine nations to complete the whole rice genome sequence, which has become the gold standard for functional genomics since 2004. Rice Science Center's team has discovered essential functional genes controlling economic traits and implemented them in rice breeding. He has developed a sizeable homogenised population to create spontaneous mutations in purple-pigmented rice. His whole career has been to complete a comprehensive gene pyramiding scheme delivering premium rice cultivars with aroma, grain qualities, and nutritional benefits with tolerance to biotic and abiotic stresses. His well-known rice cultivars are KDML105 Plus, Low Glycemic Index Plus, and Purple Pigmented Riceberry Plus. These speciality rice cultivars are key products in niche and organic markets for health-conscious consumers. Professor Apichart and his team have published over 70 original articles in internationally recognised journals, registered four new plant variety protection, registered 50 plant varieties, filed 11 international gene patents, and received 13 national honours and awards. His persistent efforts to change rice consumers' habits towards healthy whole grain pigmented rice and Rainbow rice, to shift into the new paradigm of food biofortification, and to feed highly nutritious rice to billions of people in the future climate change.

FROM A CONSPIRACY THEORY TO INNOVATION: MEDICINAL RAINBOW RICE

Apichart Vanavichit^{1*}, Phorphimon Janchai², Sukantharos Thadakittisarn², Maiporn Maiphoka¹, Kitti Walayaporn¹, Anuchart Sawasdee¹, Teerapan Singkhan^{1,3}, Thanwanit Thanyasiriwat⁴, and Siriphat Reungphayak¹

¹ Rice Science Center, Kasetsart University, Kamphaengsaen, Thailand

² Kasetsart Agricultural Product Institute (KAPI), Kasetsart University, Bangkok, Thailand

³ Graduate School, Kasetsart University, Bangkok, Thailand

⁴ Faculty of Natural Resources and Agro-Industry, Kasetsart University Chalermpkrakiat, Sakon Nakhon, Thailand

Abstract:

Among the largest and longest-lived animals on earth, including dinosaurs and elephants, are vegan by consuming green biomass all their life. These Green biomasses are more nutritious than mature biomasses, particularly those from C3 plants, which are rich in RUBISCO, the key photosynthetic enzyme. We have speculated that rice, a C3 plant, may provide nutritious and palatable green biomass for future foods and ingredients. Over-consumption of high caloric foods and stagnant lifestyles are the leading causes of over-nutrition, obesity and diabetes. The dilemma is best solved by replacing high-calorie starch with affordable, nutrient-rich ingredients, including reliable dietary fibre and plant-based protein.

In recent years, Thailand has taken on a new challenge to become the kitchen of plant-based producers. Actually, Thailand ranked as the top plant protein producer and the net protein exporter in Asia. In contrast, the imported statistics for soybean and whey protein isolates from the USA have skyrocketed recently. To fully capitalise on the economic opportunity, Thailand must compensate for the import of plant-based protein by sourcing it locally.

We reported here Rainbow Rice, the emerging class of vegetable rice, orchestrating mixed patterns of chlorophyll, flavonoids, and carotenoids. Rich in dietary fibre, protein, micronutrients, antioxidants, with minimal phytate. Rainbow Rice has become a promising genetic model for molecular, physiological, nutritional and product innovation. We successfully isolated up to 30% of hydrolysable plant protein (RBPH) and dietary fibre (RBDF) from the vegetable Rainbow Rice leaf. We also characterise the amino acid profile and biochemical characteristics. Building on experiences from Rainbow Rice, we identify additional cultivars of choice for plant-based functional foods in the future. Farmers can earn significantly more income from producing high-quality leaves, which helps avoid open-field burnout, supports regenerative agriculture, and replaces high-caloric starch to mitigate triple-burden malnutrition on a global scale.

Keywords: Rainbow Rice, Vegetable Rice, Plant-based Protein, Hydrolysable Dietary Fibre, Future Food Ingredients.



Chanakan Prom-u-thai

Lanna Rice Research Center, Chiang Mai University

Short bio: Prof. Chanakan Prom-u-thai is a leading expert in rice science and sustainable agriculture at Chiang Mai University, Thailand. She has long term experience in plant physiology, rice crop improvement, and agricultural resource management. Prof. Chanakan has published extensively on topics such as rice straw utilization, rice grain quality, nutrient fortification, and climate-smart farming practices. She has led numerous interdisciplinary research projects and actively collaborates with local and international organizations to promote innovations that benefit both farmers and the environment.

SUSTAINABLE RICE STRAW MANAGEMENT: SOLUTIONS BEYOND OPEN BURNING

Chanakan Prom-u-thai^{1,2*}, Suthaphat Khamthai^{1,3}

¹ Lanna Rice Research Center, Chiang Mai University, Chiang Mai 50200, Thailand

² Department of Plant and Soil Sciences, Faculty of Agriculture, Chiang Mai University, Chiang Mai 50200, Thailand

³ Division of Packaging Technology, School of Agro-Industry, Faculty of Agro-Industry, Chiang Mai University, Chiang Mai 50100, Thailand

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Abstract:

Rice straw is produced in vast quantities across Thailand, with estimates indicating that over 26 million tons are generated annually following rice harvests. Traditionally, more than 70% of this rice straw is disposed of by open-field burning, contributing significantly to air pollution, greenhouse gas emissions, and adverse health effects for local communities. Despite these challenges, rice straw holds tremendous potential as a resource for sustainable agriculture and rural economic development. Currently, less than 30% of rice straw in Thailand is utilized for alternative purposes, such as soil incorporation, composting, mushroom substrate, animal feed, and biogas production. In this presentation, we will share data from a literature review, farmer interviews, and our research experiments. Successful case studies from Thailand and neighboring countries will be shared to demonstrate the economic, environmental, and social benefits of effective rice straw management. Community initiatives, the sharing of agricultural machinery, and policy support play essential roles in encouraging widespread adoption. Understanding how changing the current approach to rice straw can simultaneously address environmental issues and foster community prosperity. The presentation concludes with concrete recommendations and a call to action for all stakeholders toward a more sustainable and healthy agricultural future.

Keywords: Straw bales, Straw fiber, Open-field burning

Concurrent Session: Rice Cultivation



Jens Soth

The Sustainable Rice Platform (SRP)

Short bio: Jens Soth is an agricultural scientist and environmental engineer with over 20 years of experience dedicated to enhancing the environmental sustainability of agricultural production and processing. His expertise spans sustainable and regenerative agriculture, as well as circular economy principles.

Jens has contributed his knowledge to several international expert committees, including the Sustainability Panel of the International Cotton Advisory Committee, the ISO, and the EU Ecolabelling Board.

He possesses extensive experience working with various value chains and corresponding standards and has successfully facilitated public-private partnerships involving multi-stakeholder collaboration at both farm and landscape levels.

Since mid-2025, Jens has served as the Executive Director of the Sustainable Rice Platform (SRP), where he leads efforts to advance a credible, multi-actor initiative centered on a recognized standard and label for sustainable rice production.

SUSTAINABLE RICE AND LOW CARBON INNOVATIONS

Jens Soth

Executive Director of The Sustainable Rice Platform (SRP)

Abstract:

The global rice sector faces major challenges, from greenhouse gas emissions to the need for sustainable practices that support both the environment and farmers' livelihoods. In this session, Jens Soth will share how the Sustainable Rice Platform (SRP) is promoting low-carbon innovations in rice production. Drawing on over 20 years of experience in sustainable agriculture and environmental engineering, he will discuss practical approaches for climate-smart rice farming, applying circular economy principles, and fostering collaboration among multiple stakeholders. The session will also highlight how SRP works with public and private partners to develop recognized standards and labels, helping farmers adopt low-carbon practices across rice value chains. Attendees will leave with actionable insights on advancing sustainability and reducing carbon emissions in rice production, while supporting economic and social benefits for farming communities. Keywords: Sustainable Rice Production Low-Carbon Innovation Climate-Smart Agriculture Public-Private Partnerships

Keywords: Sustainable Rice Production, Low-Carbon Innovation, Climate-Smart Agriculture, Public-Private Partnerships



Bjoern Ole Sander

Senior Scientist II – Climate Change
Country Representative – Thailand
International Rice Research Institute

Short bio: Ole is the climate change focal point of IRRI and leads the Thailand country office. His research focuses on greenhouse gas (GHG) emissions and mitigation technologies, particularly in Asia. Ole joined IRRI in 2010 and has since specialized in analyzing the GHG balance of cropping systems and evaluating mitigation strategies, such as Alternate Wetting and Drying (AWD) to reduce methane, incl. support to create enabling environments for adoption of new technologies and scaling. His broad expertise in agricultural climate change and multistakeholder engagement has strengthened IRRI's climate change research initiatives across the region, fostering partnerships with national institutions in Vietnam, Thailand, Cambodia, Bangladesh, and the Philippines.

MONITORING AND REPORTING OF GHG EMISSIONS FROM RICE: AVAILABLE TOOLS AND LATEST RESEARCH ADVANCES

Bjoern Ole Sander

International Rice Research Institute

Abstract:

The International Rice Research Institute (IRRI) has established an integrated framework of Monitoring, Reporting, and Verification (MRV) tools designed to quantitatively assess greenhouse gas (GHG) emissions from rice-based production systems. This framework aims to facilitate the achievement of methane mitigation commitments and enhance access to carbon finance mechanisms within the agricultural sector. The SECTOR GHG Calculator constitutes a central component of this framework, enabling site-specific estimation of emissions using IPCC Tier II-compliant methodologies under a range of management scenarios.

Complementary digital platforms, namely RiceMoRe (Rice Monitoring and Reporting) and FarMoRe (Farm Monitoring and Reporting), enable the collection of activity data through mobile and web-based interfaces. These systems record key management indicators such as irrigation scheduling, fertilizer application, straw management practices, and crop yield performance. The resulting datasets provide high-resolution activity data that strengthen the accuracy of national GHG inventories, contribute to NDC (Nationally Determined Contribution) progress tracking, and strengthen monitoring processes for carbon project development.

To enhance spatial coverage and improve estimation accuracy, IRRI's MRV approach integrates remote sensing and process-based modeling tools. The ORYZA rice growth model has been expanded with dedicated modules for GHG estimation, enabling the simulation of emissions in relation to biophysical and management variables. In parallel, a novel radar-based remote sensing technique has been developed to detect paddy field water regimes from satellite observations, allowing large-scale assessment of flooding dynamics—a key determinant of methane fluxes. Together, these components enable progression towards Tier 3 inventory methodologies, providing countries with more precise, science-based emission estimates.

The presentation will illustrate the practical application of these tools through case studies. It will further examine methodological strengths, data limitations, and opportunities for harmonization across spatial scales and institutional contexts. Collectively, IRRI's MRV innovations provide a robust scientific foundation for advancing climate change mitigation strategies in the global rice sector.



Chitnucha Buddhaboon

Rice Department

Short bio: Dr. Chitnucha Buddhaboon is a Former Deputy Director General of Rice Department, Ministry of Agriculture and Cooperatives. He received his M.S. in Agriculture (Agricultural Systems) International curriculum at Chiang Mai University and Ph.D. in Agricultural Systems at Chiang Mai University, University of Georgia and Washington State University. After almost 34 years as an Agricultural Research Officer, Senior Professional Level in Division of Rice Research and Development, he moved to Bureau of Rice Policy and Strategy and then Division of Rice and Rice Products Inspection and Certification, as the Director before promoted to be the Deputy Director General, Rice Department. He retired on September 30, 2025.

His research specialty and interests include the DSSAT-CSM-rice model for crop yield prediction, adaptation and mitigation strategies for rice production under climate change. He also involved team of climate change policy and planning in agricultural sector.

ASSESSMENT OF GHGS EMISSION AND LOW CARBON RICE PRODUCTION IN THAI RICE SYSTEMS

Chitnucha Buddhaboorn¹, Benjamas Rossopa²

¹ Former Deputy Director General of Rice Department, Ministry of Agricultural and Cooperatives

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Abstract:

The research on assessment of greenhouse gases emission from rice paddy field was conducted from 1994 to 1999 at Prachin Buri Rice Research Center, Department of Agriculture. The objective was to quantify methane (CH₄) emission from rice production systems in Thailand. The research found that CH₄ emission from application of rice straw compost, straw mulching and burned rice straw in deepwater rice were not significantly different ranging from 9.6 to 27.2 kg CH₄/rai/season. However, application of rice straw compost tended to give a higher emission rate those of two treatments. Under irrigated rice production system, methane emission rates range from 2.4 to 6.7 kg CH₄/rai/season. There were various of factors affecting on CH₄ emission rate from rice production systems such as rice varieties, soil types, fertilizer application, water management, rice straw management. Base on many researches during last few decades regarding to GHGs reduction from rice production activity, Alternative Wetting and Drying (AWD) technique has been dominated technology for water management to reduce GHGs emission from rice production system. It is able reduce more than 30% of CH₄ flux. More than 10 technologies are able to implement in both irrigated and rainfed systems for increase productivity, reduce cost and reduce GHGs emission. Rice Department (RD), Ministry of Agriculture and Cooperatives is able to implement these technologies along with Consolidate Farming and Community Rice Center policies. The RD has collaborated with government organizations, private sectors, and international organizations to apply suitable technologies to reduce GHGs under government policy. Low carbon rice is recently hot issue in term of environment friendly rice production system. Anyway, value of carbon credit is very low and MRV system is quite hard for farmers to record. Low carbon rice market and differentiated consumers who willing to pay and share to take care environment is the way of sustainable system.

Keywords: rice, low carbon, alternative wetting and drying (AWD), methane, technology

Concurrent Session: Vegetable Science & Innovation



Le Dong

Food and Agriculture Organization of the United Nations (FAO)

Short bio: Dr. Dong Le is Innovation Specialist (Agrobiodiversity and Food Systems) at FAO Regional Office for Asia and Pacific, based in Bangkok, Thailand, since April 2025. From 2018 to March 2025, he was Programme Officer (Module Leader on Partnership and Innovation) at FAO Representation in China. Prior to joining FAO, he worked for the Delegation of the European Union to China from 2009 to 2011, and World Wide Fund For Nature (WWF) China for a Global Shift Initiative based in Beijing and African Regional Office based in Nairobi from 2011 to 2013. He holds a doctoral degree on environmental economics and master degree on environmental management from Kyoto University, Japan.

VEGETABLE INNOVATIONS IN THE ASIA AND PACIFIC REGION

Le Dong

Regional Office for Asia and the Pacific, Food and Agriculture Organization of the United Nations (FAO)

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Abstract:

Vegetable is a cornerstone of food security, nutrition, and livelihoods in the Asia and Pacific region. However, this sector faces unprecedented challenges, including climate change impacts, pest and disease pressures, post-harvest losses, and the increasing need from growing urban population. In response, the Food and Agriculture Organization of the United Nations (FAO) is championing a suite of innovative and scalable solutions to transform the vegetable production and value chains towards sustainability.

This presentation explores key innovations that are enhancing the resilience and productivity of vegetable sector. It highlights the critical role, challenges and opportunities provided by the development of science, technology and innovation. Five main innovations are presented: 1) diversifying the vegetables, in the context that Asia has variety of high priority underutilized vegetable species, and agricultural biotechnologies can be adopted in breeding programme; 2) Protecting the vegetables with Integrated Pest Management (IPM) and Biocontrol, with case study from the region showing the risk can be reduced; 3) Urban and Peri-urban Agriculture, which is key to improving the productivity of land, generating employment, strengthening the economic status of farmers, while substituting for imports, to meet consumers' demand for high-value products, such as vegetables; 4) Reducing Post-harvest Loss and Waste, by tackling the storage, processing and packaging which witnessed the most loss and waste for fruits and vegetables for Eastern and South-eastern Asia; 5) Digital leap for vegetables, by harnessing the digital innovations for the full value chain of vegetables.

Through concrete case studies from across the Asia and Pacific region, this presentation demonstrates how these interconnected innovations are not only improving the productivity of vegetable sector, livelihoods of vegetable farmers, but also contributing to the transformation of our agri-food systems towards more resilience and sustainable.

Keywords: Vegetable, Innovation, Technology, Asia and Pacific



Concurrent Session: Vegetable Science & Innovation



Johan Van Asbrouck

Rhino Research

Short bio: Johan Van Asbrouck is the Executive President of Rhino Research Co., Ltd., Thailand, and a global expert in seed science and technology. With more than 30 years of experience, he has contributed to innovations in seed drying, storage, and physiological quality assessment. His pioneering work includes the development of Drying Beads® technology, Respirometer seed respiration measurement, and RhinoVision multispectral imaging systems—tools that are now widely used by leading seed companies and research institutes. Johan has worked extensively across Asia, Europe, and Africa to improve seed quality management systems and training through the International Seed Academy (ISA). His mission focuses on integrating data-driven analytics to enhance seed quality assurance and sustainability in modern agriculture.

ADVANCED ANALYTICS FOR VEGETABLE SEEDS

Johan Van Asbrouck

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Abstract:

The vegetable seed sector is undergoing rapid transformation as digitalization and advanced analytics redefine how quality is measured, predicted, and assured. This presentation introduces an integrated approach combining multispectral imaging (RhinoVision), oxygen consumption monitoring (Respirometer), and chlorophyll fluorescence sensors (CF-Sensor) to create a multidimensional understanding of seed quality and vigor. By leveraging these technologies through RhinoLink—a central analytics platform—seed professionals can access real-time physiological data that connect laboratory results with field performance. Examples from recent studies in tomato, pepper, and brassica seeds demonstrate how advanced analytics enable early detection of deterioration, improve process optimization, and strengthen quality control systems. The talk also highlights case studies on integrating these data pipelines into breeding and production programs to enhance decision-making and reduce variability. The goal is to showcase how “Power of Seed Analysis” can transform the vegetable seed industry from reactive testing to predictive management—supporting both sustainability and profitability.

Keywords: Multispectral Imaging, Oxygen Consumption, Chlorophyll Fluorescence, Seed Quality, Seed Analytics

Concurrent Session: Vegetable Science & Innovation



Ya-Ping Lin

World Vegetable Center

Short bio: Dr. Ya-Ping Lin is a quantitative geneticist and genomics scientist who currently serves as an omics breeder at the World Vegetable Center. She specializes in vegetable crop improvement, with a particular focus on mungbean genomics. Dr. Lin has led pioneering efforts in pan-genome assembly, multi-location association studies, and QTL mapping, uncovering key genetic loci for yield, climate resilience, and disease resistance in mungbean. Beyond mungbean, she applies multi-omics integration, advanced statistical modeling, and AI-driven breeding strategies to accelerate genetic gain in crops such as tomato and amaranth. Widely published in leading journals including *Plant Physiology*, *eLife*, and *Physiologia Plantarum*, she also collaborates globally to strengthen molecular breeding capacity. Her expertise and contributions have led to invitations to major scientific conferences, highlighting her role in advancing vegetable genomics for global food security.

DIVERSITY TO DISCOVERY, DEVELOPING A PAN-GENOME FOR MARKER DEVELOPMENT IN VEGETABLE BREEDING

Ya-Ping Lin

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Abstract:

Mungbean (*Vigna radiata*) is a protein-rich, low-input pulse crop that contributes to food security, rural incomes, and soil fertility in developing regions. However, mungbean yellow mosaic disease (MYMD) represents a major constraint to production across South and Southeast Asia. To elucidate the genetic basis of resistance, we evaluated the mungbean minicore collection across multiple environments from 2016 to 2021 within the International Mungbean Improvement Network. Thirty phenotypic datasets from Bangladesh, India, Myanmar, and Pakistan revealed significant spatiotemporal variation in disease severity, with outbreaks ranging from severe in Madaripur, Bangladesh (mean score 5.39, 2020) to mild in Rangpur, Bangladesh (mean score 1.13, 2020). Year effects were notable in Ishwardi, while Gazipur showed relatively stable resistance. Several resistant and susceptible accessions were consistently identified, including the broadly resistant VI002190BG. To complement phenotypic evaluations, we constructed a comprehensive mungbean pangenome through whole-genome resequencing of 600 elite breeding lines and nearly 200 wild accessions, thereby addressing the limitations of existing reference genomes. Across these ~800 accessions, we identified over 57,000 genes, comprising ~27,000 core genes and ~30,000 dispensable genes, which substantially enrich the previously established Crystal reference genome. Genome-wide association studies revealed multiple significant loci, with recurrent QTLs consistently detected across regions, particularly in Bangladesh, India, and Myanmar. A set of multi-marker assays is being developed to enable efficient screening of resistant lines, thereby accelerating routine breeding. Collectively, these results highlight the complexity of MYMD resistance and provide valuable genomic and phenotypic resources for molecular breeding and the development of resilient mungbean cultivars.

