# 4th International Conference on Rice for the Future

# ICRF2026

## One Health Rice: Transforming Food, Climate and Health Through Rice Innovation



# Book of Abstracts

23-24 November 2026

Centara Grand at Central Plaza Ladprao
Bangkok, Thailand



# About This Book

# Book of Abstracts

## 4th International Conference on Rice for the Future (ICRF2026)

*"One Health Rice: Transforming Food, Climate and Health Through Rice Innovation"*

**23–24 November 2026**

Centara Grand at CentralPlaza Ladprao, Bangkok, Thailand

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## Guide to abstract codes

Every abstract has a reference code of the form OS1-01 (type + topic + running number). The same code is used in the Contents, the Author Index and the page header of each abstract.

| Code | Topic | Oral | Poster |
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| **S1 (OS1 / PS1)** | Rice Genomics / Rice-omics | 9 | 14 |
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*O = Oral presentation, P = Poster presentation, S1–S6 = topic. Example: OS3-14 is the 14th oral abstract of topic 3. Within each topic the codes run consecutively, and a poster's code is also its board number.*

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ICRF2026

# Welcome Message

Rice is more than a staple food. It is a cornerstone of food security, human health, environmental sustainability, and rural livelihoods for more than half of the world's population. As global challenges such as climate change, biodiversity loss, emerging diseases, environmental degradation, and nutritional insecurity continue to intensify, the future of rice must be viewed through a broader and more integrated lens. The 4th International Conference on Rice for the Future (ICRF2026) adopts the theme “One Health Rice: Transforming Food, Climate and Health Through Rice Innovation” to highlight the interconnected health of rice production systems, ecosystems, and society. This concept recognizes that healthy soils support healthy plants; healthy plants contribute to nutritious food; nutritious food promotes human well-being; and sustainable farming systems safeguard environmental and economic resilience.

ICRF2026 will bring together researchers, policymakers, industry leaders, farmers, and development partners to explore innovative solutions across the entire rice value chain. Topics will include climate-smart rice, low-emission production systems, sustainable crop protection, rice genomics and breeding, nutrition and functional foods, digital agriculture, biodiversity conservation, and policies that strengthen resilient food systems.

Through interdisciplinary collaboration and international partnerships, ICRF2026 aims to advance a shared vision of rice that not only feeds the world, but also contributes to healthier people, healthier ecosystems, and a more sustainable future for all.



**Assoc. Prof. Dr. Siwaret Arikit**
**Convener, ICRF2026**
Director - Rice Science Center, Kasetsart University

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**Emeritus Prof. Dr. Onanong Naivikul**
Kasetsart University

**Assoc. Prof. Dr. Samak Kaewsuksaeng**
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**Dr. Sithichoke Tangphatsornruang**
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**Assoc. Prof. Dr. Sujin Patarapuwadol**
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**Assoc. Prof. Dr. Supachitra Chadchawan**
Chulalongkorn University

**Assoc. Prof. Dr. Sureeporn Kate-ngam**
Ubon Ratchathani University

**Assoc. Prof. Dr. Varaporn Sangtong**
Maejo University

**Dr. Vinitchan Ruanjaichon**
National Science and Technology Development Agency

**Dr. Watchareewan Jamboonsri**
National Science and Technology Development Agency

**Dr. Wintai Kamolsukyunyong**
National Science and Technology Development Agency

**Assoc. Prof. Dr. Parisut Chalermchaiwat**
Kasetsart University

**Assist. Prof. Dr. Chawakwan Nitikornwarakul**
Kasetsart University

**Assist. Prof. Dr. Krittiya Khuenpet**
Thammasat University

**Mr. Possawat Narumol**
Thai Farmer's Way of Life and Spirit Learning Center

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**Assoc. Prof. Dr. Patompong Saengwilai**
Mahidol University

**Dr. Wasin Poncheewin**
National Science and Technology Development Agency

## Marketing, Public Relations, Finance Committee

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Silpakorn University

**Dr. Siriphat Ruengphayak**
Rice Science Center, Kasetsart University

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## Secretary

**Mr. Sumon Hoymala**
Rice Science Center, Kasetsart University

**Mr. Anat Sukeewong**
Rice Science Center, Kasetsart University

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**Mr. Krittidech Thaworntangcharoenkit**
Rice Science Center, Kasetsart University

**Mr. Wanchana Aesomnuk**
Rice Science Center, Kasetsart University

**Ms. Oangwarin Thaworntangcharoenkij**
Rice Science Center, Kasetsart University

# Venue & Floor Plan

## Centara Grand at CentralPlaza Ladprao Bangkok

1695 Phahonyothin Rd, Chatuchak, Bangkok 10900, Thailand

**Conference venue: Vibhavadee Ballroom (Lobby Floor)**



Located in Bangkok, the venue is easily accessible from both Suvarnabhumi (BKK) and Don Mueang (DMK) airports, with direct flights across Asia. Hotel recommendations and travel guidance are published on the official website.

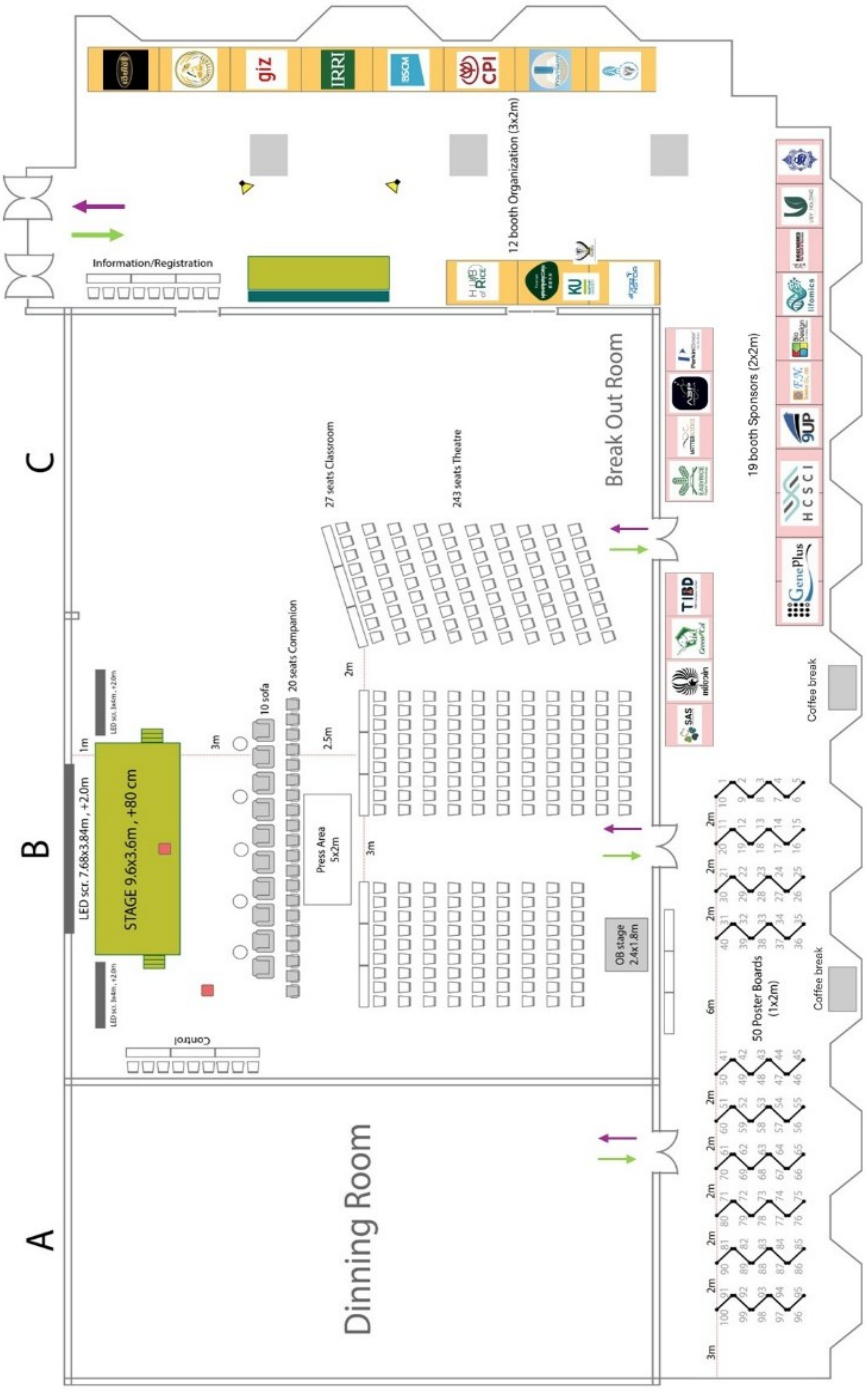
## Getting here

| From | Time | Distance / route |
|---|---|---|
| **Suvarnabhumi (BKK)** | ~45 min | ~30 km. Airport Rail Link to Phaya Thai, then BTS to Ha Yaek Lat Phrao or taxi |
| **Don Mueang (DMK)** | ~30 min | ~18 km. Direct taxi |
| **BTS / MRT** | short walk | Exit at Ha Yaek Lat Phrao (BTS) or Phahon Yothin (MRT) |

*Taxi fares are approximate and exclude tollway charges. Confirm the meter is running, or book via the Grab app for a fixed fare.*

## Floor plan

Vibhavadee Ballroom A-B-C (Lobby Level)




*Registration, plenary sessions, parallel oral sessions, poster area and exhibition are arranged as shown. Please check the on-site signage for the latest room assignments.*

## Cultural experience: Loy Krathong Night

After the closing session on 24 November 2026, Don't miss the chance to explore the Loy Krathong (Full Moon) festival, a memorable evening for international participants. Suggested locations: Wachirabenchathat Park, Chatuchak Park, Rama VIII Park, ICONSIAM, Wat Arun Ratchawararam and Asiatique The Riverfront. Dress code: casual

23-24 NOVEMBER 2026

# Program at a Glance

*Vibhavadee Ballroom, Centara Grand at CentralPlaza Ladprao.*

## Day 1 · Monday, 23 November 2026

| | |
|---|---|
| **08:30–09:00** | Registration |
| **09:00–09:35** | **Opening Ceremony**<br>Welcome & Introduction · Welcome Address & Report · Remarks on Rice Research Support · Opening Address & Official Opening Declaration · Group Photo |
| **09:35–10:00** | Exhibition & Break |
| **10:00–12:10** | **Plenary Session I** Room: Vibhavadee Ballroom B-C<br>10:00 **Howarth Bouis** (International Food Policy Research Institute (IFPRI), United States)<br>*Future Directions for Biofortification*<br>10:30 **Apichart Vanavichit** (Kasetsart University, Thailand)<br>*Thai Rice Reimagine*<br>10:55 **Byung-Hoo Lee** (Sejong University, South Korea)<br>*Advancing rice flour processing: Biocatalytic modification for the development of slowly digestible carbohydrate ingredient*<br>11:20 **Peter McAllister** (Sustainable Rice Platform (SRP), Thailand)<br>*Putting the Farmer at the Centre of Change: Challenges and Lessons Learned from Sustainable Rice Production*<br>11:45 **Nana Kuenkel** (GIZ, Thailand)<br>*GCF Thai Rice: Scaling Climate-Smart Rice Innovation through technology, finance and institutional ownership* |
| **12:10–13:10** | Lunch Room: Vibhavadee Ballroom A |
| **13:10–13:55** | **Poster Session & Exhibition Visit** |
| **13:55–15:00** | **Plenary Session II** Room: Vibhavadee Ballroom B<br>13:55 **Martin Trtilek** (Photon Systems Instruments (PSI), Czech Republic)<br>*Making the Invisible Visible: High-Throughput Phenotyping Reveals the Hidden Life of Roots*<br>14:10 **Julie Gray** (University of Sheffield, United Kingdom)<br>*Stomata and climate resilience*<br>14:35 **Antony Champion** (Université de Montpellier, France)<br>*Unraveling the Jasmonate Regulation of Adventitious Root Development and Defense Response in Rice* |
| **15:05–17:30** | **Parallel Oral Sessions**<br>**Rice Genomics / Rice-omics (I)** · Room: Vibhavadee Ballroom B<br>Chair: Samart Wanchana (NSTDA) · Co-chair: Wasin Poncheewin (NSTDA)<br>**Abiotic Stress (I)** · Room: Vibhavadee Ballroom C<br>Chair: Julie Gray (University of Sheffield, United Kingdom) · Co-chair: Kanamon Riangwong (Silpakorn University)<br>**Novel Rice Processing and Product Innovation** · Room: Ladprao Suite 1-2<br>Chair: Savitree Ratanasumawong (Kasetsart University) · Co-chair: Nongnuch Siriwong (Kasetsart University)<br>**Agri-tech** · Room: Ladprao Suite 3-4<br>Chair: Watchareewan Jamboonsri (NSTDA) · Co-chair: Chanate Malumpong (Kasetsart University)<br>Coffee break 15:55–16:15 (Rice Genomics / Rice-omics (I) 16:05–16:25) |