Keywords: *Vigna radiata*, Mungbean yellow mosaic disease, Pan-genome, Genome-wide association study

Concurrent Session: Vegetable Science & Innovation



Giancarlo Colelli

University of Foggia

Short bio: Prof. Giancarlo Colelli is Full Professor at the Department of Agricultural Sciences, Food, Natural Resources and Engineering, University of Foggia, Italy. His research focuses on the impact of equipment and innovative technologies on the postharvest quality of whole and fresh-cut

fruits and vegetables, with a strong emphasis on non-destructive quality assessment. He has led more than 20 national and international R&D projects and currently serves as Chair of the Postharvest and Quality Management Division of the International Society of Horticultural Science. A frequent invited speaker at leading international conferences, Prof. Colelli has delivered lectures in over 30 institutions worldwide, including in China, Germany, Japan, Spain, and the United States. He is the author of nearly 170 peer-reviewed articles in international journals, contributing substantially to advancing postharvest science and technology.

INNOVATION IN POSTHARVEST TECHNOLOGY TO MAINTAIN QUALITY, EXTEND SHELF-LIFE, AND INCREASE MARKET VALUE OF FRESH VEGETABLES

Giancarlo Colelli

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Abstract:

Fresh vegetables are important for their richness in biologically active compounds and should be regularly part of the human diet. They are very perishable and commercial life is often a matter of days resulting in high postharvest losses. In response to these challenges significant research have been dedicated to innovating postharvest technologies. Temperature and atmosphere management remain fundamental, but have evolved beyond simple refrigeration. Atmosphere modification technologies have been refined with improved gas permeability films and more accurate predictive models, allowing for the creation of optimal environments that slow metabolic changes for specific vegetable types. Ethylene management, through advanced scrubbing technologies or the application of inhibitors like 1-methylcyclopropene, is now more effective in delaying ripening and senescence. A promising area of innovation is non-destructive quality assessment. Near-Infrared Spectroscopy and Hyperspectral Imaging enable the rapid and accurate evaluation of internal and external quality attributes and allow to discriminate the product for a number of features, potentially relevant for the market. These systems are being integrated into automated sorting lines, ensuring consistent quality, reducing labor costs, and allowing for market segmentation based on premium quality. To address food safety and decay, novel sanitation and preservation techniques are replacing traditional treatments. The application of physical methods like UV-C, electrolyzed water, and ozone effectively reduces microbial loads on vegetable surfaces. Concurrently, the development of edible coatings, formulated from natural biopolymers contribute to create a modified atmosphere around the individual product and can be enriched with antimicrobial/antioxidant compounds, preventing decay and preserving nutritional value. Finally, the integration of these technologies demonstrates that extending shelf-life and maintaining quality directly translates to increased market value. By reducing waste, ensuring product safety, delivering a consistently superior sensory experience, and enabling access to distant markets, these innovations provide growers, distributors, and retailers with a significant competitive advantage.

Keywords: Atmosphere modification, non-destructive technologies, ethylene inhibitors, product quality

Concurrent Session: Vegetable Science & Innovation



Kulaporn Boonyaves

Mahidol University

Short bio : Dr. Kulaporn Boonyaves is a researcher specializing in plant stress adaptation, molecular biology, and crop improvement. She obtained her Ph.D. in Biology from Swiss Federal Institute of Technology in Zurich (ETHZ), Switzerland, and is currently an assistant professor at

Mahidol University, Thailand. Her current research focuses on environmental stress crosstalk in plants, particularly the role of nitrogen in regulating environmental adaptations. She has published in peer-reviewed journals and actively supervises undergraduate and graduate students, fostering scientific training in plant biology. Dr. Boonyaves also collaborates nationally and internationally to advance sustainable crop protection strategies, engaging in both fundamental biological research and translational studies that bridge basic discoveries with agricultural applications. Outside of academic work, she enjoys travelling and long walks, and finds joy in growing plants and watching them thrive.

FROM NITROGEN TO STRESS RESPONSES: BUILDING PLANT RESILIENCE

Kulaporn Boonyaves

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Abstract:

Nitrogen is an essential mineral nutrient for plant growth and development and is widely used in agriculture as a key factor determining crop productivity. However, excessive application of nitrogen fertilizers has led to serious environmental issues, including eutrophication and greenhouse gas emissions. Improving nitrogen use efficiency (NUE) in crops is therefore critical for reducing environmental impacts and achieving sustainable agricultural production. In plants, sufficient nitrogen supply supports vigorous growth and photosynthetic activity, whereas nitrogen deficiency results in chlorosis and reduced biomass accumulation. Beyond its central role in primary metabolism, nitrogen also influences plant responses to biotic and abiotic stresses through complex regulatory and signaling networks. Transcription factors such as WRKYs are known to modulate stress responses in either shared or stress-specific manners, while phytohormones coordinate overall plant adaptation under stress conditions. Despite advances in this area, the molecular mechanisms underlying nitrogen perception, assimilation, and regulation—particularly those involving transcription factors and phytohormonal control—remain incompletely understood. This talk will present insights into plant molecular and phenotypic responses to nitrogen availability, including studies in chili pepper, and introduce imaging-based tools developed to quantify these responses under varying environmental conditions.

Keywords: Nitrogen, Environmental stress, WRKYs, Chili pepper



Concurrent Session: Vegetable Science & Innovation



Jeremy Ross Shearman

National Science and Technology Development Agency (NSTDA)

Short bio : Dr. Jeremy Shearman earned his bachelor's and PhD degrees from the University of New South Wales in Sydney, where he also worked part-time at the Ramaciotti center for Genomics. His PhD project focused on disease gene discovery in dogs, where he developed a DNA test that ultimately led to the complete eradication of a disease from purebred Border Collies.

After graduating, he completed a two-year postdoc in the plant genomics lab at NSTDA, and is now a senior researcher and lab manager for the bioinformatics staff of the National Omics Center, NSTDA. He has worked on QTL analysis in rice, maize, rubber tree, and casava; RNAseq in oil palm, rice, sugarcane, maize, and mangrove; and genome assembly and annotation in sugarcane, rubber tree, and mangrove. In addition, Dr. Shearman currently serves as an Executive Editor for the Elsevier journal, Genomics.

ENSURING SEED PURITY THROUGH DATABASE MINING AND DNA MARKER INNOVATION

Jeremy R. Shearman

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Abstract:

High-quality, pure seed stock is the cornerstone of modern agriculture, directly impacting crop yield, uniformity, and resistance to environmental stresses. Farmers often buy or sell large quantities of seed from lines with high yield or known resistance genes, and the most effective way to provide quality control is through the use of molecular markers. A large market for such testing is hybrid seed testing to identify the percentage of the samples that are hybrids and the percentage of the seeds that are from parental selfing. We perform reduced representation sequencing to identify SNPs that are informative for such crosses to allow for routine SNP testing using allele-specific PCR.

In addition to seed purity testing, farmers need SNP based testing for many traits, such as disease resistance, not only to allow for marker assisted selection, but also to ensure that successive generations of established lines do not lose these traits of interest. We are in the process of mining literature and variant databases to develop SNP based testing for as many disease resistance and desirable traits as possible. It is also interesting to note that precision genomics using gene editing is now considered safe and acceptable by the world, opening up the possibility to add variants identified from other lines to local lines.

Keywords: Seed Purity, Molecular Markers, Marker-Assisted Selection, Disease Resistance, Plant Breeding, Genotyping

POSTER SESSION: RICE	
RICE-01	CALLUS INDUCTION AND REGENERATION EFFICIENCY IN THREE COMMERCIAL THAI RICE CULTIVARS
RICE-02	MODELING AND EXPERIMENTAL INSIGHTS INTO CADMIUM-INDUCED ROOT TRAIT ALTERATIONS AND THEIR IMPACT ON NITRATE UPTAKE AND CARBON ALLOCATION IN RICE
RICE-03	GENOTYPIC VARIATION IN ROOT ANATOMICAL TRAITS AND ITS ROLE IN CARBON SEQUESTRATION IN RICE
RICE-04	FARMERS' AWARENESS AND WILLINGNESS TO PARTICIPATE IN CARBON MARKETS IN THAILAND
RICE-05	COMPARATIVE STUDY ON NUTRITIONAL AND BIOACTIVE PROPERTIES OF ORGANIC BROWN SANGYOD AND JASMINE RICE
RICE-06	BRASSINOSTEROID FOLIAR SPRAYING IMPROVES THERMOTOLERANCE AND REPRODUCTIVE YIELD OF KDML105 RICE UNDER HIGH TEMPERATURE STRESS AT REPRODUCTIVE STAGE
RICE-07	USE CASE PROTOTYPES FOR A KNOWLEDGE PLATFORM PROMOTING HOME-GROWN RICE SELF-SUFFICIENCY
RICE-08	GENOME-WIDE ASSOCIATION STUDY (GWAS) REVEALS ENDOSPERM-SPECIFIC GENES (<i>OSENS</i>) AND <i>WX</i> GENE REGULATING SEED STORAGE PROTEIN (<i>SSP</i>) IN RICE GRAIN (<i>ORYZA SATIVA L.</i>)
RICE-09	DEVELOPMENT OF HIGH-FIBER DRIED RICE NOODLES FORTIFIED WITH RED SEAWEED (<i>GRACILARIA FISHERI</i>)
RICE-10	OPTIMIZING N6D MEDIA COMPOSITION FOR ENHANCED SECONDARY EMBRYOGENIC CALLUS FORMATION IN THAI RICE VARIETIES (<i>ORYZA SATIVA L.</i>)
RICE-11	IDENTIFICATION OF ROOT RESPONSIVE GENES UNDERLYING PENETRATION ABILITY IN COMPACTED SOIL USING QTL-SEQ IN RICE (<i>ORYZA SATIVA L.</i>)
RICE-12	SELECTION AND DEVELOPMENT OF A MICROBIAL CONSORTIUM PROTOTYPE FOR EFFICIENT AND SAFE DECOMPOSITION OF RICE STRAW AND STUBBLE AS AN ALTERNATIVE TO OPEN BURNING AND TO SUPPORT SUSTAINABLE RICE PRODUCTION
RICE-13	SILICON-INDUCED RESISTANCE IN RICE (<i>ORYZA SATIVA L. CV. NIAW DAM CHOR MAI PAI 49</i>): AN ECO-INNOVATIVE STRATEGY FOR SUSTAINABLE MANAGEMENT OF RUSTY PLUM APHID (<i>HYSTERONEURA SETARIAE THOMAS</i>)
RICE-14	QUANTITATIVE TRAIT LOCUS (QTLs) MAPPING FOR RICE STOMATAL MEGA-PAPILLAE USING QTL-SEQ AND GENOME-WIDE ASSOCIATION STUDIES
RICE-15	THE <i>OSCIPK9</i> GENE NEGATIVELY REGULATES SALINE-ALKALI STRESS TOLERANCE IN RICE
RICE-16	INFLUENCE OF LOW EARTH ORBIT ON AROMA, TEXTURE, AND PROTEIN DIGESTIBILITY OF THAI LANDRACE RICE (466HM) CULTIVATED ABOARD THE SHIJIAN-19 MISSION

POSTER SESSION: RICE

RICE-17	INNOVATION OF MICROBIAL FOR AGRICULTURAL RESIDUE DECOMPOSITION INTEGRATED WITH RICE PRODUCTION TECHNOLOGY TO ENHANCE PRODUCTIVITY AND SUSTAINABLE NO-BURN FARMING IN NONTHABURI PROVINCE
RICE-18	COMPARATIVE EFFECTS OF RICE VARIETIES ON THE QUALITY OF DRIED BROWN RICE PASTA
RICE-19	VALORIZATION OF RICE STRAW AND STUBBLE INTO CLEAN ENERGY THROUGH MOBILE BIOMASS PELLETIZING MACHINE INNOVATION UNDER THE BCG ECONOMY
RICE-20	MAPPING AND SPATIAL CLUSTERING OF RICE BLAST DISEASE IN THAILAND FOR TARGETED MANAGEMENT
RICE-21	ENHANCEMENT OF DROUGHT TOLERANCE IN THAI JASMINE RICE (KDML105) BY <i>STREPTOMYCES THERMOCARBOXYDUS</i> ISOLATE S3 ASSOCIATED WITH ARBUSCULAR MYCORRHIZAL FUNGUS <i>FUNNELIFORMIS MOSSEAE</i>
RICE-22	DISSECTING THE POLYGENIC BASIS OF BACTERIAL LEAF STREAK RESISTANCE IN RICE USING QTL-SEQ AND BULKED SEGREGANT WHOLE-GENOME SEQUENCING
RICE-23	EFFECTS OF PESTICIDE APPLICATION METHODS ON THE DIVERSITY OF NATURAL ENEMIES IN RICE FIELDS AT CHIANG RAI PROVINCE
RICE-24	PRODUCTION OF ANTIBODY AGAINST <i>XANTHOMONAS ORYZAE</i> PV. <i>ORYZICOLA</i> FOR EARLY SEROLOGICAL DETECTION OF RICE BACTERIAL LEAF STREAK
RICE-25	PHYTOLITH MORPHOTYPES OF SELECTED GRASS (POACEAE) SPECIES IN THAILAND FOR ARCHAEOBOTANICAL RESEARCH
RICE-26	PRODUCTION AND CHARACTERIZATION OF POLYCLONAL ANTIBODY AGAINST <i>XANTHOMONAS ORYZAE</i> PV. <i>ORYZAE</i> FOR EARLY DETECTION OF RICE BACTERIAL LEAF BLIGHT
RICE-27	INNOVATION IN REMOTE SENSING FOR AGRICULTURE: INTEGRATING FIELD SURVEYS AND SATELLITE DATA TO DEVELOP INDICES FOR MONITORING RICE YIELD IN SUPHAN BURI PROVINCE, THAILAND.
RICE-28	IDENTIFICATION OF STABLE AND HIGH-YIELDING AROMATIC GLUTINOUS RICE LINES ADAPTED TO RAINFED ECOSYSTEMS IN NORTHERN THAILAND
RICE-29	IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF BACTERIAL LEAF BLIGHT RESISTANCE CANDIDATE GENE USING CRISPR/CAS9 TECHNIQUE
RICE-30	EVALUATION OF <i>METARHIZIUM</i> STRAINS FOR RICE PLANTHOPPER CONTROL
RICE-31	CERTIFICATION OF RICE POWDER CERTIFIED REFERENCE MATERIAL (TRM-F-2003) FOR METROLOGICAL TRACEABILITY OF ELEMENTS AND ARSENIC ANALYSIS
RICE-32	METROLOGICAL TRACEABILITY AND UNCERTAINTY EVALUATION IN MOISTURE METER CALIBRATION USING CERTIFIED RICE REFERENCE MATERIALS

POSTER SESSION: RICE	
RICE-33	MULTI-TRAIT SELECTION OF PHOTOPERIOD-INSENSITIVE GLUTINOUS RICE LINES WITH HIGH YIELD AND MULTI-STRESS RESISTANCE
RICE-34	GGE BIPLLOT ANALYSIS REVEALS YIELD STABILITY AND ADAPTABILITY OF AROMATIC RICE WITH MULTI-STRESS TOLERANCE
RICE-35	PRELIMINARY STUDY ON THE GROWTH RESPONSE AND NUTRIENT DISTRIBUTION OF FIELD MAIZE VARIETY SUWAN 5821 IN PHOSPHORUS AND ZINC DEFICIENT ENVIRONMENT WITH MYCORRHIZA INOCULATION GROWN IN SAND CULTURE.
RICE-36	INSIGHT INTO THE GENETICS OF A NOVEL WHITE-STRIPED LEAF IN RICE
RICE-37	THE EFFECT OF GERMINATION ON GAMMA-AMINOBUTYRIC ACID (GABA) CONTENT IN RICE GRAINS OF 'BAO YOD MUANG' AND 'RD79' VARIETIES
RICE-38	EVALUATION OF AGRONOMIC TRAITS, YIELD COMPONENTS AND YIELD OF LANDRACE UPLAND RICE COLLECTED FROM HIGHLAND GROWN IN CENTRAL PLAIN OF THAILAND
RICE-39	HOM CHONLASIT 2: A MULTI-STRESS-RESISTANT AROMATIC RICE VARIETY FOR FUTURE SUSTAINABLE FARMING
RICE-40	DEVELOPMENT OF THE SALT-TOLERANT, BLAST- AND BACTERIAL LEAF BLIGHT-RESISTANT FRAGRANT RICE VARIETY 'HOM SIAM 3' USING MARKER-ASSISTED BREEDING
RICE-41	INTROGRESSION AND SCREENING OF HEAT TOLERANCE QTL (<i>QHT4</i>) IN RICE F1-DOUBLE CROSS POPULATIONS
RICE-42	PRESERVING INTANGIBLE CULTURAL HERITAGE: THE THAM KHWAN KHAO NA RIM LE (RICE BLESSING RITUAL) OF THE PAK PRA COMMUNITY, SOUTHERN THAILAND

POSTER SESSION: VEGETABLE

VEGETABLE-01	BIOFORTIFICATION AND BIOMASS PRODUCTION OF <i>RAPHANUS SATIVUS</i> L. MICROGREENS CULTIVATED ON ORGANIC SUBSTRATE WITH PHOTOSYNTHETIC BACTERIAL APPLICATION
VEGETABLE-02	AGROBACTERIUM TRANSFORMATION EFFICIENCY IN CHERRY TOMATO CVS. RED RUBY AND SUNSHINE
VEGETABLE-03	TARGETED AROMA VOLATILE COMPOUNDS ASSOCIATED WITH CONSUMER PREFERENCES IN CHILLI
VEGETABLE-04	ORGANIC BIOSTIMULANT SYNERGY ENHANCING GROWTH AND PRODUCTIVITY OF CHINESE CABBAGE (<i>BRASSICA RAPA</i> VAR. <i>CHINENSIS</i>) USING VERMICOMPOST AND PHOTOSYNTHETIC BACTERIA
VEGETABLE-05	OPTIMIZING LIGHTING AND ECONOMIC PERFORMANCE FOR CALENDULA PRODUCTION IN PFALS
VEGETABLE-06	ELEVATED CO ₂ DIFFERENTIALLY AFFECTS GROWTH, PHOTOSYNTHESIS, AND PHYTONUTRIENT PROFILES OF TWO KALE CULTIVARS IN THE PLANT FACTORY WITH ARTIFICIAL LIGHTING
VEGETABLE-07	ARTIFICIAL POLLINATION IMPROVES THE YIELD OF GREENHOUSE CHERRY TOMATOES UNDER HIGH SUMMER TEMPERATURE
VEGETABLE-08	MORPHOLOGICAL CORRELATION OF CHILLI FLOWERS WITH MICROSPORE DEVELOPMENTAL STAGES FOR F ₁ HYBRID OF <i>CAPSICUM ANNUUM</i> L. 'CA365' X 'CA1191'
VEGETABLE-09	IMAGE ANALYSIS FOR PREDICTING AUTISM SPECTRUM DISORDER: A DEEP LEARNING APPROACH
VEGETABLE-10	AYUR-GENOMICS MEETS NEUROINFORMATICS: NGS AND IMAGE PROCESSING APPROACHES FOR ASSESSING THE THERAPEUTIC ROLE OF BRAHMI, ASHWAGANDHA, AND SHANKHPUSHPI IN AUTISM
VEGETABLE-11	IMPROVING CUCUMBER (<i>CUCUMIS SATIVUS</i> L.) CULTIVATION PRACTICES: EVALUATING THE IMPACT OF SPUNBOND COVERS ON YIELD, DISEASE REDUCTION, AND ECONOMIC SUSTAINABILITY
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POSTER SESSION: VEGETABLE