## Day 2 · Tuesday, 24 November 2026

| | |
|---|---|
| **08:30–09:45** | **Plenary Session III** Room: Vibhavadee Ballroom B-C<br>08:30 **Toru Fujiwara** (The University of Tokyo, Japan)<br>*Introduction of a Moonshot project "Developing Environmentally Robust Crops based on Crop Design Technology"*<br>08:55 **Erik Murchie** (University of Nottingham, United Kingdom)<br>*Photosynthetic Heat Resilience Phenotyping, Scaling from Cell to Field*<br>09:20 **Inez Slamet-Loedin** (International Rice Research Institute (IRRI), Philippines)<br>*Harnessing Genome Editing for Healthier and Climate-Resilient Rice* |
| **09:45–10:05** | Coffee Break |
| **10:05–12:10** | **Plenary Session IV** Room: Vibhavadee Ballroom B-C<br>10:05 **Takeshi Izawa** (The University of Tokyo, Japan)<br>*From Molecular Mechanisms to Applications: Understanding and Controlling Flowering Time in Rice*<br>10:30 **Nese Sreenivasulu** (International Rice Research Institute (IRRI), Philippines)<br>*Artificial Intelligence aided precision breeding approaches to breed next generation high-quality nutritious rice varieties*<br>10:55 **Zhang Guangheng** (China National Rice Research Institute, China)<br>*NLSS3 Protects SHM1 from ATG8d-Mediated Autophagic Degradation to Regulate Leaf Morphology and Salt Tolerance in Rice*<br>11:20 **Fangjie Zhao** (Nanjing Agricultural University, China)<br>*Strategies to Reduce Heavy Metal Accumulation in Rice*<br>11:45 **Nitsara Karoonuthaisiri** (National Center for Genetic Engineering and Biotechnology (BIOTEC), NSTDA, Thailand)<br>*Mycotoxins in Rice: Occurrence, Detection, and Mitigation Strategies* |
| **12:10–13:10** | Lunch Room: Vibhavadee Ballroom A |
| **13:10–14:10** | **Poster Session & Exhibition Visit** |
| **14:10–16:45** | **Parallel Oral Sessions**<br>**Climate Change** · Room: Ladprao Suite 1-2<br>Chair: Piyada Theerakulpisut (Khon Kaen University) · Co-chair: Jonaliza L. Siangliw (NSTDA)<br>**Rice Genomics / Rice-omics (II)** · Room: Vibhavadee Ballroom B<br>Chair: Varodom Charoensawan (Mahidol University) · Co-chair: Pornpipat Kasemsap (Chulalongkorn University)<br>**Biotic Stresses** · Room: Vibhavadee Ballroom C<br>Chair: Phanchita Vejchasarn (Rice Department) · Co-chair: Chatchawan Jantasuriyarat (Kasetsart University)<br>**Health, Medical & Pharmaceutical + Abiotic Stress (II)** · Room: Ladprao Suite 3-4<br>Chair: Chanakan Prom-u-thai (Lanna Rice Research Center, Chiang Mai University) · Co-chair: Sompong Chankaew (Khon Kaen University)<br>Coffee break 15:25–15:45 Rice Genomics / Rice-omics (II) · 15:30–15:45 Climate Change · 15:30–15:50 Biotic Stresses · 15:35–15:55 Health + Abiotic Stress (II) |
| **17:00–17:30** | **Awards & Closing Ceremony** |
| **Evening** | Loy Krathong Night *(optional cultural experience)* |

*Oral abstracts (codes OS1–OS6) are presented in the parallel oral sessions, some in a session of a related topic; Poster abstracts (PS1–PS6) are displayed in the poster area during the poster sessions.*

# Plenary & Invited Speakers



**Howarth Bouis**
Founding Director, HarvestPlus; Emeritus Fellow International Food Policy Research Institute (IFPRI), United States

**Day 1 · 10:00–10:30**

## Future Directions for Biofortification

**Howarth Bouis**
Emeritus Fellow, International Food Policy Research Institute

### Abstract

The 20+ years of experience of developing and deploying biofortified crops globally in Low-and-Middle Income Countries (LMICs) through the HarvestPlus program has shown that biofortification can be an efficacious and cost-effective intervention in the fight against mineral and vitamin deficiencies. However, the impact of biofortification has been significantly limited by increasing the density of only one single nutrient per crop using conventional plant breeding techniques. Progress has been slow in increasing the density of these single nutrients.

There are two future strategies which can address the single-nutrient constraint. And these strategies may reinforce one another, multiplying their effects.

The first strategy is to use transgenic and other more advanced crop development techniques. A “three-nutrient-in one” high-yielding transgenic rice has been developed at the International Rice Research Institute in the Philippines, although it is not yet de-regulated in any country. If substituted one-for-one with non-biofortified rice in the Philippines – at no extra cost to consumer food budgets – the vitamin A intakes of the bottom 40% of the income distribution can be doubled. For the whole population on average, zinc intakes will be increased by 75% and iron intakes will be increased by 25%. These increases in nutrient intake are based on nutrient densities in milled rice.

The second strategy is to encourage a switch from milled rice to wholegrain rice. Densities of a range of mineral and vitamins tend to be relatively high in the outer bran layers. Indeed, the EAT-Lancet dietary recommendations published by Willet et al., (2019) argues strongly for switching from milled grain to the consumption of wholegrains. However, wholegrain rice in the Philippines is sold for a higher price than milled rice, making it difficult especially for low-income households to make the switch.

De-husking of rice starts a process of oxidation and degradation of unsaturated fatty acids in the bran layer at room temperatures, which results in an unacceptable rancid taste within less than two months after de-husking. Thus, the higher cost of storage, packaging, and marketing is the underlying cause of the higher price of wholegrain rice.

Importantly, there are several cost-saving advantages of processing/marketing unpolished rice over milled rice (lower cost of milling, no broken rice, higher economic value of bran for human consumption than as animal feed). Thus, if rancidity can be controlled through a genetic solution, there is the prospect that unpolished rice can be sold for a significantly lower price than milled rice. Such a price incentive could drive a switch to wholegrain rice – in particular, by lower income groups who are most price-sensitive and who would benefit most nutritionally from such a switch.

It is critical to explore genetic solutions through plant breeding to control rancidity and so to lengthen the shelf-life of unpolished rice at no extra cost. This is a key step to increasing the feasibility of brown rice consumption. Further, there is a need to

ensure that the unpolished rice does not contain harmful levels of heavy metals, as these can accumulate in the bran layer following exposure to degraded soils.

It can be expected that the densities of vitamin A, iron, and zinc in “three-in-one rice” in the bran layer will be exceptionally high.

### Short biography

Dr. Howarth Bouis is Founding Director of HarvestPlus and an Emeritus Fellow of the International Food Policy Research Institute (IFPRI). He holds a bachelor's degree in economics and a master's degree and PhD from the Food Research Institute at Stanford University. After three years as a volunteer in the Philippines, he joined IFPRI in 1982 as a postdoctoral researcher in its Food Consumption and Nutrition Division, where he studied how economic factors shape food demand and nutrition in Asia.

That work led him to propose biofortification in the early 1990s, and he founded HarvestPlus in 2003. Its biofortified crops now reach more than 50 million people in smallholder farming families in low-income countries. He received the 2016 World Food Prize, an honorary Doctor of Science from the University of Greenwich (2017), and was named a Nutrition Champion by the African Leaders for Nutrition initiative (2018). He chairs the Board of Trustees of the Micronutrient Forum.



**Apichart Vanavichit**
Rice Science Center
Kasetsart University, Thailand

**Day 1 · 10:30–10:55**

## Thai Rice Reimagine

**Apichart Vanavichit**
Rice Science Center, Kasetsart University, Kamphaeng Saen, Nakhon Pathom, Thailand
Email: vanavichit@gmail.com

### Abstract

Amid climate change, geopolitical conflict, malnutrition, and declining productivity, Thai rice has emerged as the next breakthrough in productivity and biofortification. If future consumers see rapidly digestible glucose-starch as the main cause of obesity, global rice prices will remain low. Thai rice industries must strive for a game changer in the value chain. We have developed three rice ideotypes that provide desirable nutrients and glycemic responses, combined with multiple resistances to biotic and abiotic stresses. These include pigmented soft-cooked, whole-grain varieties, varied in purple and red colours, with low to intermediate glycemic indexes, high antioxidant and anti-inflammatory activity, and dietary fibre. We developed RBR04, a purple waxy rice, loaded with 14% grain protein to improve masculinity and reduce sarcopenia and type-2 diabetes among seniors. Low-glycemic-index white rice varieties, PinK+, and tri-colour mixed grains (3G) strongly induced GLP-1, an important gut hormone controlling satiation and satiety. Two diet intervention programs using 3G rice with metabolic cohorts for 12 weeks improved BMI and reduced visceral and hepatic fats. In CKD patients at stage 3b-4, a 3G-based low-protein/low-GI diet intervention showed slow CKD progression by stabilising GFR, decreasing Albuminuria, and reducing the risk of Hyperkalemia, Hyperphosphatemia, and muscle mass loss. A nexus named after vibrant leaf colours is Rainbow Rice (RBR), which expresses stripe-wise arrays of anthocyanins, flavonoids, and chlorophyll, and is rich in antioxidants, high protein (20%), dietary fibre (60-65%), and bioavailable micronutrients, including Fe, Mg, and Mn. Most importantly, vegetative leaves contain no rapidly digestible starch and phytate to block micronutrient absorption. We focused on unique combinations of phytochemicals in the reddish leaves of RBR02: Protein Hydrolysate, Anthocyanins-Fisetin, and Dietary Fibre, serving as functional ingredients to maximise the value chain, alleviating triple-burden malnutrition and mitigating climate change.

**Keywords:** *Pigmented Rice and Leaf, Glycemic Response, Protein; Anthocyanin, Dietary Fibre, Metabolic Syndrome*

### Short biography

Dr. Apichart Vanavichit is a professor in plant breeding and Senior Adviser at the Rice Science Center, Kasetsart University. His expertise is precision breeding by integrating biodiversity, gene discovery and genomics. The best-known products are discovering economically important genes and innovative rice varieties. He has registered 54 speciality rice varieties, mainly pigmented rice, suitable for developing novel food products and resiliency to global warming. Rainbow Rice is the latest innovation, designed for developing specialized therapeutic products and enabling agro-tourism. He has published more than 100 publications in international journals.