VEGETABLE-17	LOCAL WISDOM ON HERBAL UTILIZATION FOR COMMUNITY HEALTH IN PAPHAYOM AND THE THANAE RIVER BASIN, PHATTHALUNG PROVINCE
VEGETABLE-18	URBAN FOOD ENVIRONMENTS AND FRUIT AND VEGETABLE INTAKE AMONG VULNERABLE GROUPS IN BANGKOK: EVIDENCE FROM SENIORS, MIGRANTS, AND MONKS
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VEGETABLE-20	MALDI-FINGERPRINT PROFILING REVEALS MOLECULAR SIGNATURE OF CUCUMBER SEED AGING
VEGETABLE-21	IDENTIFICATION OF <i>COLLETOTRICHUM</i> SPP. CAUSING ANTHRACNOSE DISEASE ON CHILI AND EVALUATION OF RESISTANCE IN IMPROVED BREEDING LINES
VEGETABLE-22	DEVELOPMENT OF METHODS FOR SEED QUALITY ASSESSMENT DURING SEED PRODUCTION
VEGETABLE-23	IMPACT OF HOME GARDENING AND NUTRITION SUPPORT ON WOMEN IN REFUGEE CAMPS IN COX'S BAZAR, BANGLADESH
VEGETABLE-24	QUANTIFICATION OF HERBICIDE RESIDUES IN FRUITS AND VEGETABLES USING ISOTOPE DILUTION BY GC-MS AND MULTIPOINT CALIBRATION
VEGETABLE-25	A COMPARATIVE STUDY OF FIVE IMPORTANT METABOLIC COMPOUNDS IN THAI HOLY BASIL GERmplasm
VEGETABLE-26	CHILLING INJURY TOLERANCE SCREENING IN THE THAI HOLY BASIL GERmplasm
VEGETABLE-27	DEVELOPMENT OF AN OPTIMISED <i>IN VITRO</i> POLLEN GERMINATION PROTOCOL FOR HOLY BASIL (<i>OCIMUM TENUIFLORUM</i> L.)
VEGETABLE-28	PYRAMIDING OF TWO QTLs FOR BACTERIAL WILT RESISTANCE IN A SEEDATIP TOMATO CULTIVAR BY MARKER ASSISTED BACKCROSSING (MAB)
VEGETABLE-29	ASSESSMENT OF GENETIC DIVERSITY AND POPULATION STRUCTURE IN HOLY BASIL USING WHOLE-GENOME SEQUENCING
VEGETABLE-30	PHENOTYPIC DISTRIBUTION OF THE AROMATIC TRAIT IN A BI-PARENTAL POPULATION OF HOLY BASIL (<i>OCIMUM TENUIFLORUM</i> L.)
VEGETABLE-31	IMPACTS OF BEAN COMMON MOSAIC VIRUS INFECTION ON QUALITY AND QUANTITY OF BUTTERFLY PEA (<i>CLITORIA TERNATEA</i> L.) FLOWERS
VEGETABLE-32	EFFECT OF GAMMA IRRADIATION ON SEED GERMINATION AND EARLY GROWTH IN <i>OCIMUM</i> SPECIES

CALLUS INDUCTION AND REGENERATION EFFICIENCY IN THREE COMMERCIAL THAI RICE CULTIVARS

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Abstract:

Rice is a vital crop in Thailand, serving as a primary source of consumption, export, and manufacturing. To maintain competitiveness in rice production, it is necessary to develop new varieties with targeted traits. Genome editing provides a significant advantage over conventional breeding by enabling precise modifications within the rice genome. Three commercial rice cultivars, RD79, RD85, and RD111, were selected based on their high yield and disease resistance. Four callus induction media (C11-C14) and three regeneration media were evaluated. The progression of rice callus and embryonic callus formation was systematically monitored. C13 medium produced the highest rates of callus induction (90-92.5%) and embryogenic callus induction (55-65%). Callus induction and regeneration efficiency varied by genotype, with RD111 demonstrating the highest efficiency, followed by RD79 and RD85.

Keywords: *Oryza sativa*, genome editing, callus induction

MODELING AND EXPERIMENTAL INSIGHTS INTO CADMIUM-INDUCED ROOT TRAIT ALTERATIONS AND THEIR IMPACT ON NITRATE UPTAKE AND CARBON ALLOCATION IN RICE

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Abstract:

Cadmium (Cd) contamination in agricultural soils threatens rice productivity by impairing root development and nutrient uptake. To investigate these effects, a root pouch experiment with two rice varieties (IR64 and KDML105) was combined with OpenSimRoot simulations to assess Cd-induced changes in root traits, nitrate uptake, and carbon (C) allocation. At 10 ppm Cd, IR64 showed a 21.5% reduction in primary root growth rate and a 19.2% decrease in seminal root growth rate, whereas KDML105 displayed a 2% increase in primary root growth rate but a 12% decrease in seminal root growth rate. Both varieties exhibited significantly reduced lateral root branching density (LBD) on seminal roots. Simulations revealed that Cd-affected root growth rates reduced nitrate uptake by 28.4% in IR64 and 11.2% in KDML105. The strongest reduction in C allocation to roots occurred in IR64 (39.2%). In contrast, reduced LBD had little effect on nitrate uptake, but in KDML105 it caused the greatest reduction in C allocation to roots (39.1%). Additionally, IR64 exhibited the largest decrease in C allocation to shoots. When Cd and N stresses co-occurred, simulations identified an optimal phenotype with 60 seminal roots and a 30° growth angle that maximized nitrate uptake and C allocation to both shoot and root. Overall, Cd toxicity alters root growth and function in genotype- and root class-specific ways. Model-guided insights, integrated with experimental validation, highlight root phenotypes that could support breeding of rice varieties resilient to heavy metal stress.

Keywords: cadmium, carbon allocation, nitrogen, OpenSimRoot, *Oryza sativa*

GENOTYPIC VARIATION IN ROOT ANATOMICAL TRAITS AND ITS ROLE IN CARBON SEQUESTRATION IN RICE

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Abstract:

Developing low-carbon rice is an emerging strategy to enhance soil carbon sequestration while improving crop sustainability. Rice roots play a central role in this process, as their anatomical traits influence carbon investment in the root system and rhizosphere. Lignification and suberization in the hypodermis and endodermis form barriers to radial oxygen loss and promote carbon accumulation belowground. In this study, we evaluated Specific Root Length (SRL), defined as root length per unit dry weight, as an indicator of carbon allocation in rice roots. A panel of 102 rice varieties was assessed for SRL alongside Casparian strip, hypodermis, and stele traits. Results revealed wide genotypic variation, with high-SRL varieties such as KDML105 (140,848 cm.g⁻¹) and RD103 (62,980 cm.g⁻¹), and low-SRL varieties including Riceberry (10,976 cm.g⁻¹) and Gra Dang Ngah Plus 17F3 (6,932 cm.g⁻¹). Principal Component Analysis indicated that Casparian strip ratio, hypodermis ratio, and stele ratio strongly influence carbon investment in roots. Notably, Casparian strip and hypodermis ratios were positively correlated, while stele ratio was independent of other traits. These findings highlight that rice root anatomical characteristics significantly shape carbon allocation patterns. Insights from this study provide a foundation for breeding rice varieties with root structures that are efficient in water and nutrient uptake while simultaneously maximizing carbon sequestration in soils.

Keywords: Root anatomical traits, Specific root length, Carbon investment, Carbon Sequestration

FARMERS' AWARENESS AND WILLINGNESS TO PARTICIPATE IN CARBON MARKETS IN THAILAND

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Abstract:

Thailand is one of the leading producers and exporters of rice, and at the same time contributes substantially to greenhouse gas (GHG) emissions. Rice cultivation is the main GHG contributor in Thailand's agriculture sector. At present, reducing GHG emissions in rice farming is voluntary, and there is no carbon market for rice farming in Thailand. A well-designed carbon market for rice farmers is needed to ensure their engagement in GHG emission reduction program.

This study aims to assess rice farmers' willingness to accept (WTA) carbon credit incentives and participate in the carbon market by adopting climate-smart agriculture (CSA) practices including Alternate Wetting and Drying (AWD), Direct-Seeded Rice (DSR), and Rice Straw Management (RSM). The choice experiment, which included hypothetical carbon market systems, was undertaken with 401 rice farmers from Thailand's irrigated production areas during the 2023/2024 dry cropping season. The results show that most farmers had at least heard of AWD, DSR, and RSM concepts. Financial incentives were a major reason to adopt CSA practices. On average, farmers estimated they would need about 1,228 THB/ha as an incentive to participate. The choice experiment revealed that financial incentives are important, but that shorter contract duration is generally preferred. Training and technical support are also valued, but to a lesser extent than financial considerations and contract duration. Participation in carbon markets was found to also be influenced by neighboring farmers; thus, achieving a critical mass of adopters within each community is key, along with capacity building to raise awareness and understanding of the carbon market.

Keywords: Carbon market, Choice experiment, Alternative wetting and drying, Climate smart agriculture

COMPARATIVE STUDY ON NUTRITIONAL AND BIOACTIVE PROPERTIES OF ORGANIC BROWN SANGYOD AND JASMINE RICE

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Abstract:

This experimental study compared the nutritional properties and health benefits of organic Sangyod and Jasmine brown rice varieties, analyzing proximate compositions, vitamins, minerals, and bioactive compounds while evaluating antioxidant and anticancer activities. Results revealed significant differences ($p < 0.05$) between the two varieties, with Sangyod brown rice exhibiting higher protein content and vitamin B1 levels, while Jasmine rice contained more fiber and carbohydrates. Sangyod demonstrated superior bioactive compound concentrations, including phenolic compounds (100.52 mg GAE/100g) and anthocyanins (18.35 mg CG/100g) compared to Jasmine rice, though gamma-oryzanol levels showed no significant difference. Regarding health properties, Sangyod brown rice displayed significantly stronger antioxidant activity ($p < 0.05$) with an IC₅₀ value of 2.06 mg/ml versus Jasmine's 4.43 mg/ml, and proved more effective against colon cancer cells, achieving 61.32% growth inhibition at 200 µg/ml concentration compared to Jasmine's 78.94% cell viability. The study concluded that organic Sangyod brown rice possesses outstanding nutritional value and bioactive compounds, particularly excelling in protein, vitamin B1, phenolic compounds, and anthocyanins, while demonstrating superior antioxidant capacity and anti-colon cancer properties compared to brown Jasmine rice, making it a promising candidate for health food product development.

Keywords: Nutritional value, Bioactive compound, Brown rice, Organic

BRASSINOSTEROID FOLIAR SPRAYING IMPROVES THERMOTOLERANCE AND REPRODUCTIVE YIELD OF KDML105 RICE UNDER HIGH TEMPERATURE STRESS AT REPRODUCTIVE STAGE

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Abstract:

Heat stress during the reproductive stage exposes a critical threat to rice productivity, particularly in Thai aromatic rice such as KDML105. This study evaluated the role of brassinosteroid (BR) foliar application (0, 0.05, 0.1 and 0.5 nM) in mitigating the adverse effects of high temperature stress (at 42°C for 7 days) on the photosynthetic performance, membrane stability, yield components and yield in KDML105 at booting and 50% flowering stages. Results showed that heat stress significantly reduced photosynthetic efficiency, membrane integrity, and grain yield. However, BR application, especially at 0.5 nM BR, alleviated these negative impacts by enhancing PSII efficiency, photosynthetic gas exchange and yield, while reducing electrolyte leakage and lipid peroxidation under heat stress. In addition, these physiological improvements in KDML105 contributed to enhance reproductive performance, with increased filled grains and higher grain yield under both unheat and heat stress conditions, especially at 50% flowering stage. The findings suggest that exogenous BR application at the reproductive stage is an effective strategy to improve thermotolerance and sustain yield in rice, offering a potential adaptation approach to future climate change scenarios.

Keywords: Brassinosteroid, heat, physiology, rice, reproductive stage

USE CASE PROTOTYPES FOR A KNOWLEDGE PLATFORM PROMOTING HOME-GROWN RICE SELF-SUFFICIENCY

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Abstract:

Amidst economic slowdown and rising unemployment, rice cultivation and self-consumption have become pivotal for household food security and self-reliance. Various types of rice, such as brown rice and Riceberry, offer robust nutritional benefits, including high fiber, essential vitamins, minerals, and antioxidant compounds that support sustainable health. As land for agriculture becomes limited, efficient growing techniques such as vertical rice farming and container planting allow people in urban environments to produce rice for their own needs. However, a lack of consolidated practical guidelines and advisory systems prevents individuals from maximizing these benefits. This review highlights the economic and health challenges driving the urgent need for an integrated knowledge platform focused on rice-based self-sufficient nutrition. The proposed solution includes clear cultivation tutorials, nutritional information, and community knowledge sharing, enabling urban and rural residents to grow diverse rice varieties at home, improve dietary quality, and reduce reliance on external food sources. By addressing these gaps, the system supports resilience in the face of economic instability and empowers individuals toward long-term food and health security.

Keywords: self-reliance, household rice farming, brown rice, Riceberry, food security

GENOME-WIDE ASSOCIATION STUDY (GWAS) REVEALS ENDOSPERM-SPECIFIC GENES (OSENS) AND WX GENE REGULATING SEED STORAGE PROTEIN (SSP) IN RICE GRAIN (*ORYZA SATIVA* L.)

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Abstract:

Rice (*Oryza sativa* L.) is a crucial source of carbohydrates and protein, essential for human nutrition. Seed storage proteins (SSPs) play a significant role in determining rice's nutritional and culinary attributes. Despite the importance of SSPs, the genetic basis for these traits remains unclear. This study aimed to identify SSP-related genes through the analysis of 2 seasons of indica rice varieties, including 2018 and 2019, using 189 and 210 accessions of indica rice varieties from the Thai rice germplasm, respectively. The SSPs were quantified using Bradford's method, and genotype-phenotype associations were examined via a Genome-Wide Association Study (GWAS) using GLM models. We identified 9 quantitative trait loci (QTLs) associated with SSPs across 7 chromosomes (2, 6, 7, 8, 9, 11, and 12). Interestingly, a QTL on chromosome 7 (qSSP7) was consistently identified in 2 seasons. Within a 400-kb window, linkage disequilibrium analysis (LD) revealed 27 genes, with 8 containing functional SNPs. Gene expression analysis (RiceXpro database) identified 5 candidate genes that are highly expressed in the rice endosperm. Based on Co-expression network analysis (RiceFRIEND database), our 4 identified candidate genes (Os07g0213600, Os07g0213800, Os07g0214100, and Os07g0214300) are involved in essential endosperm-specific regulation with seed storage protein regulatory genes such as GLUD1 (Glutelin type-D 1) and prolamin-related genes. Therefore, these candidate genes are suggested to be involved in SSPs regulation. Our findings provide novel insights into the genetic mechanisms controlling protein synthesis and accumulation in rice, which may aid breeding programs focused on improving SSPs content.

Keywords: GWAS, Seed storage protein

DEVELOPMENT OF HIGH-FIBER DRIED RICE NOODLES FORTIFIED WITH RED SEAWEED (*GRACILARIA FISHERI*)

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Abstract:

Rice noodles, made from rice flour, are widely consumed as a staple food in Asia however, they are typically low in nutrients, particularly dietary fiber his study aimed to enhance the fiber content of dried rice noodles by fortifying them with red seaweed (*Gracilaria fisheri*), which contains approximately 64% dietary fiber. Red seaweed powder was incorporated into rice noodle formulations at concentrations of 0–25% (w/w). The addition of 25% red seaweed significantly increased dietary fiber content by approximately 32-fold compared with the control, allowing the product to meet the criteria for a “high-fiber” claim under Thai FDA regulations. The cooking time of dried rice noodles decreased significantly when the red seaweed content exceeded 25%. However, the incorporation of red seaweed disrupted the starch matrix, resulting in higher cooking loss, and decreased noodle firmness and extensibility. These findings indicate that the incorporation of red seaweed can enhance the nutritional of rice-based noodles, offering a promising approach to developing healthier rice-derived products.

Keywords: rice noodles, seaweed, gluten-free, dietary fiber, texture

OPTIMIZING N6D MEDIA COMPOSITION FOR ENHANCED SECONDARY EMBRYOGENIC CALLUS FORMATION IN THAI RICE VARIETIES (*ORYZA SATIVA* L.)

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Abstract:

Rice (*Oryza sativa* L.) is one of the most vital staple crops worldwide, providing the main source of calories for more than half of the global population. Beyond its nutritional value, rice quality traits such as texture, flavor, and particularly aroma play a significant role in consumer preference and market value. Recent advances in genome editing technologies, especially CRISPR-Cas9, have opened new possibilities for precise genetic improvement in rice, including the enhancement of desirable traits such as aroma. However, the successful application of CRISPR-Cas9 in rice remains limited by challenges in tissue culture preparation, especially the development of suitable embryogenic callus tissues required for transformation and regeneration.

In this study, two modified N6D media were formulated and evaluated for their effectiveness in inducing callus formation from three Thai rice varieties: RD79, RD85, and RD111. The results revealed that increasing the concentration of casein hydrolysate, an organic nitrogen source, while decreasing the level of L-proline, significantly improved the induction and development of secondary embryogenic calli. These calli are crucial for efficient gene editing and subsequent plant regeneration. This finding highlights the importance of optimizing culture media composition to enhance tissue culture responses, which could ultimately facilitate more effective CRISPR-Cas9-based genome editing in rice. Such improvements in callus induction protocols may accelerate the breeding of rice varieties with superior aroma and other desirable traits.

Keywords: Rice, Callus induction, Secondary embryogenic calli

IDENTIFICATION OF ROOT RESPONSIVE GENES UNDERLYING PENETRATION ABILITY IN COMPACTED SOIL USING QTL-SEQ IN RICE (*ORYZA SATIVA* L.)

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Abstract:

Nowadays, many agricultural areas have been becoming modern agriculture, where heavy machinery and equipment have been intensively used. According to increasing crop intensity and reducing labor. Meanwhile, heavy machinery loads result in soil compaction, which has been affecting plant growth, which influence plant yield. The stunning root growth under compacted soil is directly contributed by restricted ethylene diffusion and the crosstalk between auxin, ABA, and ethylene. This study aims to screen and evaluate root-responsive characteristics under ethylene treatment and to identify genomic regions associated with root sensitivity to compaction by using three different systems. Firstly, the ethylene chamber system was used to evaluate the ethylene sensitivity in the root. Next, we developed a bi-parental population by crossing Dharia and PTT1 and used the F2 progeny to perform QTL-seq for root penetrating ability (RPA) under a compacted gel-based system. As a result, significant QTLs on chromosome 3 were identified for RPA ($p < 0.01$). Ten promising candidate genes for RPA were identified based on annotation, variant effect and literature mining. Notably, LOC_Os03g18600 (OsPYL/RCAR4), an ABA receptor, LOC_Os03g18910 (OsBCL1), COBRA-Like (COBL) family protein and LOC_Os03g19310 (OsGT4), a galactosyl transferase family protein, were identified as potential regulators of root responses under stress conditions. In addition, we also evaluated the root response between control and soil compaction treatments among parents. The results in this study pave the way for further research into the genetic mechanism of root penetration ability in rice at the seedling stage and could be used as breeder-friendly markers in future breeding programs.