He was honoured as the National Distinguished Researcher in Agriculture and Biological Science in 2006; Outstanding Biotechnologist from the Foundation for Promotion of Science and Technology under the Royal Patronage of His Majesty the King in 2010; Distinguished Person of Thailand for Science and Technology from the National Distinctive Committee in 2012; and the Distinguished Research and Innovation Award at the 60th Anniversary of National Research Council Thailand in 2019.



**Byung-Hoo Lee**
Department of Food Science & Biotechnology
Sejong University, South Korea

**Day 1 · 10:55–11:20**

## Advancing rice flour processing: Biocatalytic modification for the development of slowly digestible carbohydrate ingredient

**Byung-Hoo Lee**
Department of Food Science & Biotechnology and Carbohydrate Bioproduct Research Center, Sejong University, Seoul 05006, Republic of Korea

### Abstract

Rice has traditionally been a major staple food in Korea as well as in many parts of Asia; however, per-capita consumption has steadily declined owing to dietary diversification and changes in eating habits. Accordingly, expanding the utilization of rice through processed foods and rice flour has become increasingly important. Conventional rice flour production has largely relied on wet milling to minimize starch damage. To overcome the limitations associated with this process, floury rice cultivars such as Baromi 2 have been developed in Korea, featuring a soft endosperm and loosely packed, rounded starch granules that facilitate dry milling. In addition to improving processing efficiency, enhancing the functionality of rice flour is also important because its starch is rapidly digested, resulting in sharp postprandial increases in blood glucose that may contribute to the risk of metabolic diseases such as obesity and type 2 diabetes. In this study, rice flour was directly modified using a glycogen branching enzyme derived from Rhodothermus obamensis (RoGBE) as a clean-label approach to produce slowly digestible carbohydrate ingredients. The RoGBE-modified rice flour exhibited a reduced molecular size distribution and degree of polymerization, together with an increased proportion of α-1,6 linkages. Notably, the content of highly branched α-limit dextrins produced by α-amylase was markedly elevated, leading to slow hydrolysis and sustained energy release with attenuated glucose spike at the in vitro and in vivo levels. Overall, the RoGBE-treated rice flour has the potential to be utilized as a functional food ingredient to prevent metabolic diseases such as type 2 diabetes and obesity.

**Keywords:** *Rice flour, Baromi 2, Glycogen branching enzyme, Slowly digestible carbohydrate*

### Short biography

Dr. Byung-Hoo Lee is a Professor in the Department of Food Science and Biotechnology at Sejong University in Seoul, Republic of Korea. He received his Ph.D. from Purdue University in 2012 under the guidance of Dr. Bruce Hamaker, and subsequently worked as a Postdoctoral Researcher at the Whistler Center for Carbohydrate Research until 2015. After serving as a faculty member at Gachon University, he joined Sejong University, where he is also affiliated with the Carbohydrate Bioproduct Research Center (CBRC).

Building upon his foundational research on slowly digestible carbohydrates at Purdue, Dr. Lee's research group focuses on modulating carbohydrate digestion to extend the glycemic response and attenuate postprandial glucose spikes. His primary research programs include: 1) the development and application of slowly digestible carbohydrates utilizing various glycosyltransferases, 2) the production of α-glucan-type microbial exopolysaccharides, 3) the expression of recombinant human α-glucosidases and development of digestive models, and 4) the altered functionality of prebiotic ingredients through the digestive tract, including gut hormone (e.g., GLP-1) modulation.



**Peter McAllister**
Executive Director
Sustainable Rice Platform (SRP), Thailand

**Day 1 · 11:20–11:45**

## Putting the Farmer at the Centre of Change: Challenges and Lessons Learned from Sustainable Rice Production

**Peter McAllister**
Sustainable Rice Platform (SRP) Secretariat, Bangkok, Thailand
Email: Peter.mcallister@srpglobal.org

### Abstract

Rice feeds more than half of humanity and supports hundreds of millions of farmers. Climate change, water scarcity and greenhouse gas emissions make a strong case for transforming how rice is grown, to reduce the impact on the planet. But the livelihoods of those who grow rice matter just as much. Environmental ambition will only last if farmers also see their incomes, resilience and wellbeing improve. Therefore, it is essential that farmers are at the centre of change.

This presentation shares practical lessons from the Sustainable Rice Platform (SRP), a multi-stakeholder alliance of more than 130 member organizations in over 30 countries. It is not a research report. It draws on the experience of members working directly with farmers to put the SRP Standard for Sustainable Rice Cultivation into practice. It looks at what farmers must weigh when changing how they farm, including costs, risks, labour, access to markets and finance, and at what helps: understanding the farmers perspective and aspirations, building trust, effective training, peer learning and fair returns that farmers can see for themselves.

The central message is that environmental and farmer outcomes are not competing priorities, but farmer must be real partners in change. When farmers are treated as partners rather than recipients of solutions, better practices can mean better yields, lower costs and stronger incomes, alongside climate and environmental benefits. But most importantly the solutions can be adapted to the farmers reality and therefore are more likely to be effective and sustained. This session also considers how governments, companies, development partners and researchers can align behind this approach, and how tools such as the SRP Verification can connect farmer effort to market recognition.

Participants will take away practical insights on building partnerships in which farmers, national stakeholders, the rice value chain and the planet can benefit.

**Keywords:** *Sustainable rice, Farmer livelihoods, Mutual benefit, Climate resilience, Partnership*

### Short biography

Peter is an independent expert on responsible business, business ethics and multi-stakeholder initiatives. Currently engaged as the Executive Director of the Sustainable Rice Platform on an interim basis, to support the development of this important initiative.

He provides support on strategy development, responsible business, fostering relevant partnerships, supporting practical solutions to supply chain challenges and takes non-executive roles on relevant boards.

For 14 years Peter led the Ethical Trading Initiative (ETI), a leading multi-stakeholder initiative working with business, trade unions and NGOs on Human Rights and responsible business. This included engagement with a variety of supply chains, from textiles to food and manufactured goods, across Asia, Africa, Europe and Latin America.