Keywords: QTL-Seq, Rice, Root, Compaction, Penetration ability

SELECTION AND DEVELOPMENT OF A MICROBIAL CONSORTIUM PROTOTYPE FOR EFFICIENT AND SAFE DECOMPOSITION OF RICE STRAW AND STUBBLE AS AN ALTERNATIVE TO OPEN BURNING AND TO SUPPORT SUSTAINABLE RICE PRODUCTION

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Abstract:

The open burning of rice straw and stubble is a major source of environmental degradation, air pollution, and health risks, while depleting soil organic matter and nutrients. This study aimed to isolate, select, and develop microbial prototypes for straw and stubble decomposition as a sustainable alternative to burning. Microorganisms were isolated from 240 soil and straw samples collected from Chiang Mai, Phitsanulok, Chainat, and Phetchabun provinces. Screening was conducted through plate and enzyme assays, followed by species identification using 16S rRNA and ITS sequencing. Selected strains were evaluated in a 60-day simulated composting system and safety-tested on rice cultivar RD43. A total of 126 isolates (68 bacterial, 58 fungal) were obtained. Among them, *Bacillus subtilis* (cellulase 4.2 ± 0.3 U/mL; xylanase 3.8 ± 0.4 U/mL) and *Trichoderma harzianum* (laccase 2.7 ± 0.2 U/mL; lignin peroxidase 1.9 ± 0.1 U/mL) showed the highest enzyme activities ($p < 0.01$). Co-inoculation of *B. subtilis* + *T. harzianum* accelerated decomposition, reducing straw mass by 42.6% within 45 days compared to 26.9% in the control ($p < 0.05$). The C/N ratio declined from 48.2 to 24.5 after 60 days. No mycotoxin or inhibition of rice germination (>92%) was observed. The consortium remained stable for six months at room temperature (> 10^7 CFU/g). In conclusion, *B. subtilis* + *T. harzianum* (1:1) exhibited the highest efficiency and is suitable for bio-inoculant development, reducing CH₄ and N₂O emissions by 28% and 19%, respectively, while enhancing soil organic carbon (0.35–0.48 t C rai⁻¹ season⁻¹).

Keywords: microbial decomposition, *Bacillus subtilis*, *Trichoderma harzianum*, rice stubble management, no-burn, GHGs emissions, sustainability agriculture

SILICON-INDUCED RESISTANCE IN RICE (*ORYZA SATIVA* L. CV. NIAW DAM CHOR MAI PAI 49): AN ECO-INNOVATIVE STRATEGY FOR SUSTAINABLE MANAGEMENT OF RUSTY PLUM APHID (*HYSTERONEURA SETARIAE* THOMAS)

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Abstract:

Sustainable rice production requires innovative, environmentally friendly strategies to manage insect pests while minimizing chemical pesticide use. This study investigated the role of silicon (Si) supplementation in enhancing insect resistance in the Thai indigenous rice cultivar Niew Dam Chor Mai Pai 49. Plants were grown under greenhouse conditions and treated with calcium silicate (Ca_2SiO_4) at 0%, 2%, and 4% (w/w). The effects on silicon accumulation, aphid infestation, and defense-related enzyme activities—peroxidase (POD), polyphenol oxidase (PPO), and phenylalanine ammonia-lyase (PAL)—were evaluated. Results revealed that Si-treated plants exhibited higher silicon accumulation in leaf tissues, increased silica cell area, and significantly lower aphid populations compared with untreated controls. Moreover, Si supplementation activated key defense enzymes associated with induced resistance mechanisms. These findings demonstrate that Si fertilization not only strengthens the physical and biochemical defense systems of rice but also provides a sustainable and innovative approach for integrated pest management (IPM). Incorporating silicon into nutrient management programs could therefore reduce pesticide dependence and promote resilient rice cultivation systems in Southeast Asia.

Keywords: sustainable rice production, silicon fertilization, aphid resistance, integrated pest management, plant defense enzymes

QUANTITATIVE TRAIT LOCUS (QTLs) MAPPING FOR RICE STOMATAL MEGA-PAPILLAE USING QTL-SEQ AND GENOME-WIDE ASSOCIATION STUDIES

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Abstract:

Rice, the world's second largest cereal, plays a crucial role in human food security. Climate change is affecting rice production, particularly through water shortages. Similar to other plants, rice uses stomata to maintain the balance between CO₂ uptake and water loss depending on climatic conditions. Unique to rice are special epidermal protrusions on the subsidiary, the so-called papillae. We have observed a large number of papillae on the stomata of subsidiary, known as "mega-papillae", which partially cover the stomata. This structure potentially enhances water use efficiency. However, the genetic components that control the development of mega-papillae are still undiscovered. In this study, we identified quantitative trait loci (QTLs) that control mega-papillae development. We performed QTL-seq analysis in the F₂ population of Pathum Thani 1, a variety with normal papillae, and Dharia, a variety with mega-papillae, and identified 1 QTLs on chromosomes 5 based on the delta SNP index. In addition, genome-wide association studies (GWAS) for QTL identification were performed with a diversity panel, resulting in the identification of seven associated regions on chromosomes 2 and 5 across three statistic models (GLM, MLM and FarmCPU). The most promising QTL is located on chromosome 5, which is stable in both the QTL-seq and GWAS approaches. This candidate QTL could be useful in future breeding programs to improve water use efficiency.

Keywords: Rice, stomata, mega-papillae, GWAS, climate change

THE OSCIPK9 GENE NEGATIVELY REGULATES SALINE-ALKALI STRESS TOLERANCE IN RICE

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Abstract:

Saline-alkali stress is a major abiotic constraint on rice growth, causing nutrient deficiency and oxidative damage. The calcium-signaling CBL-CIPK network is a key mediator of stress responses, in part through the regulation of reactive oxygen species (ROS). In this study, we identify *OscIPK9* as a critical negative regulator in the rice saline-alkali stress response. Transcriptomic profiling and qRT-PCR analysis showed that *OscIPK9* is rapidly upregulated in roots under stress conditions. Phenotypic assessment under saline-alkali stress revealed that *Oscipk9* loss-of-function mutants had significantly improved germination rates, root length, and recovery, whereas overexpression lines were hypersensitive. Furthermore, mutants maintained higher chlorophyll content and photosynthetic efficiency, alongside elevated activities of ROS-scavenging enzymes and gene expression, resulting in lower malondialdehyde (MDA) accumulation. Overexpression lines showed the opposite trends. Our findings establish that *OscIPK9* negatively modulates saline-alkali tolerance by impairing ROS homeostasis.

Keywords: CIPK9, Rice, ROS scavenging, Saline-alkali stress

INFLUENCE OF LOW EARTH ORBIT ON AROMA, TEXTURE, AND PROTEIN DIGESTIBILITY OF THAI LANDRACE RICE (466HM) CULTIVATED ABOARD THE SHIJIAN-19 MISSION

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Abstract:

Developing sustainable and nutritious food sources is a prerequisite for supporting extended human presence in space. Thai landrace rice 466HM, recognized for its nutritional quality and resilience to stress, represents a potential crop for extraterrestrial farming systems. Nevertheless, there is limited understanding of how spaceflight alters its compositional and functional properties. In this study, rice grains cultivated on Earth were compared with those grown during the Shijian-19 (SJ-19) low Earth orbit mission, which maintained an altitude of approximately 336 km for 13.5 days under microgravity conditions ($2-7 \times 10^{-7}$ g). Environmental monitoring indicated an absorbed radiation dose of ~ 0.153 rad (Si), measured using an integrated silicon dosimeter. Analyses encompassed volatile compound profiling, assessment of cooked grain texture, and in vitro gastrointestinal digestion followed by peptide mass fingerprinting. Results revealed that space-grown rice exhibited greater adhesiveness while maintaining comparable hardness to Earth controls. Notable differences were also detected in volatile organic compounds and peptide digestion profiles, with principal component analysis clearly separating Earth and orbital samples, signifying microgravity-associated shifts in peptide composition. Cytotoxicity assays using HT-29 and HepG2 cell lines confirmed that both sample types were non-toxic, underscoring their safety for dietary use. Overall, these findings demonstrate that orbital cultivation modifies the sensory, biochemical, and nutritional attributes of rice, providing essential insights into crop adaptation and food security strategies for future space missions.

Keywords: space-grown rice, microgravity, nutritional properties, peptide profiling, volatile compounds

INNOVATION OF MICROBIAL FOR AGRICULTURAL RESIDUE DECOMPOSITION INTEGRATED WITH RICE PRODUCTION TECHNOLOGY TO ENHANCE PRODUCTIVITY AND SUSTAINABLE NO- BURN FARMING IN NONTHABURI PROVINCE

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Abstract:

Rice cultivation in irrigated areas faces major challenges in managing post-harvest residues, especially straw and stubble that are often disposed of by open burning, leading to greenhouse gas emissions, PM_{2.5} pollution, and nutrient loss. Microbial technology offers a sustainable solution by decomposing cellulose- and lignin-rich residues into organic matter and returning nutrients to the soil. This study aimed to promote sustainable straw and stubble management using microbial decomposition technology integrated with rice production innovations under the Technology Verification Experiment (TVE) in Nonthaburi Province during 2023–2024 with 24 participating farmers. The application of microbial inoculants (100 g/rai) significantly ($p < 0.05$) increased soil organic matter (4.02–4.04%), available phosphorus (23.2–37.0 mg/kg), and potassium (207.7–263.5 mg/kg). Rice yield increased by 117–236 kg/rai (21.0–29.4%), production costs decreased by 699–1,870 THB/rai (17.5–34.0%), and net profit rose by 3,573–6,083 THB/rai (49.0–93.1%) compared with conventional practice. Microbial treatment also reduced volunteer rice and ratoon regrowth significantly ($p < 0.05$). Farmers reported the highest satisfaction and acceptance ($= 4.45–4.46$), especially for microbial decomposition, alternate wetting and drying, and drone-based seeding and spraying technologies. Overall, microbial decomposition of rice residues enhanced soil fertility, yield, and profitability while eliminating residue burning and reducing environmental impacts. The integration of microbial technology with smart rice farming practices demonstrates strong potential for scaling up at both field and policy levels toward sustainable, no-burn rice production systems.

Keywords: innovation, microbes, rice straw and stubble, no-burn, sustainability

COMPARATIVE EFFECTS OF RICE VARIETIES ON THE QUALITY OF DRIED BROWN RICE PASTA

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Abstract:

This study investigated the effects of three rice varieties—Chainat1, Pinkaset4.1, and Pinkaset4.2—on the cooking quality, textural properties, and sensory evaluation of dried brown rice pasta. Among the samples, pasta from Pinkaset4.1 showed the lowest proportion of broken strands after cooking. The optimal cooking time of Chainat1 pasta was approximately one minute shorter than that of the other varieties, while cooking loss did not differ significantly. Pinkaset4.1 pasta exhibited superior textural properties, with firmness and tensile strength comparable to commercial wheat pasta, and it demonstrated the highest elongation ($147.46 \pm 5.97\%$). Sensory evaluation revealed that Pinkaset4.1 pasta received the highest scores for flavor, elasticity, and stickiness. These results indicate that Pinkaset4.1 is the most promising variety for producing high-quality, gluten-free brown rice pasta.

Keywords: gluten-free, low GI, rice pasta, texture

VALORIZATION OF RICE STRAW AND STUBBLE INTO CLEAN ENERGY THROUGH MOBILE BIOMASS PELLETIZING MACHINE INNOVATION UNDER THE BCG ECONOMY

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Abstract:

Rice is Thailand's major economic crop, cultivated on over 70 million rai with an annual production of 31 million tons. However, about 42 million tons of rice residues (straw and stubble) are generated yearly, most of which are burned, causing severe environmental and climate impacts. This project aimed to transfer and scale up non-burning residue management technology using microbial decomposition integrated with an innovative mobile biomass pelletizing machine under the BCG economy model. Implemented in Nonthaburi, Pathum Thani, and Bangkok, the project covered 150 farmers across 3,000 rai through three main activities. (1) Knowledge transfer: Before training, residue burning was practiced by 42% of farmers, while 28.7% plowed residues and 13.3% sold straw. After training, farmers showed very high satisfaction (mean = 4.86) and requested continued government support. (2) Technology verification: The integrated microbial-mechanization approach reduced burning on 1,872 rai (87 farmers), decreased production costs by 1,114–1,968 Baht/rai, and increased net income by 2,424–3,471 Baht/rai—equivalent to 2.09–3.68 million Baht in total economic benefit. (3) Technology extension: 92 farmers (2,091 rai) gained additional income (209,100 Baht) from selling straw for biomass pellet production via the mobile machine collaboration with VRP Development Holdings Co., Ltd. Environmentally, the project reduced approximately 1,464 tons CO₂e emissions (0.7 ton CO₂e/rai) and mitigated PM 2.5 pollution, promoting sustainable rice farming. In conclusion, the project enhanced productivity, lowered costs, reduced open burning, and added value to agricultural residues, demonstrating strong potential for sustainable, low-carbon agriculture under the BCG economy framework.

Keywords: agricultural residues, microbial, biomass pellet, sustainability, BCG economy

MAPPING AND SPATIAL CLUSTERING OF RICE BLAST DISEASE IN THAILAND FOR TARGETED MANAGEMENT

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Abstract:

Rice blast disease remains a major constraint to rice production across Thailand, yet its spatial distribution has not been well characterized at the national scale. Identifying where disease clusters occur is essential for developing cost-effective and site-specific management strategies. Between 2023 and 2024, rice blast incidence was surveyed across 1,381 farmers' paddy fields nationwide. Geostatistical analyses combining Inverse Distance Weighting (IDW) interpolation and Local Moran's I statistics were applied to examine spatial distribution and clustering patterns and to identify high-risk areas for rice blast. Results from the Local Moran's I analysis revealed that most provinces exhibited positive spatial autocorrelation ($I > 0$), particularly across the northern and lower northern regions, indicating strong local clustering of disease incidence. In contrast, several western and lower northeastern provinces displayed negative spatial association ($I < 0$), reflecting isolated or low-risk areas. Significant positive spatial dependence ($p < 0.05$) was detected in Nan, Phitsanulok, Lamphun, and Chai Nat, whereas negative dependence ($p > 0.05$) occurred in Buriram and Surin. Spatial interpolation further supported these patterns, with IDW providing finer resolution of disease gradients across the landscape. The disease was most widespread in the northern and upper central regions, with moderate clustering in parts of the east. Conversely, the northeast and south showed localized foci of infection, particularly near Udon Thani, Ubon Ratchathani, and Sakon Nakhon, where outbreaks were spatially limited. These results underscore the spatial heterogeneity of rice blast distribution and provide practical insights for prioritizing surveillance and implementing targeted management in high-risk zones.

Keywords: Rice blast disease, Spatial distribution, Geostatistical interpolation, Thailand, Targeted disease management

ENHANCEMENT OF DROUGHT TOLERANCE IN THAI JASMINE RICE (KDML105) BY STREPTOMYCES THERMOCARBOXYDUS ISOLATE S3 ASSOCIATED WITH ARBUSCULAR MYCORRHIZAL FUNGUS FUNNELIFORMIS MOSSEAE

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Abstract:

Water deficit stress imposes a range of negative impacts on the biochemistry, morphology, and physiological processes that are directly related to plant development and crop yield in rice (*Oryza sativa*). The rice life cycle can be classified into three growth stages, among which the maturity phase or reproductive phase has been shown to be the most sensitive to reduced water availability. *Streptomyces thermocarboxydus* isolate S3 was isolated from the spores of *Funneliformis mosseae*, and evidence suggests its potential agricultural use as a plant growth promoter both in vitro and in vivo. It exhibited variable capacities for indole-3-acetic acid (IAA) production, phosphate solubilization, and siderophore production. Inoculation with the drought-tolerant *S. thermocarboxydus* isolate S3 significantly improved the growth of Thai jasmine rice KDML105 cultivated under induced drought during both the reproductive and ripening stages. This improvement was observed in various growth parameters, including plant length, dry weight, relative water content (RWC), proline content, total chlorophyll content, and grain yield. Our results demonstrate that the arbuscular mycorrhizal spores of *F. mosseae* serve as a promising source of novel rare actinobacterial taxa, and the isolated endophytic actinobacterial strain is capable of promoting the growth of Thai jasmine rice KDML105 under drought conditions. Overall, this study supports the view that inoculation of rice with a plant growth-promoting actinobacterial strain can mitigate the adverse effects of drought stress on rice.

Keywords: actinobacteria, arbuscular mycorrhizal spore, *Funneliformis mosseae*, Plant growth-promoting activity, Rice (*Oryza sativa*), Reproductive stats, Drought stress

DISSECTING THE POLYGENIC BASIS OF BACTERIAL LEAF STREAK RESISTANCE IN RICE USING QTL-SEQ AND BULKED SEGREGANT WHOLE-GENOME SEQUENCING

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Abstract:

Rice, a crucial staple crop, is highly vulnerable to various stresses, including bacterial leaf streak (BLS), caused by *Xanthomonas oryzae* pv. *oryzicola* (Xoc), which can lead to up to 32% yield loss. Despite the importance of utilizing host plant resistance genes as a management strategy, only a limited number of resistance and defense -related genes have been identified to confer protection against BLS. In this context, a whole-genome resequencing and QTL-seq approach was employed on an F2 population derived from the cross between two Thai rice varieties Homcholasit (HCS- BLS susceptible variety) and Niaw Dam Chaw Mai Pai 49 (NDCMP49- BLS resistant variety) to explore the genetic underpinnings of resistance to this disease. Using the Thai Xoc isolate (1NY2-2), a critical QTL region on chromosome 2 was identified, encompassing 9,668 single nucleotide polymorphisms (SNPs), underscoring the complexity of BLS resistance. To refine candidate SNPs, nonsynonymous SNPs and insertions/deletions (InDels) were selected, with gene annotation performed using the Rice Annotation Project Database. This strategic filtration prioritized 16 candidate genes, including Os02g0597300 (NBS-LRR protein), Os02g0627100 (OsPAL1), Os02g0650500 (OsRLCK80), Os02g0726700 (OsBHLH034), and Os02g0606200 (OsBBX4), based on their known roles in pathogen response. RNA-seq further confirmed that these genes were significantly and differentially expressed during early infection stages, indicating their involvement in the resistance mechanism. This study offers valuable insights into the genetic basis of BLS resistance in rice, highlighting potential candidate genes for breeding programs aimed at developing BLS-resistant Thai rice varieties.

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

EFFECTS OF PESTICIDE APPLICATION METHODS ON THE DIVERSITY OF NATURAL ENEMIES IN RICE FIELDS AT CHIANG RAI PROVINCE

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Abstract:

Unmanned Aerial Vehicles (UAVs), or drones, play crucial roles in substituting manual labor in agricultural sector. This study examined effects of pesticide application methods on diversity of natural enemies in rice fields. The experiment was conducted at Chiang Rai Rice Research Center during the 2025 Dry season. The rice variety San-pah-tawng1 was cultivated using wet broadcasting method. A 3 × 2 + 1 factorial experiment was conducted using RCBD, comprising seven treatments with three replications, including a control treatment (water spraying) applied at the seedling stage. Insecticide carbaryl 85% WP and post-emergence herbicide fenoxaprop-P-ethyl 6.9% EW were applied either as single agents or in combination at recommended rates, using both XAG P100 drone (Model 3WWDZ-40AT) and motorized backpack mist blower. Insect populations were randomly sampled using D-vac suction device one day before spraying and at 3, 7, and 15 days after spraying. Insects were identified and counted, focusing on rice pests and natural enemies. Results showed that before pesticide application, six orders of natural enemies were recorded—Hemiptera, Araneae, Coleoptera, Hymenoptera, Diptera, and Odonata. After the application, an increase in Orthoptera was observed, and abundance of all orders increased, with Hemiptera being the most dominant. The Shannon–Wiener diversity index increased after pesticide application in both application methods, with the highest value observed in the control treatment and the lowest in manual application of carbaryl 85% WP. Overall, all application methods were generally harmless to natural enemies, except for a slight adverse effect observed in drone application of fenoxaprop-P-ethyl 6.9% EW.

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

PRODUCTION OF ANTIBODY AGAINST *XANTHOMONAS ORYZAE PV. ORYZICOLA* FOR EARLY SEROLOGICAL DETECTION OF RICE BACTERIAL LEAF STREAK

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Abstract:

Xanthomonas oryzae pv. *oryzicola* (XOA), the causal agent of rice bacterial leaf streak, represents a significant threat to rice production, with symptoms often mistaken for physiological disorders in rice plants. Accurate and early diagnosis is essential for effective management and disease containment. This study focused on generating a specific polyclonal antibody (PAb) against XOA by immunizing white New Zealand rabbits with glutaraldehyde-fixed XOA cells (10⁹ cells/ml). Antiserum was collected at two-week intervals over ten rounds, yielding high titers ranging from 1,000,000 to 2,560,000. Specificity analysis showed no cross-reactivity with other rice pathogens, including *X. oryzae* pv. *oryzae* and *Burkholderia glumae*, confirming the antibody's specificity for XOA. Sensitivity testing using indirect ELISA demonstrated that the antibody could detect XOA at concentrations as low as 10⁷ cells/ml. These results underscore the potential of this antiserum for reliable, early-stage detection of XOA infections. The specific antibody developed here offers promising applications in the creation of rapid diagnostic kits, which could greatly enhance disease monitoring and management strategies, supporting sustainable rice production.

Keywords: Rice bacterial leaf streak, *Xanthomonas oryzae* pv. *oryzicola*, polyclonal antibody, early detection, rapid diagnostic kit

PHYTOLITH MORPHOTYPES OF SELECTED GRASS (POACEAE) SPECIES IN THAILAND FOR ARCHAEOBOTANICAL RESEARCH

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Abstract:

Phytoliths—microscopic silica bodies formed within plant tissues—occur in various morphologies and are highly resistant to decomposition in soils and sediments. Owing to their preservation and taxonomic specificity, phytoliths serve as valuable proxies in paleo-ecological and archaeobotanical studies. Among plant families, Poaceae phytoliths produce the most abundant and diagnostic phytoliths in sediments. Wide-ranging research on grass phytoliths has greatly enhanced understanding of past vegetation and plant–human interactions. Rice (*Oryza sativa* L.), a major Poaceae crop, has long been central to human culture and subsistence. Nevertheless, archaeobotanical investigations in Thailand remain limited, particularly those that integrating botanical analysis as a key approach to advancing knowledge and interpretation within archaeological context. This study aims to develop a comprehensive phytolith reference collection from selected Poaceae species, emphasizing rice because of its considerable cultural and dietary importance. Phytoliths were extracted using wet oxidation technique from 3 plant parts —leaf, husk, and rachis—across 36 accessions including cultivated and wild rice, local landraces and grass weeds commonly found in Thai rice fields. Phytoliths were classified based on their morphological features (morphotypes), providing a reference framework for identifying and interpreting phytoliths recovered from archaeological sediments. The resulting collection represents a valuable resource for paleo-botanists, paleoecologists and archaeobotanists investigating ancient ecosystems and agricultural practices.

Keywords: Archaeobotany, Paleobotany, Phytolith, Rice, Thailand

PRODUCTION AND CHARACTERIZATION OF POLYCLONAL ANTIBODY AGAINST *XANTHOMONAS ORYZAE* PV. *ORYZAE* FOR EARLY DETECTION OF RICE BACTERIAL LEAF BLIGHT

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Abstract:

Rice bacterial leaf blight, caused by *Xanthomonas oryzae* pv. *oryzae* (XOO), poses a significant threat to rice cultivation globally, leading to substantial yield losses. Timely and accurate diagnosis is critical for effective disease management, and serological methods have proven valuable in this regard. This study reports the production of polyclonal antibody (PAb) specific to XOO, developed by immunizing New Zealand White rabbits with glutaraldehyde-fixed XOO cells (108 cells/ml). Antiserum was collected five times at two-week intervals, with the fifth collection showing the highest titer at 2,048,000. Specificity assays revealed that the produced antiserum could recognize other *Xanthomonas* species, including *X. oryzae* pv. *oryzicola* and *X. campestris* pv. *glycine*, without cross-reactivity to other non-*Xanthomonas* plant pathogens tested. Sensitivity evaluation by indirect ELISA demonstrated detection of XOO at a minimum concentration of 107 cells/ml. The high specificity and sensitivity of this antiserum make it a valuable tool for early disease detection in rice fields, enabling proactive management strategies to mitigate the impact of bacterial blight. The application of this antibody in field diagnostics promises to facilitate rapid and efficient disease surveillance, ultimately supporting food security in rice-dependent regions.

Keywords: Rice bacterial blight, *Xanthomonas oryzae* pv. *oryzae*, polyclonal antibody, early detection, serological diagnostics

INNOVATION IN REMOTE SENSING FOR AGRICULTURE: INTEGRATING FIELD SURVEYS AND SATELLITE DATA TO DEVELOP INDICES FOR MONITORING RICE YIELD IN SUPHAN BURI PROVINCE, THAILAND.

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Abstract:

Accurate monitoring of rice yield is crucial for food security and informed agricultural planning, especially in major rice-producing countries such as Thailand. Integrating remote sensing technology with ground-truth data offers a robust approach for precise rice yield assessment and forecasting, which is essential for sustainable resource management and production planning. This study aims to establish a rice yield forecasting system by combining satellite imagery with ground-truth yield data from the Suphan Buri province, Thailand. The research focuses on enhancing rice yield monitoring across 300 sites within this region during the 2018 growing season by integrating satellite-based remote sensing data with field survey information. Collaborations with key institutions, including the Geo-Informatics and Space Technology Development Agency (GISTDA), Kasetsart University (KU), and the National Science and Technology Development Agency (NSTDA), enabled the analysis of 39 satellite indices, such as ARVI, BI, EVI, GNDVI, NDVI, SAVI, and others, across the rice growth cycle. The results indicate that the average rice yield in Suphan Buri province was 587.9 kg/rai, with a minimum of 182.8 kg/rai and a maximum of 914.7 kg/rai. Ten indices showed highly significant association with rice yield, with MSAVI, NDRE2, MCARI demonstrating the strongest association (R^2 values of 0.434, 0.422, and 0.313, respectively). The multiple regression model achieved an R^2 value of 0.860, with a highly significant difference (p -value < 0.05). These correlations were used to develop a linear regression model for forecasting rice yield in Suphan Buri province.

Keywords: Remote Sensing, rice, MSAVI, NDRE2, MCARI

IDENTIFICATION OF STABLE AND HIGH-YIELDING AROMATIC GLUTINOUS RICE LINES ADAPTED TO RAINFED ECOSYSTEMS IN NORTHERN THAILAND

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Abstract:

Rice is a staple food worldwide, and glutinous rice is widely cultivated in the rainfed lowlands of Thailand and Laos. This study aimed to evaluate the yield stability of newly developed aromatic glutinous rice lines with resistance to blast disease, bacterial leaf blight, and submergence tolerance, bred through marker-assisted selection (MAS). Yield stability under variable environments remains a major challenge in sustainable rice production, with genotype × environment (G×E) interaction influencing grain yield and adaptability. Five elite aromatic glutinous rice lines were tested in multi-location trials at five sites (two in Lampang and three in Chiang Rai provinces) during 2019 using a randomized complete block design (RCBD). Grain yield data were analyzed using ANOVA and the Eberhart and Russell regression model to assess G×E interaction and yield stability. Significant effects of genotype, environment, and their interaction ($P < 0.05$) were observed. Mean yields ranged from 783 to 1,071 kg/rai, with GA1 and GA2 yielding 935 kg/rai, while GA5 and GA4 achieved the highest yields of 1,071 and 1,039 kg/rai, respectively. Although no genotype was fully stable across environments, GA1 ($b = 0.920$) exhibited better adaptability and consistent yield performance. These findings indicate that GA1 and GA2 have strong potential for wider adaptation and could be considered for release as stable, high-yielding aromatic glutinous rice varieties for rainfed regions of northern Thailand.

Keywords: Rice breeding, Glutinous rice, Yield stability, Marker-assisted selection

IDENTIFICATION AND FUNCTIONAL CHARACTERIZATION OF BACTERIAL LEAF BLIGHT RESISTANCE CANDIDATE GENE USING CRISPR/CAS9 TECHNIQUE

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Abstract:

Rice is one of the most important staple crops worldwide, particularly in Asia. However, its production is often limited by various abiotic and biotic stresses. In Thailand, bacterial leaf blight (BLB), caused by *Xanthomonas oryzae* pv. *oryzae* (Xoo), is a major biotic factor leading to severe yield losses. One of the most effective strategies against bacterial leaf blight is the use of resistance genes in rice. Given this importance, this research aims to identify and characterize a gene function using the CRISPR/Cas9 technique. Among 93 candidate genes identified from a GWAS dataset, LOC_Os1lg40840 showed significant expression in quantitative PCR (qPCR) analysis and was selected for functional characterization. This gene is predicted to encode a receptor-like protein kinase 2 precursor. CRISPR/Cas9 constructs targeting the first exon of LOC_Os1lg40840 were introduced into the rice variety Nipponbare through Agrobacterium-mediated transformation. Sequence analysis revealed that one edited line (Nipponbare 17/1) contained a 1-bp deletion. A pathogenicity assay will be conducted to evaluate the effect of this mutation on BLB resistance.

Keywords: Rice, Bacterial Leaf Blight, CRISPR/Cas9, *Xanthomonas oryzae* pv. *oryzae*

EVALUATION OF METARHIZIUM STRAINS FOR RICE PLANTHOPPER CONTROL

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Abstract:

The brown planthopper (BPH), *Nilaparvata lugens* (Stål) (Hemiptera: Delphacidae), is an important pest in rice cultivation, especially in the Asian region. Biological control is warranted as an environmentally friendly method to control infestations. Entomopathogenic fungi, such as the *Metarhizium* fungi, have received growing attention as biocontrol agent against BPH. In this study, BPH populations from 40 provinces of Thailand were sampled. *Metarhizium* fungi and BPH were sequenced to understand their genomes. Three geographical BPH populations of Thailand (Pathum Thani, Buriram, and Phetchabun provinces) were selected for pathogenicity tests, assessing the virulence of *Metarhizium* fungi. The objective was to select *Metarhizium* strains suitable for effective control of the BPH in Thailand. The results showed that certain *Metarhizium* strains, particularly BCC4849 (*M. neoanisopliae*) and ARSEF 7450 (*M. neoanisopliae*), exhibited consistent pathogenicity towards different BPH populations. In contrast, other strains such as ARSEF11637 (*M. clavatum*) and ARSEF7486 (*M. acridum*) showed relatively low pathogenicity.

Keywords: rice, *Metarhizium*, virulence, brown planthopper, biocontrol

CERTIFICATION OF RICE POWDER CERTIFIED REFERENCE MATERIAL (TRM- F-2003) FOR METROLOGICAL TRACEABILITY OF ELEMENTS AND ARSENIC ANALYSIS

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Abstract:

The accurate and internationally comparable measurement of heavy metals and arsenic species in rice is of paramount importance for global food safety and adherence to regulatory requirements, particularly the Codex Alimentarius standards. Ensuring the reliability and international acceptance of analytical results hinges on establishing metrological traceability.

To address this need and bolster the capabilities of testing laboratories, the National Institute of Metrology (Thailand) (NIMT), an internationally recognized National Metrology Institute (NMI) with demonstrated Calibration and Measurement Capabilities (CMCs), has developed and certified a Rice flour Certified Reference Material (CRM), designated TRM-F-2003.

This matrix-matched CRM, produced under the "TRM – Thailand Reference Material" brand, was prepared in strict compliance with ISO 17034, ensuring the highest standards of quality and consistency. TRM-F-2003 provides certified values for a critical range of analytes: essential and toxic elements (Cadmium (Cd), Copper (Cu), Calcium (Ca), Manganese (Mn), Magnesium (Mg), Zinc (Zn), total arsenic (As), as well as elemental species such as inorganic arsenic (iAs) and dimethylarsinic acid (DMA)). The metrological traceability for all certified values has been rigorously established through NIMT's validated certification procedures.

TRM-F-2003 effectively fills a crucial analytical gap, providing an essential quality control tool for method validation and routine monitoring. Its availability ensures the continued accuracy and global comparability of laboratory testing results for rice, thereby supporting consumer protection and facilitating international trade.

Keywords: Metrological traceability, Certified Reference Material, Arsenic, Heavy metal

METROLOGICAL TRACEABILITY AND UNCERTAINTY EVALUATION IN MOISTURE METER CALIBRATION USING CERTIFIED RICE REFERENCE MATERIALS

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Abstract:

Moisture meters are widely used in agricultural quality control, particularly for rice and paddy products. This study presents a traceable calibration procedure for moisture meters based on ISO 7700:2008 and ISO 712:2009, utilizing certified reference materials (CRMs) of rice and paddy. The calibration covers three types of moisture meters—resistance, capacitance, and near-infrared (NIR)—with moisture content ranging from 10% to 29% (w.b.).

The calibration method includes environmental conditioning, CRM homogenization, and repeated measurements to assess reproducibility and refilling effects. Measurement uncertainty is evaluated according to JCGM 100:2008 and EA-4/02, incorporating components such as CRM uncertainty, resolution, repeatability, ambient temperature variation, sample non-uniformity, and filling density. The expanded uncertainty ranges from 0.28% to 0.46%, depending on the meter type and moisture level.

This approach ensures metrological traceability and supports quality assurance through inter-laboratory comparisons. The results contribute to enhancing confidence in moisture measurements, which are critical for trade, storage, and processing of rice-based products.

Keywords: Moisture meter calibration, Certified reference material (CRM), Measurement uncertainty, Metrological traceability, Rice and paddy

MULTI-TRAIT SELECTION OF PHOTOPERIOD- INSENSITIVE GLUTINOUS RICE LINES WITH HIGH YIELD AND MULTI-STRESS RESISTANCE

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Abstract:

The development of non-photosensitive glutinous rice cultivars with durable resistance to pests and diseases, alongside high yield potential, is essential for sustainable rice production in the rainfed lowland ecosystems of the Mekong Basin. This study evaluated 25 photoperiod-insensitive glutinous rice lines under rainfed conditions in Northeastern Thailand during the 2024 wet season. The lines, developed through marker-assisted selection (MAS) and pedigree breeding, were selected for resistance to rice blast, bacterial blight, brown planthopper, and submergence tolerance. A randomized complete block design with three replications was used, with commercial cultivars RD6, RD10, and RD22 as checks. Significant genetic variation was observed for grain yield and agronomic traits. Grain yield showed positive correlations with key yield components, including panicles per plant, panicle length, biomass, filled grain percentage, plant height, and thousand-grain weight. These correlations suggest strong potential for simultaneous genetic improvement of multiple traits. Using the Smith-Hazel Index (SHI) at 20% selection intensity, four superior lines (G21, G12, G1, and G8) were identified for their enhanced yield and robust resistance to pests and submergence. These photoperiod-insensitive lines demonstrate potential for stable cultivation year-round under rainfed condition, where water supply is available, offering a reliable solution for regions with fluctuating seasonal conditions. The results underscore the importance of further multi-location trials to assess their adaptability and yield stability across diverse agroecosystems in Thailand. This research provides valuable genetic resources for sustainable rice breeding, contributing to food security in the Mekong Basin.

Keywords: Glutinous rice, photoperiod-insensitive rice, multi-trait selection, Smith-Hazel index

GGE BIPLLOT ANALYSIS REVEALS YIELD STABILITY AND ADAPTABILITY OF AROMATIC RICE WITH MULTI-STRESS TOLERANCE

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Abstract:

Genotype-by-environment interaction (GEI) is a major constraint in evaluating complex quantitative traits such as grain yield, which is crucial for varietal improvement. Multi- location yield trials are therefore essential to identify superior and stable genotypes prior to cultivar release. This study evaluated the effects of GEI and identified high-yielding, stable rice genotypes using GGE biplot analysis. Forty-four improved rice lines pyramided for blast and bacterial blight resistance and submergence tolerance, along with the check variety KDML105, were evaluated at two locations—Ubon Ratchathani University (UBU) and Ubon Ratchathani Rice Research Center (UBN)—using an augmented design with two replications. Combined analysis of variance revealed highly significant effects of genotype, environment, and GEI for grain yield. The mean yield–stability view of the GGE biplot identified genotype A33 (4.17 t ha⁻¹ at UBU and 5.21 t ha⁻¹ at UBN) as both high-yielding and stable across environments. The polygon view separated the environments into two mega- environments, with genotypes A35 and A22 performing best at UBU, and A5, A27, and A44 showing superior performance at UBN, indicating specific adaptability. Overall, A33 was recognized as the most desirable genotype, combining above-average yield with exceptional stability. The GGE biplot effectively classified genotypes into three groups: (i) high yield with high stability (A33, A21), (ii) high yield with low stability (A5, A35), and (iii) high stability with low yield (A42). These results demonstrate the usefulness of GGE biplot analysis in identifying both broadly adapted and environment-specific rice genotypes, providing valuable insights for rice breeding and cultivar recommendation.

Keywords: Rice, genotype-by-environment interaction, multi-environment trials, yield stability

PRELIMINARY STUDY ON THE GROWTH RESPONSE AND NUTRIENT DISTRIBUTION OF FIELD MAIZE VARIETY SUWAN 5821 IN PHOSPHORUS AND ZINC DEFICIENT ENVIRONMENT WITH MYCORRHIZA INOCULATION GROWN IN SAND CULTURE.

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Abstract:

Zinc and phosphorus are essential elements in the growth of plants. Arbuscular mycorrhiza fungi (AMF) can form symbiosis with plants. This symbiotic relationship aids plants in acquiring nutrients, such as phosphorus and zinc, in nutrient-deficient environments. They serve as biofertilizers in the sustainable production of crops. The aim of this experiment was to observe the impact of zinc and phosphorus-deficient environment in the presence of AMF on: (i) the growth and development of maize (ii) the colonisation of AMF (iii) zinc and phosphorus accumulation. A pot experiment was conducted in sand culture using SUWAN 5821 maize seeds inoculated with mycorrhiza with 2 levels of nutrient using Hoagland's solution: full Hoagland (+Zn+P) and modified Hoagland without zinc and phosphorus (-Zn- P), with 3 replications arranged in RCBD. The results showed significantly higher agronomic characteristics in full Hoagland treatment for most parameters including leaf area (+29.87%), leaf dry weight (+29.63%), stem dry weight (+29.1%), root dry weight (+77.47%). There was no significant growth in plant height. Moreover, a significantly higher root colonisation percentage (62.3%) was observed with the modified Hoagland treatment compared to full Hoagland (34.0%). Zinc accumulation in the roots did not change in both treatments (~74%) but differed between stem and leaves. Phosphorus accumulated more in the leaves in -Zn-P (56.46%) treatment but more in the stem (59.89%) in full Hoagland. Further studies would determine the effect of mycorrhiza on the accumulation pattern of phosphorus and zinc, and the impact of individual nutrient omission on the accumulation pattern and colonisation percentage.

Keywords: AMF, Zinc, Phosphorus, Hoagland

INSIGHT INTO THE GENETICS OF A NOVEL WHITE-STRIPED LEAF IN RICE

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Abstract:

Rice is mainly consumed by half of the world's population. The imminent climate change and population growth expected in the next 30 years will outpace the current rice production capacity, posing risks to food and nutrition security in developing nations. One simplified approach to address this challenge is to improve photosynthetic capacity by increasing chlorophyll content in leaves. In this study, we identified a unique white-striped leaf (wsl) mutant, RBR05, characterized by a productive, stage-specific, and temperature-sensitive phenotype with reduced chlorophyll content during the mature stage. We utilised RNA sequencing between the wsl and solid green leaf (SGL) rice to identify differentially expressed genes and QTL sequencing to identify genes responsible for the wsl phenotype. The causative mutation is a novel missense mutation in OsSAMHD1, converting arginine to histidine at amino acid position 310. This mutation disrupts chloroplast development, leading to chlorophyll deficiency and the formation of non-chlorophyllous cells in the whitened region of the leaf blade and sheath. The wsl310 (qws1_503564) was associated with the downregulation of genes involved in the formation of photosynthetic machinery and the chlorophyll biosynthetic pathway, while the upregulation of the OsRNRS1 and genes involved in the expression of plastid-encoded genes was observed. A SNP marker specific to wsl310 completely co-segregated with the wsl phenotype, confirming its causal role. The functional marker developed in this study provides a useful tool for rice breeders aiming to improve leaf colouration and productivity in RBR05 and related cultivars.