Previously Peter established the International Cocoa Initiative bringing together the global chocolate industry, with Trade Unions and NGOs to tackle child labour and promote responsible business practices. Peter's earlier career involved roles spanning development, emergency relief and rights-based work with the NGO CARE and he served as a VSO volunteer in Malawi. Peter qualified as an Industrial Engineer.



**Nana Kuenkel**
Cluster Director Agriculture and Food
GIZ, Thailand

**Day 1 · 11:45–12:10**

## GCF Thai Rice: Scaling Climate-Smart Rice Innovation through technology, finance and institutional ownership

**Dr. Nana Kuenkel**
Deutsche Gesellschaft für internationale Zusammenarbeit (GIZ), Bangkok, Thailand
Cluster Coordinator – Agriculture and Food-Systems, Program Director "GCF-Thai Rice"
Email: nana.kuenkel@giz.de

### Abstract

Rice sustains Thailand's food security and rural livelihoods, yet it faces growing water stress and extreme weather while remaining a significant source of agricultural greenhouse gas emissions. Advances in rice research only reach their potential if farmers can adopt them at scale. This presentation argues that scaling climate-smart rice requires institutional and financial innovation alongside technical and biological innovation.

The Green Climate Fund supported Thai Rice project, implemented by GIZ Thailand with Thai government agencies, financial institutions, research organizations and private sector partners, applies this logic across 21 provinces, aiming to reach approximately 253,400 smallholder farmers. Together with the International Rice Research Institute (IRRI), the project screens innovations for their potential to scale, both in preparation and throughout implementation, and tests the most promising ones in pilots before wider roll-out.

The project promotes a portfolio of ten proven climate-smart technologies (CST) covering improved water, nutrient and crop management and more efficient use of inputs and biomass. Each is matched with financial products designed around its cost and risk profile and strengthened extension services and local service providers support farmers in applying them. Finance is an innovation in its own right, aimed at changing decisions rather than only funding them. Climate-smart incentives lower the cost and risk of a first trial, so farmers can see on their own fields that new practices work. Climate-smart loans then finance the investments needed to sustain and expand them. As adoption grows, results become visible to other farmers and communities, and climate-smart practices move from exception towards norm. BAAC's decision to raise its Climate-Smart Loan credit line to THB 5 billion (about USD 155 million), from the roughly THB 1 billion originally planned, illustrates this dynamic, as a major agricultural lender now treats climate-smart rice as bankable and is expanding its commitment. The aim is lower emissions and resource use, better soil and water quality, and stronger health and resilience of farming communities and rice-based food systems.

**Keywords:** *Rice innovation, Climate-smart agriculture, Sustainable rice production, Agricultural resilience, Smallholder farmers*

### Short biography

Since August 2022, Dr. Nana Kuenkel has headed the Agriculture and Food Cluster at GIZ. She oversees a portfolio of agriculture, food and health projects in Thailand and ASEAN, which are implemented on behalf of the German government and co-financed by various international donors and the private sector. Dr. Kuenkel has extensive experience in developing, implementing, and overseeing climate change and biodiversity projects with a focus on natural resources management for GIZ worldwide. Previously, she served as program and project director at GIZ for climate change and agriculture projects, GIZ's focal point to the Green Climate Fund, negotiator in United Nations Framework Convention on Climate Change (UNFCCC) negotiations on adaptation to climate change, and advisor to German ministries in the field of climate change adaptation in international cooperation. She has a background in agricultural economics and political science, holding doctorate and master degrees from Humboldt University Berlin and Freie Universität Berlin in Germany.



**Martin Trtilek**
Photon Systems Instruments (PSI), Czech Republic

**Day 1 · 13:55–14:10**

## Making the Invisible Visible: High-Throughput Phenotyping Reveals the Hidden Life of Roots

**Martin Trtilek [1]*, Klára Panzarová [1], Lamis Abdelhakim [1], Ivan Kashkan [1], Sajid Ullah [1], Katarzyna Retzer [2]**

1 PSI (Photon Systems Instruments), spol. s r.o., Prumyslova 470, 66424 Drásov, Czech Republic

2 Department of Ecosystem Management, Climate and Biodiversity, Institute of Forest Ecology, University of Natural Resources and Life Sciences (BOKU), Peter-Jordan Straße 82, Vienna, 1190, Austria

### Abstract

High-throughput phenotyping has substantially advanced our understanding of shoot-level stress responses, while one of the most critical parts of the plant has largely remained hidden from view—the root system. Traditional root studies are destructive, time-consuming, and poorly suited for monitoring dynamic responses to environmental changes.

Here, we demonstrate how the PlantScreen™ Root System brings the hidden below-ground phenotype into view. This automated, non-invasive platform enables parallel monitoring of root and shoot growth across multiple plant species and experimental conditions. Precise control of rhizobox soil moisture allows defined waterlogging and drought treatments, as well as controlled application of nutrients and biostimulants.

Within the BarleyMicroBreed project, root growth dynamics of ten barley genotypes were characterized during early developmental stages under optimized moderate drought conditions. Simultaneous monitoring of below- and above-ground development complements field-trial evaluations and provides new opportunities to assess how root traits contribute to plant performance and yield stability under drought.

Morphological traits of both shoots and roots were captured using RGB imaging, while multispectral and near-infrared sensors provided additional information on physiological properties, including root water content. Automated image segmentation using sensor-specific pipelines and pretrained models, followed by quantitative trait extraction, enabled efficient analysis of complex root and shoot phenotypes.

The results revealed distinct genotype-dependent responses to drought and different strategies of stress resilience. Importantly, high-throughput phenotyping at early seedling stages captured divergent root growth dynamics that may be predictive of later field performance under drought conditions.

By integrating above- and below-ground phenotyping with advanced imaging and automated analysis, we can now observe plant responses that previously remained concealed beneath the soil. Making these hidden traits visible opens new opportunities for understanding root–shoot regulation, identifying stress-resilient phenotypes, and accelerating trait selection for crop improvement.