Keywords: white-striped leaf, *Oryza sativa* L., chloroplast development, SAMHD1, nucleotide metabolism

THE EFFECT OF GERMINATION ON GAMMA-AMINOBUTYRIC ACID (GABA) CONTENT IN RICE GRAINS OF 'BAO YOD MUANG' AND 'RD79' VARIETIES

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Abstract:

This research aimed to investigate and compare the effect of the germination process on the changes in Gamma-Aminobutyric Acid (GABA) content in the Thai landrace rice 'Bao Yod Muang' and the improved variety 'RD79'. Brown rice of both varieties was germinated for 48 hours and compared with non-germinated rice (0 hours). The GABA content was then analyzed using HPLC.

The results revealed that germination had markedly different effects on the GABA content in the two rice varieties. In the 'RD79' variety, germination led to a significant 2.5-fold increase in GABA content, rising from 28.50 mg to 73.23 mg per 100 g. Conversely, an interesting finding was observed in the 'Bao Yod Muang' variety, which initially possessed a high GABA content of 100.88 mg/100 g. After germination, its GABA content decreased to 78.42 mg/100 g. However, despite this reduction, the germinated 'Bao Yod Muang' still contained a higher GABA level than the germinated 'RD79'.

This study concludes that germination is an effective technique for enhancing the nutritional value of 'RD79' rice. However, for the 'Bao Yod Muang' variety, which is naturally rich in GABA, consumption as non-germinated brown rice provides the maximum GABA content. These findings underscore the importance of selecting appropriate rice varieties and processing methods to maximize the nutritional benefits in the development of health-oriented rice products and functional foods.

Keywords: GABA, Germinated brown rice, Bao Yod Muang, RD79, Germination

EVALUATION OF AGRONOMIC TRAITS, YIELD COMPONENTS AND YIELD OF LANDRACE UPLAND RICE COLLECTED FROM HIGHLAND GROWN IN CENTRAL PLAIN OF THAILAND

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Abstract:

Landrace upland rice varieties collected from farmers growing in the highlands of Phetchabun Province were another source of genetic resources that can be used in breeding projects. Therefore, the objective of this experiment was to evaluate the agronomic traits, yield components, and yield of 9 landrace upland rice varieties collected from the highlands of Phetchabun Province. They were grown in the central plains, namely the Lopburi Research Center and the National Corn and Sorghum Research Center, compared to those grown in the highlands, namely the Phetchabun Research Station. The results of the experiment showed that all 9 rice varieties grew well. Rice grown at the National Corn and Sorghum Research Center produced higher yields per plant than those grown at the Lopburi and Phetchabun Research Stations. When considering the number of grains per panicle, which is an important yield component, it was found that KhaoJaoKao and KhaoJaoPlueakDaengPom had more than 200 grains. However, the disadvantage of all 9 rice varieties is that the plants were quite tall, which was not suitable for promoting planting in the central region because the tall plants are easily broken. However, the results of this experiment will be base information to selecting genetic material for upland rice breeding projects in the future

Keywords: Rice, Landrace upland rice, Adaptation

HOM CHONLASIT 2: A MULTI-STRESS-RESISTANT AROMATIC RICE VARIETY FOR FUTURE SUSTAINABLE FARMING

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Abstract:

The Thai aromatic rice variety 'Hom Chonlasit 2' was developed to integrate resistance to submergence (SUB), brown planthopper (BPH), bacterial leaf blight (BLB), and blast disease with high yield and premium grain quality. Breeding began in the 2018 dry season by crossing line RGD14326-MS241-MS205, derived from the original Hom Chonlasit possessing submergence tolerance (*Sub1*) and BPH resistance (*Bph3*, *TPS*, *Bph32*), with Pin Kaset plus 4, a high-yielding variety tolerant to submergence and resistant to BLB (*xa5*, *Xa21*) and BPH (*Bph3*, *TPS*, *Bph32*). Molecular markers confirmed F₁ hybrids and monitored target genes. A second cross with RGD13297-124-8-2-MS3-MS1, carrying BLB resistance (*xa5*, *Xa21*, *Xa33*) and blast resistance (*qBL1*, *qBL11*), produced three-way F₁ hybrids. Generations F₂-F₆ were selected using morphological traits and 12 molecular markers. Preliminary yield trials of 105 F₅ lines in 2021 produced yields of 476-1,014 kg/rai; 21 lines were advanced. In 2022, the selected F₇ line, Hom Chonlasit 2, yielded 918 kg/rai at Nakhon Pathom, 1,073 kg/rai at Songkhla, and 887 kg/rai at Yala, with uniform grain quality. The line showed moderate to high resistance (MR-R) to six BLB isolates and was resistant to seven groups of 39 blast isolates. and 76.9% survival under 120 cm submergence for two weeks. Hom Chonlasit 2 has 18.16% amylose, an alkali digestion value of 6.33 (70-74°C), aroma of 0.92 ppm 2AP, and 92% genetic similarity with KDML105. Hom Chonlasit 2' is a non-photoperiod-sensitive, soft-textured, high-yielding aromatic rice variety suitable for year-round cultivation, exhibiting resistance to multiple stresses.

Keywords: rice breeding, Hom Chonlasit 2, molecular marker, cooking quality, A Multi-Stress-Resistant

DEVELOPMENT OF THE SALT-TOLERANT, BLAST- AND BACTERIAL LEAF BLIGHT-RESISTANT FRAGRANT RICE VARIETY 'HOM SIAM 3' USING MARKER-ASSISTED BREEDING

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Abstract:

The non-glutinous rice variety Hom Siam 3 is a fragrant, soft-textured, photoperiod-insensitive variety with medium height, high yield potential, and excellent cooking quality comparable to Khao Dawk Mali 105 (KDML105). It was developed through backcross breeding and marker-assisted selection (MAS) to incorporate salinity tolerance, blast, and bacterial leaf blight resistance while maintaining desirable grain quality. The initial cross between KDML105 and the salt-tolerant line RGD07727-3R produced the F₁ population in 2011. Successive generations were selected using DNA markers for salinity tolerance (qST1a, qST1b), aroma, low amylose (Wx), and gelatinization temperature (SSIIa). In 2013, selected F₂ plants were crossed with UBN03004-16-20-19-21-26-KPS-5 carrying qBL11 and xa5 genes, followed by three backcrosses to recover the maternal genome. Marker-assisted and phenotypic selection from BC₁F₁ to BC₃F₄ identified plants with strong panicles and high seed set. Sixty-two BC₃F₅ lines were evaluated under 150 mM NaCl at the seedling stage, and 36 salt-tolerant lines were identified, showing moderate to high resistance to 39 blast isolates. Yield trials (BC₃F₆) revealed 31 lines producing 337–1,100 kg/rai, exceeding KDML105. The best line also showed field resistance to bacterial leaf blight. Grain quality of BC₃F₇ lines showed 19.2% amylose, 122 mm gel consistency, <70°C gelatinization temperature, and 1.36 ppm 2-AP fragrance. On-farm trials in Songkhla (2023) averaged 620 kg/rai (max 1,100 kg/rai). Hom Siam 3 thus combines high yield, fragrance, and salt and disease tolerance, ideal for salt-affected rice areas.

Keywords: *Oryza sativa* L., Marker-assisted backcrossing, salinity tolerance, blast resistance, bacterial leaf blight, rice breeding, fragrant rice

INTROGRESSION AND SCREENING OF HEAT TOLERANCE QTL (QHT4) IN RICE F1-DOUBLE CROSS POPULATIONS

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Abstract:

Climate change poses a severe threat to rice production, characterized by unpredictable water scarcity and excess, and critically, by elevated night-time temperatures that significantly reduce yield. This research sought to mitigate these impacts by developing multi-stress-tolerant rice lines through a targeted hybridization program. Heat tolerance was conferred by a donor line (RGD19003-MS280-MS22-B) and tracked using DNA markers developed from SNPs discovered on Chromosome 4.

The heat-tolerant donor was strategically crossed with varieties providing genes for Nitrogen Use Efficiency (NUE) and Water Use Efficiency (WUE), resulting in three F1 single-crosses (F1-SC_RGD24064, F1-SC_RGD24065, F1-SC_RGD24067). Subsequent intercrossing produced two F1 double-cross (F1-DC) populations: RGD25023 and RGD25025 (totaling 112 plants).

Screening for heat tolerance was performed using an Augmented Experimental Design under controlled stress conditions, where the average greenhouse temperature was 40.2°C. The heat-tolerant donor line showed no significant decrease in seed setting, like the tolerant check N22 (3.8% reduction), while susceptible varieties experienced reductions between 74% and 100%. At heat stress, the F1-DC population maintained average seed settings of 30% (RGD25023) and 33% (RGD25025). Critically, 40 F1-DC lines surpassed the heat tolerance donor (RGD19003-MS280-MS22-B), with up to 111% higher percentage seed setting. These results successfully demonstrate the development of promising, heat-tolerant F1-DC lines which will be advanced to F5 generation for future field trials.

Keywords: Heat tolerance, F1 double cross, percentage seed setting

PRESERVING INTANGIBLE CULTURAL HERITAGE: THE THAM KHWAN KHAO NA RIM LE (RICE BLESSING RITUAL) OF THE PAK PRA COMMUNITY, SOUTHERN THAILAND

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Abstract:

This study aims to (1) collect knowledge and document the *Tham Khwan Khao* (rice blessing ceremony) of the coastal farming community in Pak Pra, and (2) analyze and interpret the verses chanted by the *mor phithikam* (ceremonial master) during the ritual. A qualitative research method was employed through in-depth interviews and focus group discussions with key informants. The findings reveal that the *Tham Khwan Khao*, also known as *Somphot Mae Phosop* (celebration of the Rice Goddess), represents an intangible cultural heritage that has been transmitted through generations of farmers in the Songkhla Lake basin. However, this wisdom has gradually declined due to changes in agricultural systems and the introduction of modern technology. Recently, the Pak Pra community has revived coastal rice cultivation and organized the "New Rice and Abundant Fish" (*Khao Mai Pla Man*) festival. The *Tham Khwan Khao* ritual expresses gratitude to *Mae Phosop*, the spirit of rice, after harvest. It serves to thank the goddess for abundance, strengthen farmers' morale, foster community unity, and enhance cultural learning among visitors. During the ritual, the *mor phithikam* prepares offerings such as cooked food, newly harvested rice, and farming tools, which are bound with sacred threads (*sai sin*). The chants invoke *Mae Phosop*, rice varieties, and associated animals and plants, symbolizing fertility and the spiritual essence (*khwan*) of rice. The ceremony thus reflects the coexistence of belief, wisdom, and cultural revival among the coastal rice-farming community.

Keywords: Intangible cultural heritage; Rice blessing ritual; Mae Phosop; Coastal farming community; Pak Pra

BIOFORTIFICATION AND BIOMASS PRODUCTION OF *RAPHANUS SATIVUS* L. MICROGREENS CULTIVATED ON ORGANIC SUBSTRATE WITH PHOTOSYNTHETIC BACTERIAL APPLICATION

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Abstract:

Microgreens of *Raphanus sativus* L., known for their dense nutrient content and short cultivation cycle, are increasingly regarded as promising candidates for functional food production within sustainable agriculture. This study assessed the combined effects of organic growing media enriched with vermicompost and applications of photosynthetic bacteria (PSB) on growth dynamics, phytochemical profiles, and nutritional quality of radish microgreens. A completely randomized design (CRD) was implemented with ten treatment combinations, varying in peat moss to vermicompost ratios and PSB concentrations (ranging from 1.25 to 5.00 mL/L), including co-application treatments. Cultivation was conducted under controlled environment conditions, and key parameters were evaluated, including plant height, fresh and dry biomass, total phenolics, anthocyanins, carotenoids, antioxidant activity, and macronutrient composition. Results revealed that microgreens grown in a 1:1 mixture of vermicompost and peat moss, combined with 1.25 mL/L PSB, exhibited significantly enhanced growth performance and functional phytochemical content compared to the control. This treatment yielded the highest levels of total phenolics (13.7 mg GAE/g), anthocyanins (2.4 mg/g), carotenoids (3.7 mg/g), and antioxidant capacity (31.2 μ mol TE/g). Additionally, notable improvements were recorded in protein (20.1%), crude fiber (12.3%), ash content (9.7%), and caloric value (319 kcal/100 g dry weight). The findings suggest that integrating vermicompost and PSB not only improves biomass yield but also enhances the functional and nutritional quality of microgreens. Such integration offers a sustainable, peat-reducing cultivation strategy aligned with global food security and nutrition goals, particularly in the context of eco-friendly crop production systems.

Keywords: Microgreens, vermicompost, photosynthetic bacteria, bioactive compounds, biofortification

AGROBACTERIUM TRANSFORMATION EFFICIENCY IN CHERRY TOMATO CVS. RED RUBY AND SUNSHINE

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Abstract:

Cherry tomato cvs. Red Ruby and Sunshine are Thai commercial varieties developed locally through cooperation between the National Center for Genetic Engineering and Biotechnology and TK R&D Ltd. These varieties are bred using marker-assisted selection to be resistant to Tomato yellow leaf curl virus (TYLCV). Additionally, they have a high carotenoid content and a long shelf life. However, its major drawback is sensitivity to high temperatures, which adversely affects fruit set and yield. Therefore, it is only productive in the winter season (between November and February). Our goal is to utilize genome editing to develop a tomato variety with enhanced heat tolerance. Prior to the target CRISPR/CAS construct, the transformation protocol was established with reporter gene transformation. Explants from cotyledons were used for pGFPGUSplus transformation using Agrobacterium strain EHA105. Our results showed high transformation efficiency at 85% for cv. Red Ruby and 80% for cv. Sunshine.

Keywords: Tomato, genome editing, heat tolerance

TARGETED AROMA VOLATILE COMPOUNDS ASSOCIATED WITH CONSUMER PREFERENCES IN CHILLI

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Abstract:

Aroma is a key driver of consumer preference for chilli (*Capsicum* spp.), yet the volatile compounds underlying this response remain poorly defined. This study profiled three chilli cultivars—'Karen', 'Khee Noo Suan', and 'Jinda'—using GC-MS and GC-O, combined with sensory evaluation by a nine-member trained panel and preference testing with 170 consumers. Fifty-seven volatile compounds were identified, with clear differences in acceptance across cultivars. 'Khee Noo Suan' achieved the highest liking score (52.9%), while 'Karen' and 'Jinda' received markedly lower ratings (31.8% and 15.3%, respectively). Multivariate analysis highlighted key volatiles associated with consumer responses: methyl 4-methylpentanoate, (E)-2-hexenal, 4-methyl-1-pentanol, 4-methylpentyl 2-methyl, 4-methylpentyl 8-methylnon-6-enoate, isohexyl isocaproate, fumaric acid, cis-hex-3-enyl pentyl ester, 2-decanol, hexyl hexanoate and methyl palmitate conferring floral notes, were consistently linked to higher liking, whereas (E)-3-hexen-1-ol, 1H-benzocycloheptene, trans- β -ionone, nerolidol and hexanoic acid with musty attributes reduced acceptance. These findings identify specific aroma compounds that shape consumer preference, providing actionable targets for breeding and product development to align chilli varieties with market demand.

Keywords: *Capsicum* spp., Volatile compounds, GC-MS, GC-O, Consumer preference

ORGANIC BIOSTIMULANT SYNERGY ENHANCING GROWTH AND PRODUCTIVITY OF CHINESE CABBAGE (*BRASSICA RAPA* VAR. *CHINENSIS*) USING VERMICOMPOST AND PHOTOSYNTHETIC BACTERIA

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Abstract:

This study investigated the effects of vermicompost and photosynthetic bacteria on the growth and yield performance of Chinese cabbage (*Brassica rapa* var. *chinensis*) under organic farming conditions. The experiment was conducted using a completely randomized design (CRD) with seven treatments and four replications. The treatments included: no fertilizer as control (T1), chemical fertilizer 15-15-15 (T2), vermicompost at 250 kg/rai (T3), vermicompost at 500 kg/rai (T4), foliar application of photosynthetic bacteria at 50 mL per 20 liters of water (T5), 100 mL per 20 liters (T6), and a combination of vermicompost at 500 kg/rai with photosynthetic bacteria at 100 mL per 20 liters (T7). At 40 days after transplanting, plants receiving chemical fertilizer (T2) exhibited the highest growth and yield. However, statistical analysis revealed no significant differences between T2 and T7. This indicates that the integrated application of vermicompost and photosynthetic bacteria can be a viable substitute for chemical fertilizer in Chinese cabbage production. The findings highlight the potential of organic biostimulants in promoting plant growth and yield without reliance on synthetic inputs. Moreover, this integrative approach supports sustainable agriculture through reduced chemical use, enhanced environmental quality, and improved economic returns for smallholder farmers. Such organic practices can also enhance consumer health and market value of produce. Before widespread application, further studies in open- field and on-farm conditions are recommended to validate the results and adapt the method to diverse agricultural systems.

Keywords: Vermicompost, Photosynthetic bacteria, Chinese cabbage, Organic farming, Growth and yield

OPTIMIZING LIGHTING AND ECONOMIC PERFORMANCE FOR CALENDULA PRODUCTION IN PFALS

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Abstract:

Edible flowers are considered promising high-value crops for Plant Factories with Artificial Lighting (PFALs), offering opportunities for market differentiation and year-round production. Among the key production factors in PFALs, electricity for lighting represents the most significant portion of operational costs. Therefore, this study aimed to optimize lighting strategies for calendula (*Calendula officinalis* L.), a model edible flower, by evaluating plant growth, yield, and economic performance. Calendula seedlings were cultivated in a PFAL and subjected to four lighting treatments: two photoperiods 12 h/12 h and 18 h/6 h (light/dark) and two continuous lighting conditions with different light intensities (24 h–200 and 24 h–400). The results indicated that extending the photoperiod beyond 12 h led to earlier flowering and increased flower yield, both in terms of number and fresh weight. In addition, total phenolic content and DPPH radical scavenging activity were enhanced under longer light exposure. Among all treatments, the 24 h–200 condition exhibited the highest energy use efficiency of lighting (EUE) in terms of flower production and secondary metabolite accumulation. Economic analysis presented that the benefit-cost ratio for fresh calendula flowers was above 2, whether sold by flower count or weight, under the 24 h–200 condition. These results suggest that lighting strategies can be used to optimize calendula production and maximize energy efficiency. Furthermore, calendula cultivation in PFALs is economically feasible, supporting its potential as a viable high-value crop.

Keywords: pot marigold, edible flower, artificial lighting, controlled environment agriculture, cost performance

ELEVATED CO₂ DIFFERENTIALLY AFFECTS GROWTH, PHOTOSYNTHESIS, AND PHYTONUTRIENT PROFILES OF TWO KALE CULTIVARS IN THE PLANT FACTORY WITH ARTIFICIAL LIGHTING

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Abstract:

Enrichment of carbon dioxide (CO₂) is known to enhance to the growth and biomass of vegetables in the Brassicaceae family. This study aimed to investigate the impact of CO₂ concentration on the growth, biomass, and phytonutrient production of kale grown in a plant factory with artificial lighting (PFAL) in 2 kale cultivars ('Curly Kale' and 'Red Ursa'). Plants were grown under 3 concentrations of CO₂ : 400 (ambient CO₂), 800, and 1200 μmol mol⁻¹, using a completely randomized design with 4 replications/treatment. The results revealed that increasing CO concentration to 1200 μmol mol⁻¹ significantly increased the growth and biomass in both kale cultivars compared to others CO₂ 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 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 was most effective at increasing total vitamin C, soluble protein, and total phenolic contents in both kale cultivars. Notably, 1200 μmol mol⁻¹ CO treatment caused a significant reduction in vitamin C content. Furthermore, both elevated CO 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 optimizes for growth, biomass, and photosynthesis, while at 800 μmol mol⁻¹ CO is superior for enhancing phytonutrient quality.

Keywords: Brassica, carbon fixation, elevated CO₂, phytonutrients, photosynthesis

ARTIFICIAL POLLINATION IMPROVES THE YIELD OF GREENHOUSE CHERRY TOMATOES UNDER HIGH SUMMER TEMPERATURE

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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, Heat stress

MORPHOLOGICAL CORRELATION OF CHILLI FLOWERS WITH MICROSPORE DEVELOPMENTAL STAGES FOR F1 HYBRID OF *CAPSICUM ANNUUM* L. 'CA365' X 'CA1191'

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Abstract:

Identifying the appropriate pollen developmental stage is essential for successful double haploid (DH) production in *Capsicum annuum*. This study aimed to determine the optimal microspore stage for androgenesis induction in chili cultivar 'CA365' x 'CA1191'. Chili flowers of different sizes were collected and classified based on flower length and anther characteristics. Microscopic observation using orcein staining was performed to examine microspore development stages, including uninucleate and binucleate stages. The results showed a strong correlation between flower size and microspore stage. Uninucleate microspores, which are considered the most responsive to androgenesis, were predominantly found in chili flowers measuring 4–5 mm in length. These findings provide essential information for selecting suitable floral material for DH induction in *Capsicum annuum* breeding programs, particularly for the 'CA365' x 'CA1191' cultivar. Further research on culture media and environmental conditions is recommended to enhance the efficiency of androgenic response and plant regeneration.

Keywords: *Capsicum annuum*, double haploid, microspore stage, androgenesis, chili flower

IMAGE ANALYSIS FOR PREDICTING AUTISM SPECTRUM DISORDER: A DEEP LEARNING APPROACH

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Abstract:

Autism Spectrum Disorder (ASD) is a complex neurodevelopmental condition that affects communication, social interaction, and behaviour. Its early diagnosis remains challenging due to variability in symptom presentation, overlap with other developmental conditions, and reliance on subjective behavioural assessments. Conventional methods often delay intervention, which can limit opportunities for improving long-term developmental outcomes. To address this gap, the present study explores an image-based computational framework for supporting ASD prediction. A publicly available dataset containing facial images of autistic and non-autistic individuals was utilised for experimentation. The images were pre-processed through resizing, normalization, and augmentation techniques to enhance quality and increase robustness. The study employed a DenseNet201 model with modifications tailored for binary classification of ASD and non-ASD categories. Transfer learning was integrated to leverage prior knowledge, while dropout and batch normalization layers were applied to reduce overfitting and stabilize training. The model was trained and validated using structured splits of the dataset, with the Adamax optimizer and categorical cross-entropy loss function guiding parameter updates. A custom learning rate adjustment mechanism was employed to balance convergence and generalization. Performance evaluation was carried out through accuracy and loss plots across epochs, supported by separate testing on unseen samples. Experimental results demonstrated that the model achieved high training accuracy approaching near-perfect performance, with validation accuracy stabilizing around 90%. Despite fluctuations in validation loss, the framework showed strong potential for identifying autistic features from facial data. Visualization of sample predictions and error trends highlighted areas requiring refinement, particularly in enhancing consistency on unseen data.

This study underscores the significance of computational screening tools in complementing conventional behavioural assessments. By extracting subtle facial patterns that may escape manual observation, such methods can serve as effective early indicators, particularly in resource-limited settings where specialist diagnosis is scarce. The findings also point to opportunities for future enhancement through larger datasets, additional regularization strategies, and integration with multimodal behavioural or neuroimaging data. In conclusion, the proposed approach provides an efficient and scalable foundation for supporting early ASD detection. While not intended as a standalone diagnostic tool, it offers valuable supplementary insights to clinicians, educators, and caregivers, ultimately contributing to improved developmental interventions and outcomes.

Keywords: ASD, CNN, Training, Validation, Epoch, Accuracy, Model generalization

AYUR-GENOMICS MEETS NEUROINFORMATICS: NGS AND IMAGE PROCESSING APPROACHES FOR ASSESSING THE THERAPEUTIC ROLE OF BRAHMI, ASHWAGANDHA, AND SHANKHPUSHPI IN AUTISM

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Abstract:

Autism Spectrum Disorder (ASD) is a multifactorial neurodevelopmental condition characterized by impairments in communication, social interaction, and behaviour. Its early detection and effective management remain challenging due to heterogeneity in symptoms and the absence of definitive biomarkers. Conventional diagnostic methods largely rely on behavioural assessments, often delaying timely interventions. This study proposes an integrative bioinformatics framework combining image-based computational analysis and next-generation sequencing (NGS) to enhance the understanding of ASD and explore therapeutic avenues. Image processing techniques were employed on publicly available datasets containing facial and behavioural image data of autistic and non-autistic individuals. Pre-processing, normalization, and feature extraction enabled the identification of subtle phenotypic patterns that may serve as potential early biomarkers. In parallel, NGS-based bioinformatics analysis was conducted to investigate genomic variations associated with ASD and to assess the molecular mechanisms by which Ayurvedic herbs—Brahmi (*Bacopa monnieri*), Ashwagandha (*Withania somnifera*), and Shankpushpi (*Convolvulus pluricaulis*)—exerts neuroprotective and neuro-modulatory effects. Candidate gene pathways implicated in synaptic function, oxidative stress, and neuroinflammation were mapped with phytochemical-gene interaction networks derived from these herbs. The integration of imaging biomarkers with genomic insights provides a holistic perspective on both early detection and potential therapeutic strategies. The findings highlight the complementary role of bioinformatics-driven image processing in ASD screening and underscore the therapeutic relevance of Brahmi, Ashwagandha, and Shankpushpi as supported by NGS-based pathway analysis. This study lays the groundwork for developing multimodal diagnostic and treatment frameworks that bridge traditional knowledge systems and modern genomics, ultimately contributing to more personalized interventions for autism management.

Keywords: Autism Spectrum Disorder (ASD), Bioinformatics, Image Processing, Next- Generation Sequencing (NGS), Ayurvedic Herbs, Brahmi (*Bacopa monnieri*), Ashwagandha (*Withania somnifera*), Shankpushpi (*Convolvulus pluricaulis*), Neuroprotection, Phytochemical-gene interaction, Early detection, Multimodal diagnostics

IMPROVING CUCUMBER (*CUCUMIS SATIVUS* L.) CULTIVATION PRACTICES: EVALUATING THE IMPACT OF SPUNBOND COVERS ON YIELD, DISEASE REDUCTION, AND ECONOMIC SUSTAINABILITY

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Abstract:

Cucumber (*Cucumis sativus* L.) is an important crop in Asia but is vulnerable to yield loss from viral diseases spread by insect vectors. Preventive strategies such as insect control and row covers are used, though conventional spunbonded polypropylene covers must be removed at flowering to allow pollination and are not reapplied due to heat buildup, limiting season-long protection. This study evaluated light-converting polypropylene spunbond covers (20 g/m²) for their effectiveness in pest and disease management, yield improvement, and economic return in cucumber cultivation. Two resistant varieties, Speed Max and Northern C (East-West Seed, Thailand), were tested under a randomized complete block design with three replicates, comparing open-field and protected cultivation. Seedlings were transplanted and covered immediately after an insecticide spray (Lambda-cyhalothrin) to prevent pest entrapment. Disease incidence and severity were significantly lower in Spunbond-protected plants (33.32% and 1.17, respectively). Marketable yield increased by 64.7–67.6% compared with open-field conditions, underscoring the productivity benefits of Spunbond protection. However, higher initial costs, susceptibility of the fabric to damage, and limited reusability present economic challenges for farmers. The findings highlight the potential of Spunbond technology to reduce disease pressure, enhance yield, and improve farmer income, especially during off-season production. To improve cost-effectiveness and sustainability, complementary practices such as organic mulching and recycling of materials are recommended.

Keywords: spunbond, cucumber, protected cultivation, viral diseases, economic analysis

INHERITANCE OF SEED COAT TEXTURE IN LUFFA ACUTANGULA

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Abstract:

Luffa acutangula is an important vegetable crop for promoting well-being. Seed germination in *L. acutangula* is influenced by several factors, one of which is seed coat texture. Most accessions possess a rough seed coat, while some have a smooth seed coat, the latter often associated with slower germination. This study aimed to investigate the inheritance pattern of seed coat texture in *L. acutangula*. A cross and its reciprocal were performed between LA051 (rough seed coat) and LA080A (smooth seed coat). The F_1 seeds from both cross and reciprocal crosses exhibited the same phenotype as the maternal parent. In the F_2 generation, all seeds displayed a rough seed coat. These results indicate that seed coat texture in *L. acutangula* is under maternal effect. However, further evaluation of the F_3 generation is required to confirm this finding.

Keywords: Cucurbitaceae, maternal effect, seed morphology

MORPHOLOGICAL AND MOLECULAR IDENTIFICATION OF COLLETOTRICHUM ATLANTICUM CAUSING ANTHRACNOSE ON TORCH GINGER (*ETLINGERA ELATIOR*) IN SOUTHERN THAILAND: IMPLICATIONS FOR SUSTAINABLE HORTICULTURAL CROP PRODUCTION

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Abstract:

Torch ginger (*Etilingera elatior*), a high-value ornamental and culinary crop in tropical Asia, has gained increasing importance as part of sustainable diversification in horticultural systems. However, in 2024, symptoms of anthracnose—characterized by brown lesions and flower blight—were observed on torch ginger in Songkhla Province, southern Thailand. This study aimed to identify the causal agent using a polyphasic approach combining morphological, pathogenic, and multilocus phylogenetic analyses (*act*, *cal*, *ITS*, *gapdh*, *tub2*). The pathogen was identified as *Colletotrichum atlanticum*, marking the first global report of this species infecting torch ginger. Pathogenicity tests confirmed Koch's postulates, and all isolates reproduced typical symptoms on inoculated plants. The discovery of *C. atlanticum* on torch ginger highlights the emerging threat of *Colletotrichum* species to tropical horticultural crops and underscores the need for accurate pathogen diagnosis for sustainable disease management. Early detection and integrated control strategies, including the use of biological control agents and cultural practices, will be essential to reduce fungicide reliance and promote sustainable floriculture and vegetable-based agroecosystems in Southeast Asia.

Keywords: Anthracnose, *Colletotrichum*, morphology, PCR, torch ginger

PHYTOCHEMICAL OF THAI INDIGENOUS VEGETABLE IN RAINY SEASON

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Abstract:

In Thailand, indigenous vegetables are becoming increasingly valuable. These plants have been widely consumed as healthy food and they can be grown in all seasons in Thailand. However, information on the bioactive compounds in these plants are remain limited. Therefore, this research aims to determine the amount of some phytochemicals of indigenous vegetables. Seventeen indigenous vegetables consist of Niam Hu Suea (NHS), Niam Hu Suea Dang (NHSD), Phak Chi Chang (PCC), Cha Phlu (CP), Ching Chu Chai (CCC), Phu Khao (PK), Sa Ra Nae (SRN), Phak Phraeo (PP), Ba Ya (BY), Ba Ya Dang (BYD), Ya Nuat Maeo (YNM), Pae Tam Pueng (PTP), Ya Pak King (YPK), Hwan Ngok (HN), Som Kung (SK), Khon Thi So (KTS), and Di Pla Chon (DPC) were planted during rainy season in 2024 of Thailand. Total phenolic contents (TPC), antioxidant activity (DPPH assay), chlorophyll a, b and total carotenoid contents were analyzed. The TPC and DPPH assay were ranking from 239.11–5,781.97 mg GA/100 g FW and 39.65–1,798.07 mg TE/100 g FW, respectively. Chlorophyll a, b and total carotenoids were ranking from 0.29–2.55 mg/g FW, 0.15–0.98 mg/g FW and 0.06–6.03 mg/g FW. The indigenous vegetable that were KTS, SK, PP and CP were suggested for high phytochemical and indigenous vegetable could be consumed in all species which depend on consumers preference and their accessible in each area.

Keywords: Phenolic, Antioxidant, Chlorophyll, Carotenoid

IN SITU PARTHENOGENETIC HAPLOID PRODUCTION IN MELON FOR BREEDING PURPOSES

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Abstract:

This study aimed to induce parthenogenetic embryo development in muskmelon (*Cucumis melo* L.) by pollinating with gamma-irradiated pollen and to evaluate the embryonic development and ploidy levels of regenerated plantlets. Two cultivars, green-fleshed Jasmine (JMG) and orange-fleshed Jasmine (JMO), were used. Pollen was irradiated with gamma rays at doses of 250 and 350 Gy before pollination. Fruits were harvested, and embryos were rescued and cultured in vitro. A total of 86 embryos were obtained, with a fruit set rate of 84.4% from 96 pollinations. The 250 Gy treatment induced more embryos than the 350 Gy treatment. Of the rescued embryos, 67 successfully developed into plantlets (77.91%). Among them, three haploid plants (4.5%) were identified two from JMO and one from JMG all derived from the 350 Gy treatment. Stomatal characteristics including chloroplast number in guard cells, stomatal size, and stomatal density were used as primary indicators for haploid identification. Haploid plants exhibited fewer chloroplasts (4–7), smaller stomatal size, and higher stomatal density compared to diploid plants. These results were confirmed by flow cytometric analysis. This study demonstrates that the combination of irradiated pollen pollination, embryo rescue, and ploidy screening using stomatal traits and flow cytometry is an effective approach for producing haploid and potentially doubled haploid muskmelon plants. However, due to the low and genotype-dependent efficiency, further optimization and the application of molecular markers are recommended to distinguish between true diploids and spontaneous dihaploids for breeding purposes.

Keywords: Irradiated pollen pollination, *Cucumis melo* L., Parthenogenesis, Embryo culture, Stomatal analysis

GENETIC PURITY ASSESSMENT OF F1 GALIA MELON USING SIMPLE SEQUENCE REPEAT (SSR) MOLECULAR MARKERS

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Abstract:

Genetic purity of F1 hybrid seeds is crucial for commercial melon production. This study aimed to develop a reliable method for assessing the genetic purity of 'Galia' melon hybrid F1-GG-13 using Simple Sequence Repeat (SSR) markers. Ten SSR primers were screened against the parental lines (IL-GG-1 and IL-GG-3) and their F1 hybrid. Two primers, CMGA104 and CMTCl60a+b, were identified as polymorphic and co-dominant, capable of clearly distinguishing the parents from the true F1 hybrid. A selected marker was then used to analyze 50 seedlings from the F1-GG-13 seed lot, which revealed a genetic purity level of 100%. The findings demonstrate that this SSR-based method is an efficient, accurate, and powerful tool for routine quality control in the SUT melon breeding program, providing a reliable alternative to the conventional Grow-Out-Test.

Keywords: molecular marker, genetic purity, hybrid melon, parental lines, SSRs.

LOCAL WISDOM ON HERBAL UTILIZATION FOR COMMUNITY HEALTH IN PAPHAYOM AND THE THANAE RIVER BASIN, PHATTHALUNG PROVINCE

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Abstract:

The ThaNaе River Basin covers four districts: Pa Phayom, Si Banphot, Khuan Khanun, and Mueang Phatthalung. The river is connected to 13 canals, with a total length of 42 kilometers, originating from the western Bantad Mountain Range and flowing into Thale Noi. A study of plant diversity and local wisdom revealed more than 60 families and 183 species. The results identified 60 families, 183 species, and five categories of utilization: (1) household medicinal plants for treating chronic and general diseases, (2) food and nutrition, (3) household equipment, (4) cosmetics, and (5) natural colorants for food and dyeing. Examples include *Alyxia reinwardtii* Blume var. *lucida* Markgr., *Thottea tomentosa* (Blume) Ding Hou, *Chloranthus erectus* Buch.-Ham. Verdc., *Claoxylon longifolium* (Blume) Endl. ex Hassk., *Mucuna macrocarpa* Wall., *Litsea glutinosa* (Lour.) C.B. Rob., *Bauhinia scandens* L., *Sida acuta* Burm. f., *Cissampelos pareira* Linn. var. *hirsutus*, *Passiflora foetida* Linn., *Plagiopteron saveolens* Griff., *Ventilago denticulata* Willd., *Morinda coreia* Ham., and *Poikilospermum suaveolens* (Blume) Merr.

Keywords: Tha Nae River Basin, Herbs, Local Wisdom

URBAN FOOD ENVIRONMENTS AND FRUIT AND VEGETABLE INTAKE AMONG VULNERABLE GROUPS IN BANGKOK: EVIDENCE FROM SENIORS, MIGRANTS, AND MONKS

Piraorn Suvanbenjakule, Pepijn Schereinemachers, Ee Von Goh

World Vegetable Center

Abstract:

Rapid urbanization has reshaped food environments in cities like Bangkok, where affordable and convenient meals are often low in fruits and vegetables (FV). This study employed a mixed-method approach to examine factors associated with FV intake among three vulnerable groups, namely, seniors, migrants, and monks, who each face unique contextual challenges within this urban setting. Data from three cross-sectional surveys were analyzed to identify psychosocial and environmental determinants of FV intake in each group. Results showed that all groups ate less than half of the WHO-recommended FV intake (400 grams). Seniors reported barriers related to age, household size, and reliance on prepared foods. Migrants faced long working hours and limited access to fresh produce near workplaces or accommodations. Monks, whose diets depend mainly on alms offerings, reflected broader urban dietary patterns dominated by rice and meat but lacking FV. Across populations, higher self-efficacy, stronger intention to eat FV, and frequent home cooking were associated with greater FV intake. However, these individual-level factors were insufficient to counteract structural and environmental barriers to achieving healthy diets within the urban food environment. The findings suggest that addressing diet in Bangkok requires both motivating the individuals and reshaping the food environment so that healthier options become more accessible and realistic in daily life.

Keywords: food environment, dietary behavior, healthy diet, urbanization

EFFECT OF COLD PLASMA ON GERMINATION AND CONTROLLING OF SEED- BORNE FUNGI IN CEYLON SPINACH SEED

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Abstract:

Basella alba (*Ceylon spinach*) is a nutritious local vegetable; however, its seeds often show uneven germination and contamination with seed-borne fungi after storage. Cold plasma has been reported to stimulate germination and inhibit fungi in various plants. This study aimed to investigate the effects of cold plasma on seed quality, α -amylase activity, and seed-borne fungi in *Basella alba* seeds. Seeds of *B. alba* (BA008) were treated with dielectric barrier discharge (DBD) plasma for 0 (control), 5, 10, 15, and 20 minutes. Seed quality parameters, including germination percentage, germination index, mean germination time, α -amylase activity, and incidence of seed-borne fungi, were evaluated using standard procedures and the blotter test. Cold plasma treatment for 5, 10, and 15 minutes increased seed germination to 97.33, 93.33, and 88.00%, respectively, compared with 85.33% in the control, whereas 20-minute treatment showed no statistical difference. Germination index was higher in the 5–15-minute treatments than in the control and 20-minute treatment, while mean germination time ranged from 7.50 to 8.06 days with no significant difference. α -Amylase activity was highest in the 5-minute treatment (78.0 $\mu\text{mol/g FW}$) compared with 70–71 $\mu\text{mol/g FW}$ in the control. The incidence of seed-borne fungi decreased with longer plasma exposure, with percentages of 86.67, 86.67, 73.33, 60.00, and 53.33% for control, 5, 10, 15, and 20 minutes, respectively. In conclusion, cold plasma treatment for 5–15 minutes effectively improved germination, germination index, and α -amylase activity, while 15–20 minutes were most effective in reducing seed-borne fungi in *B. alba* seeds.