**Julie Gray**
School of Biosciences
University of Sheffield, United Kingdom

**Day 1 · 14:10–14:35**

## Stomata and climate resilience

**Julie Gray**
School of Biosciences, University of Sheffield, United Kingdom
Email: j.e.gray@sheffield.ac.uk

### Abstract

Rice production is water intensive and vulnerable to climate change. Stomata are microscopic pores that regulate gas exchange and water loss and are key determinants of plant water use. By manipulating epidermal patterning factors that control stomatal development, we have generated rice and wheat plants with altered stomatal densities and conductance.

Crops with reduced stomatal density lose less water while maintaining photosynthetic performance and yield. Rice lines with approximately 50% fewer stomata use only 60% of the water required by wild-type plants and show improved tolerance to drought, combined drought and heat, and salt stress. These findings demonstrate that engineering stomatal development offers a strategy to improve crop water use efficiency and climate resilience while maintaining productivity.

**Keywords:** *Stomata, Water, Drought*

### Short biography

Dr. Julie Gray is a Professor in the School of Biosciences at the University of Sheffield. She is interested in plant environmental signalling responses, particularly those that trigger the closing of stomatal pores, or determine how many stomata develop on the leaf surface. She has applied these findings to engineer crop plants with greater drought tolerance and water-use efficiency. Julie studied Biochemistry at Liverpool University and was a PhD student at Nottingham University where she researched genes that control fruit ripening. She carried out postdoctoral work at the University of Melbourne investigating how flowers prevent self-pollination. Julie is a member of the European Molecular Biology Organisation (EMBO) and was awarded a Leverhulme Senior Fellowship.




**Antony Champion**

Research Director, DIADE
Institut de Recherche pour le Développement (IRD),
Université de Montpellier,
France


**Day 1 · 14:35–15:00**

## Unraveling the Jasmonate Regulation of Adventitious Root Development and Defense Response in Rice


**Mohammad CHEAIB [1], Anne-Sophie PETITOT [1], Antony CHAMPION [1*]**

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### Abstract

Jasmonate signaling plays a central role in balancing plant growth, defense and environmental adaptation, yet how distinct jasmonate receptors coordinate these processes remains poorly understood in monocots. Here, we uncover a remarkable functional specialization among rice OsCOI receptors, revealing OsCOI2 as a major regulator of root development and stress responses. Unlike its paralogs OsCOI1a and OsCOI1b, OsCOI2 predominantly controls jasmonate-dependent crown root growth and orchestrates extensive transcriptional and metabolic reprogramming, including the activation of defense-related pathways. Strikingly, we reveal an unexpected role for jasmonate perception in the regulation of aquatic adventitious roots during partial submergence. OsCOI2 maintains root primordium dormancy under non-submerged conditions, while jasmonate and ethylene signaling jointly regulate their emergence upon submergence. In contrast, OsCOI1a/b contribute to the subsequent growth of emerging roots. Together, our findings uncover a previously underappreciated subfunctionalization of jasmonate receptors, providing new insights into how hormonal signaling coordinates root developmental plasticity and adaptation to flooding in rice.



**Keywords:** *Jasmonate signaling, OsCOI receptors, Subfunctionalizatio,; Root development, Flooding adaptation*


### Short biography

Dr. Antony CHAMPION is a Research Director at the French National Research Institute for Sustainable Development (IRD) and co-leader of the CERES (Cereal Root Systems) research team within UMR DIADE at the University of Montpellier, France.

His research explores the molecular and physiological mechanisms governing root development and plant adaptation to environmental stresses, with a particular focus on rice (*Oryza sativa*). He is especially interested in hormonal signaling pathways, notably jasmonates, and their roles in root system architecture, developmental plasticity, and the balance between growth and defense.

By integrating molecular genetics, genome editing, transcriptomics, metabolomics, and plant physiology, his work investigates the regulatory networks that enable cereals to respond to challenging environments, including flooding and salinity. Recent findings have highlighted the functional specialization of jasmonate receptors in rice, identifying OsCOI2 as a key regulator of root development and stress-responsive signaling. These discoveries contribute to a deeper understanding of how plants adjust their developmental programs to changing environmental conditions.

Alongside his research, Antony Champion develops international scientific collaborations, particularly with partners in Africa and Asia. He is actively involved in capacity building, knowledge sharing, and training young scientists, while also contributing to national initiatives in plant genome editing.

His overarching objective is to connect fundamental advances in plant biology with innovative strategies to strengthen cereal resilience and promote sustainable agriculture in the context of climate change.



**Supachitra Chadchawan**
Chulalongkorn University, Thailand

**Day 1 · 15:05–15:25**

## Promoter Editing of *OsGTL1* Affects Stomatal Development and Water Use Efficiency

**Widya Fajariani [1,2], Kansinee Hungsaprug [2], Anchalee Chaidee [2], Peter G. Lynagh [3], Putut R. Purnama [4], Luca Comai [2,3] and Supachitra Chadchawan [2]***

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### Abstract

Using a proteomic approach, we identified OsGTL1 as a protein involved in drought tolerance in a mutated line of the Thai rice cultivar 'Leung Pratew 123'. The gene-editing approach to knock out this gene failed because no transgenic plants were obtained. Promoter editing of the *OsGTL1* gene with a 754 bp deletion decreased *OsGTL1* expression and stomatal density. The edited allele regulated stomatal density recessively. It also contributed to plant height as the dominant allele, suggesting a pleiotropic effect of this gene. Lower *OsGTL1* expression did not affect meristemoid formation, but it arrested complete stomatal formation, leading to lower stomatal density. However, this trait did not decrease the photosynthesis rate; instead, it increased water use efficiency (WUE) in mature leaves at the tillering stage under normal growing conditions. However, at the reproductive stage, the significantly higher WUE was not detected in the flag leaves of normally grown plants, but it was observed under drought stress conditions, suggesting different physiological adaptations related to stomatal density and developmental stage. Further investigation into the balance between leaf morphology and physiological adaptation will improve our understanding of plant life.