Keywords: *Ceylon spinach*, dielectric barrier discharge plasma, seed germination, alpha-amylase activity, seed-borne fungi

MALDI-FINGERPRINT PROFILING REVEALS MOLECULAR SIGNATURE OF CUCUMBER SEED AGING

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Abstract:

Seed aging is a significant factor limiting germination and vigor during long-term storage. Conventional methods to determine seed viability rely on germination tests or biochemical assays, which are often time-consuming and less predictive. In this study, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) was employed to profile molecular fingerprints associated with cucumber (*Cucumis sativus*) seed aging. Mass spectra were acquired in the m/z range of 5,000–20,000 for two seed lots: Y67_CUC (expired in 2024) and Y70_CUC (expiring in 2027). Distinct spectral profiles were observed between the two groups, with major peaks at m/z 5235, 7784, 8035, and 11845 differing in intensity. Principal component analysis (PCA) revealed group separation, particularly along PC2 and PC3 ($p < 0.01$), indicating statistically significant molecular divergence between aged and non-aged seeds. Hierarchical clustering analysis (HCA) further supported this discrimination, grouping samples according to storage age with high consistency. These findings demonstrate that MALDI-fingerprint analysis can effectively detect molecular changes during seed aging and provides a rapid, label-free approach for seed quality assessment. Hence, the MALDI-TOF MS fingerprinting approach offers a promising indicative tool for monitoring seed viability and predicting storage longevity in cucumber and possibly other crop species.

Keywords: Matrix-assisted laser desorption/ionization (MALDI), molecular fingerprint, seed aging, principal component analysis (PCA)

IDENTIFICATION OF *COLLETOTRICHUM* SPP. CAUSING ANTHRACNOSE DISEASE ON CHILI AND EVALUATION OF RESISTANCE IN IMPROVED BREEDING LINES

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Abstract:

Anthracnose disease caused by *Colletotrichum* spp. is a major constraint affecting chili production in Thailand. This study aimed to identify the causal fungi of anthracnose from chili-growing areas in Thailand and evaluate the resistance of improved breeding lines. *Colletotrichum* isolates were successfully obtained from symptomatic chili samples. Fungal identification using morphological characteristics and molecular analyses based on the ITS region, actin, and chitin synthase 1 gene sequences classified the isolates into two groups: the *C. truncatum* species complex and the *C. gloeosporioides* species complex. Pathogenicity tests on bird's eye chili and bell pepper revealed that *C. truncatum* isolate KRI015 exhibited the highest virulence, followed by *C. gloeosporioides* isolate RBR009. Resistance evaluation was conducted on four chili varieties: breeding lines CA758×CA1355 and CA365×CA1163, commercial variety CA365, and Amphawa Gold. Against *C. truncatum* KRI015, Amphawa Gold showed the highest resistance, with lesion sizes of 2.08 and 2.55 cm at 9 and 11 days post-inoculation, respectively, while breeding lines CA758×CA1355 and CA365×CA1163 exhibited moderate resistance. However, statistical analysis revealed no significant differences among the three varieties. For *C. gloeosporioides* RBR009, breeding line CA365×CA1163 displayed superior resistance, with lesion sizes of 0.44 and 0.65 cm at 9 and 11 days post-inoculation, respectively, which were significantly smaller than those of the commercial variety CA365 (2.16 and 2.34 cm). These findings demonstrate that chili resistance varies among different *Colletotrichum* species, providing valuable baseline information for breeding programs aimed at developing anthracnose-resistant chili cultivars.

Keywords: Anthracnose disease, *Colletotrichum* spp., Chili, Plant breeding

DEVELOPMENT OF METHODS FOR SEED QUALITY ASSESSMENT DURING SEED PRODUCTION

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Abstract:

Thailand is an important hub for seed production of the world. To maintain competitiveness in seed industry, skills in seed production with high quality, including high genetic purity, high vigor and free from diseases, must be established. Molecular techniques such as Single Nucleotide Polymorphism (SNP) genotyping and Real-time Polymerase Chain Reaction (RT-PCR) have been developed to use in testing genetic purity test in seeds. However, genomic information of plant germplasms used as parental lines for hybrid seed production is required prior to marker development. In this project, we sequenced genomes of 223 parental varieties used in seed production in 15 plant species to develop 150 SNP markers for genetic seed purity tests. We validated these markers for genetic seed purity tests in parental lines and their hybrid seeds and elevating testing standards to international acceptance. These developments can lead to provision of a service lab in seed quality assessment and help improve the quality of seed production in Thailand.

Keywords: seed, molecular, Nucleotide Polymorphism (SNP), seed purity, seed production

IMPACT OF HOME GARDENING AND NUTRITION SUPPORT ON WOMEN IN REFUGEE CAMPS IN COX'S BAZAR, BANGLADESH

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Abstract:

The number of displaced people worldwide is rising due to conflict and climate change. The Myanmar civil war has forced millions to flee, including nearly one million Rohingya refugees living in densely populated camps in Cox's Bazar, Bangladesh. While food aid meets the immediate needs of these refugees, other solutions are essential to promote self-reliance. Gardening is one such approach that can potentially improve diets, food security, and incomes, but evidence for the impact of home gardens in refugee camps remains limited. This study used a quasi-experimental design to assess the impact of a program that trained pregnant and lactating women in home gardening and nutrition. Baseline and endline data were collected from a sample of 525 control and 525 intervention women. A difference-in-differences estimator was employed to quantify the intent-to-treat effect on fruit and vegetable consumption and various secondary benefits. At the endline, 94% of households in the intervention reported having a garden, up from 58% at baseline. The intervention led to a 17-point increase in garden adoption (p -value=0.018) and a 57-point rise in households sourcing fruits and vegetables from the garden (p -value < 0.001). The intervention improved nutrition knowledge by 23 percentage points (p -value < 0.001), and household food security also saw enhancements. However, there was no significant increase in fruit and vegetable intake based on a 24-hour recall method. These findings demonstrate that gardening and nutrition training provided to pregnant and lactating women in a densely populated refugee camp improves their food security and knowledge, thereby contributing towards increased resilience.

Keywords: Rohingya, homestead food production, displacement, conflict

QUANTIFICATION OF HERBICIDE RESIDUES IN FRUITS AND VEGETABLES USING ISOTOPE DILUTION BY GC-MS AND MULTIPOINT CALIBRATION

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Abstract:

Ensuring food safety and promoting sustainable agricultural practices require accurate monitoring of pesticide and herbicide residues in crops. This study presents a validated analytical method for the quantification of herbicide residues (Atrazine, Ametryn and Pendimethalin) in apple using gas chromatography-mass spectrometry (GC-MS) with Isotope Dilution Mass Spectrometry (IDMS) and multipoint calibration. Samples were extracted using an optimized QuEChERS procedure, followed by a cleanup step to minimize matrix interferences. Calibration curves constructed across five concentration levels (0.1-1.0 µg/g) exhibited excellent linearity ($R^2 > 0.994$). Method validation demonstrated high sensitivity, with limits of detection (LOD) of 0.04 µg/g for Atrazine and Pendimethalin, and 0.05 µg/g for Ametryn. The recoveries ranged from 99% to 105%, and the repeatability was below 6% relative standard deviation (RSD). The proposed method will be applied to various fruit and vegetable samples to detect low-level herbicide residues within regulatory limits. This developed approach offers a reliable, robust, and sustainable strategy for food safety surveillance and contributes to quality assurance in agricultural produce.

Keywords: Herbicide, Isotope Dilution Mass Spectrometry, QuEChERS

A COMPARATIVE STUDY OF FIVE IMPORTANT METABOLIC COMPOUNDS IN THAI HOLY BASIL GERMLASM

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Abstract:

Holy basil (*Ocimum tenuiflorum* L.) has been widely used as a flavoring ingredient and utilized in the pharmaceutical industry. In this study, a germplasm collection was grown during the dry (winter 2023) and wet (rainy 2024) seasons at a field site in Nakhon Pathom province, Thailand. Five important metabolic compounds (MCs) were analyzed, including total phenolic content (TPC, mg GAE/g DW), total flavonoid content (TFC, mg/g DW), DPPH radical scavenging activity (%), anthocyanin content (AC, $A_{530}-0.33 \times A_{657}$), and total terpenoid content (TTC, mg/g DW). All MCs were extracted using dry leaves at flowering stage and measured using a spectrophotometer. The results showed that the levels of all MCs varied depending on the growing season (TPC, TFC, AC, and TTC showed $R^2 = 0.037, 0.033, 0.034, 0.033,$ and $0.026,$ respectively). In the dry season, 13 and 6 varieties showed AC and TTC levels exceeding 1 and 1032.72, respectively, whereas in the wet season, AC and TTC values did not exceed 0.75 and 656.48, respectively. Meanwhile, high levels of TPC, TFC, and DPPH across both seasons were observed in 4, 6, and 2 varieties, respectively. Notably, the holy basil variety OC019_p1 exhibited high levels of three MCs (TPC, TFC, and DPPH) in both seasons, while OC059A_p1 and OC024_p1 showed high levels of two MCs, TPC and DPPH, and TPC and TFC, respectively. These findings could be useful for improving cultivation management of holy basil in Thailand and for guiding future research.

Keywords: Holy basil, metabolic compound, phenolic content, flavonoid content, DPPH, anthocyanin content, terpenoids content

CHILLING INJURY TOLERANCE SCREENING IN THE THAI HOLY BASIL GERMPLASM

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Abstract:

Holy basil (*Ocimum tenuiflorum* L.) is a native tropical plant and sensitive to low temperatures. Transportation and storage temperature for fresh vegetables are commonly used at 10–15 °C. These conditions induce chilling injury (CI) in holy basil, resulting in deterioration of visual quality and a shortened storage life. To survey CI tolerance cultivars, this study evaluated 122 accessions of holy basil germplasm in a controlled room at 15 °C for 30 days. Shoots were washed thoroughly with tap water, then air-dried at room temperature (25 ± 2 °C) to remove excess surface moisture. The samples were packed into non-perforated polyethylene (PE) bags containing four shoots per bag with four replications. All bags were tightly sealed and stored in a cold room maintained at 15 ± 2 °C. CI symptoms were evaluated daily using a visual score base on percentage of CI symptoms as 0 (tolerance: 0%) to 5 (susceptible: 80–100%). The results showed that no CI symptoms were observed within 6–11 days after storage (DAS) or 8.4 DAS by average ($p < 0.05$). Among these, three accessions OTIN006, OC180B_p1, and OC095_p1 presented the slowest initial development of CI at 11 DAS. The progression of CI from score 0 to 5 varied significantly among accessions ($p < 0.05$) ranging from 15 to 29 DAS or 23.4 DAS by average. The longest storage duration was found on OC095_p1, OC133_p5, and OC112_p5 which reach a score 5 at 29 DAS. These accessions may serve as sources for breeding CI tolerance in future.

Keywords: Holy basil, chilling injury, tolerance, screening, germplasm

DEVELOPMENT OF AN OPTIMISED IN VITRO POLLEN GERMINATION PROTOCOL FOR HOLY BASIL (*OCIMUM TENUIFLORUM* L.)

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Abstract:

Pollen viability and vigour are essential indicators of pollen quality, directly affecting the success of pollination and fertilisation processes. These factors, along with pistil receptivity and pollen–pistil compatibility, are key determinants of breeding success in basil (*Ocimum* spp.). This study aimed to establish an optimised in vitro pollen germination medium (PGM) for Holy basil (*Ocimum tenuiflorum* L.), an economically important aromatic and medicinal plant. The classical Brewbaker and Kwack (BK) medium was modified by adding 12% polyethylene glycol (PEG), which significantly improved pollen germination and tube elongation. The effects of different concentrations of sucrose, boric acid, calcium nitrate, and potassium nitrate were assessed using a completely randomised design (CRD). All experiments were conducted at 37 °C, the optimal temperature for pollen germination in this species. The optimised formulation, containing 12% PEG, 15% sucrose, 6.4 mM boric acid, 1.8 mM calcium nitrate, and 0.5 mM potassium nitrate, achieved the highest pollen germination rate of 29.47%. The improved medium showed consistent and reproducible results across replicates, confirming its reliability for in vitro germination tests. This protocol, combined with standard viability staining, enables a thorough assessment of pollen fertility and vigour—crucial parameters for breeding efficiency in *Ocimum* species. The findings deepen understanding of reproductive biology in Holy basil and offer a practical basis for enhancing hybridisation and genetic improvement strategies in aromatic and medicinal plants.

Keywords: Pollen viability, Germination medium, Holy basil (*Ocimum tenuiflorum*), Polyethylene glycol (PEG), Reproductive biology

PYRAMIDING OF TWO QTLs FOR BACTERIAL WILT RESISTANCE IN A SEEDATIP TOMATO CULTIVAR BY MARKER ASSISTED BACKCROSSING (MAB)

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Abstract:

Tomato is among the world's most popular fruit and vegetable crops, producing over one hundred thousand tons annually in Thailand. The variety 'Seedathip6', valued for its pink skin, ovoid shape, and sour taste, is economically important but highly susceptible to bacterial wilt (BW). BW, caused by the *Ralstonia solanacearum* species complex (RSSC), is a major vascular disease severely limiting tomato production. Molecular markers linked to resistance genes offer an efficient tool for breeding programs aimed at pyramiding resistance loci. This study aimed to develop bacterial wilt resistant tomato lines by pyramiding two resistance loci (genes or QTLs) through marker-assisted backcrossing (MAB). Two SNP markers were applied to select for BW resistance and to fix the resistance loci in homozygous condition. Selection was performed until the BC₂F₂ generation, where tomato lines carrying all resistance loci were identified. Subsequent evaluation against *R. solanacearum* demonstrated resistance stability in advanced generations. Among the four BC₂F₄ lines tested, one line, BC₂F₄-333-5, showed promising resistance. This line exhibited low disease incidence and severity across five *R. solanacearum* strains, indicating its potential as a resistant tomato line.

Keywords: Bacterial wilt disease, Marker-Assisted Backcrossing (MAB), Tomato

ASSESSMENT OF GENETIC DIVERSITY AND POPULATION STRUCTURE IN HOLY BASIL USING WHOLE-GENOME SEQUENCING

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Abstract:

Holy basil (*Ocimum tenuiflorum* L.) has been used in Ayurvedic medicine and Thai cuisine for ages. It is distributed across Southeast Asia and commonly cultivated as a home-grown vegetable in Thailand. This study aimed to assess the genetic diversity and population structure of holy basil using genome-wide variation derived from whole-genome sequencing. A total of 129 accessions including 120 Thai native, 4 Thai commercial and 5 Indian accessions were sequenced using next-generation sequencing (NGS) platforms. The chromosome-scale genome assembly of the Thai accession OC194_p1 was used as the reference for variant calling with the Genome Analysis Toolkit (GATK). Most accessions exhibited over 90% homozygous SNPs, while only nine accessions showed > 10% heterozygosity. After filtering homozygous alleles, a minor allele frequency (MAF) \geq 0.05, and 0% missing data, 252,964 SNPs were retained for population structure analysis. ADMIXTURE analysis revealed an optimal population structure at $K = 4$, with low genetic admixture among groups. The number of accessions in each subpopulation (K1-K4) was 5, 9, 72, and 43, respectively. Neighbor-joining analysis grouped the accessions into two clusters (C1 and C2), consistent with the ADMIXTURE results, where K2 and K3 belonged to C1, and K1 and K4 to C2. Genetic clustering showed unclear association with leaf/stem color, but a trend was observed linking shorter plant height with C1 and strong aromatic traits with C2. These findings provide valuable insights into the genetic structure of holy basil and offer a foundation for future molecular breeding and genomic studies in this species.

Keywords: Holy basil, Diversity, Population structure, Whole genome sequence, SNP

PHENOTYPIC DISTRIBUTION OF THE AROMATIC TRAIT IN A BI-PARENTAL POPULATION OF HOLY BASIL (*OCIMUM TENUIFLORUM* L.)

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Abstract:

Holy basil (*Ocimum tenuiflorum* L.) is an important medicinal plant used as an ingredient in many types of food because of its unique aromatic character. This study aimed to investigate the phenotypic variation and inheritance pattern of the aromatic trait in holy basil. A total of 271 F₂ generation plants from a cross between a non-aromatic female parent (OC210_p1) and an aromatic male parent (OC143_p1) were evaluated an aroma intensity by sensory testing. The evaluation was conducted on fresh leaf collected from 100 days old plant grown during summer of 2025. Aroma intensity was scored on a scale from 0 (no aroma) to 5 (strong aroma). Chi-square analysis of the F₂ population showed that the numbers of plants with strong (score 4-5), medium (score 2-3), and no (score 0-1) aroma were 49, 184, and 38, respectively. This segregation ratio significantly deviated from the expected 1:2:1 ratio ($p = 1.9E-08$), suggesting that the aromatic trait in holy basil is controlled by multiple genes. These findings provide essential phenotypic data for selecting extreme aroma phenotypes (strong and non-aromatic) to be used in subsequent bulk segregant analysis (BSA) and QTL-seq approaches for identifying loci governing aroma expression in holy basil.

Keywords: Holy basil, Phenotypic distribution, Aroma, Sensory test, Bi-parental population

IMPACTS OF BEAN COMMON MOSAIC VIRUS INFECTION ON QUALITY AND QUANTITY OF BUTTERFLY PEA (*CLITORIA TERNATEA* L.) FLOWERS

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Abstract:

Butterfly pea (*Clitoria ternatea* L.) has recently been identified as a new host of bean common mosaic virus (BCMV) in Thailand. The primary use of butterfly pea lies in its flowers, which are widely utilized for food decoration and as a natural colorant. Therefore, this study aimed to investigate the impact of BCMV infection on the numbers, morphology, cytology, and anthocyanin content of butterfly pea flowers. BCMV was mechanically inoculated into butterfly pea seedlings, and the plants were maintained in a greenhouse until flowering. The number of flowers produced by BCMV-infected plants was significantly lower than that of the healthy control. Morphological observations showed that BCMV-infected flowers were smaller than those of healthy plants and exhibited mosaic symptoms on the petals, resulting in color breaking and abnormal petal development. Cytological examination under a compound microscope revealed that both palisade and spongy mesophyll cells in infected flowers were reduced in number and size compared with the control. Furthermore, the anthocyanin content in BCMV-infected flowers was significantly lower than that in healthy ones. In summary, BCMV infection adversely affected both the quality and yield of butterfly pea flowers.

Keywords: Butterfly pea, cytology, anthocyanin, bean common mosaic virus, virus infection

EFFECT OF GAMMA IRRADIATION ON SEED GERMINATION AND EARLY GROWTH IN OCIMUM SPECIES

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Abstract:

Radiation-induced mutation has been widely applied in crop improvement enhancing genetic variability and developing novel desirable traits. Ocimum species, including holy basil, sweet basil, and hairy basil, are valued for both medicinal and culinary uses. However, low genetic diversity has been observed among Thai Ocimum germplasm. To introduce new genetic variation, mutation induction using gamma irradiation was employed. This study aimed to evaluate the effects of radiation on seed germination and early seedling growth. Acute irradiation was performed using a Cs-137 gamma source at a dose rate of 3.13 Gy/min across twelve doses ranging from 150 to 700 Gy, with 50 Gy increments. Seven accessions, including five holy basil genotypes (HB2, Baiyai, OC113_p5, OC194_p1, and OC210_p1), one Thai sweet basil, and one hairy basil, were subjected to treatment. Irradiated seeds were sown in plastic trays, and data were recorded for germination percentage at 7 and 14 days after germination (DAG), and for plant height at 21, 35, and 49 DAG. The results indicated that germination percentage and seedling height were significantly affected by the radiation dose. Generally, higher doses resulted in a lower germination percentage and delayed germination time, evident in cultivars OC113_p5 and OC194_p1. In contrast, Baiyai and OC210_p1 showed no significant impact on germination. For all cultivars, dose-dependent reduction in average plant height significantly. The lowest mean height of 49 DAG (2.7 cm) recorded at the 700 Gy dose. This research demonstrates that increasing doses of gamma radiation negatively correlate with seed germination and subsequent seedling growth.

Keywords: Ocimum, Basil, Mutation, Gamma ray, Irradiation