**Keywords:** *Flag leaf, Photosynthesis, Stomata, Tillering*

### Short biography

Dr. Supachitra Chadchawan is a professor at the Department of Botany, Faculty of Science, Chulalongkorn University. She is currently Associate Dean of Interdisciplinary and Integrative Studies at Chulalongkorn University. Her research focuses on plant molecular biology and rice physiology, using omics approaches to identify genes and understand the mechanisms that regulate plant phenotypes.



**Hiroko Yano**
Graduate School of Organic Materials Science
Yamagata University, Japan

**Day 1 · 15:05–15:25**

## Properties of Amorphous Rice Flour Produced by SHMM (Shear and Heat Milling Machine) and Application in Rice Gels

**Hiroko Yano [1], Tomonori Koda [1], Akihiro Nishioka [1]***
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### Abstract

Shear and Heat Milling (SHM) technology, originally conceived and developed by Professor Akihiro Nishioka at Yamagata University, enables the production of amorphous rice flour within a few seconds by applying heat and mechanical shear to rice grains, without requiring conventional rice cooking or the addition of water. This process is performed using a specially developed apparatus known as the Shear and Heat Milling Machine (SHMM).

The first part of this presentation examines the effects of SHM treatment on the structural characteristics of rice flour, with particular emphasis on starch crystallinity and molecular structure. Analyses of molecular weight and chain-length distributions revealed a reduction in molecular weight and preferential cleavage of amylopectin chains with a degree of polymerization (DP) of 35 or higher following SHM treatment.

The second part focuses on rice gel as a potential application of SHM-produced amorphous rice flour. Rice gels were successfully prepared without a conventional rice-cooking process. During storage at 4 °C for five days, these gels exhibited smaller changes in the magnitude of the complex modulus (|G*|) and wide-angle X-ray diffraction (WAXD) patterns compared with conventionally prepared one. These findings suggest that SHM-produced amorphous rice flour can improve the structural and viscoelastic stability of rice gels during refrigerated storage.

Overall, SHM technology offers a promising approach for producing amorphous rice flour with potential applications in a wide range of rice-based food products.

**Keywords:** *Amorphous rice flour; Shear and Heat Milling Machine (SHMM); Rice gel; Retrogradation*

**Acknowledgments:** This work was supported by the Yamagata University Advanced Agri-Food System Research Center (YAAS) and JSPS KAKENHI (Grant Number 24K00350).

### Short biography

Dr. Hiroko Yano is an Assistant Professor at the Graduate School of Organic Materials Science, Yamagata University, Japan. She received her bachelor's degree in engineering in 2016, master's degree in 2017, and doctoral degree in 2020 from Yamagata University. She was a JSPS Research Fellow (DC1) from 2018 to 2020 and an Assistant Professor at Akita Prefectural University before joining her current institution in May 2022. Her research explores the relationships between starch molecular architecture, rheological properties, and food shaping and processing behavior, with applications to rice-based and gluten-free foods. In July 2026, she received an Encouragement Award from the Tohoku Branch of the Japanese Society of Applied Glycoscience.



**Chanchana Thanachayanont**
National Metal and Materials Technology Center (MTEC), NSTDA, Thailand

**Day 1 · 15:05–15:25**

## Structure-Property-Performance Relationships of Lignocellulosic Biochar in Agricultural Soils

**Chanchana Thanachayanont [1]*, Sakonsupa Damdib [1], Nuttakron Keratipaiboon [1], Visittapong Yordsri [1], Umaporn Sanewirush [1], Premrudee Kanchanapiya [1], Onuma Santawitee [1], and Jonaliza Lanceras Siangliw [2]**

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### Abstract

Biochar is a charcoal-like, carbon-rich material produced through pyrolysis—the thermal decomposition of biomass such as crop residues, wood waste, or animal manure under oxygen-limited conditions. While known to help crop yield enhancement, nutrient retention, and contaminant immobilization, biochar is stable carbon that can remain sequestered in soil for hundreds to thousands of years.

Optimizing biochar applications in soil requires understanding of the structure–property–performance relationships of lignocellulosic biochar in agricultural soils. This mechanistic understanding enables the targeted selection of feedstocks and pyrolysis parameters to engineer specific physical and chemical characteristics, including porosity, specific surface area, aromaticity, surface functional groups, and mineral ash content. These structural features dictate key physiochemical properties—such as pH, cation exchange capacity (CEC), water-holding capacity, sorption affinity, and recalcitrance.

To promote Net Zero local community biochar activities, the National Metal and Materials Technology Center (MTEC) initiated a dedicated research theme on Net Zero Emission Biochar in 2024. Key milestones achieved to date include low-emission pyrolysis, Thai biochar standards, Thai Biochar Database, and Biochar Map. Ensuring traceability, a digital Measurement, Reporting, and Verification (dMRV) framework for sustainable community-scale biochar production has been developed and demonstrated through the integrated B-Cycle, B-IoT, and B-VER platforms.

Although lignocellulosic biochar has been promoted as a circular, nature-based carbon capture and sequestration, field responses remain strongly context dependent. From systematic review, across 13 field studies (20 treatment–control contrasts), crop-residue biochars produced at moderate temperatures (≈400–500 °C) increased soil organic carbon (SOC) by a median of 32.6% and dissolved organic carbon by 29.1%, and frequently improved nutrient indicators and crop yield. In contrast, high-ash, Si- and Ca–P-rich biochars produced at 500–600 °C generated stronger liming responses (median soil pH +16.6%), enhanced phosphorus availability, and immobilized cadmium and other metals through Ca–P-, Si-, and sorption-mediated pathways. Mechanistic analyses implicated three interacting processes in SOC accrual: aggregate-mediated physical protection, an enhanced plant–microbe carbon pump (rhizodeposition → microbial necromass), and biochemical recalcitrance coupled to microbial and gene-level regulation. Stratified response maps and correlation analyses further highlighted strong biases toward crop residues and moderate pyrolysis temperatures, as well as major evidence gaps for woody, high-temperature, and Si- or Ca–P-rich biochars.

Preliminary trial of rice straw biochar in rice cultivation by National Center for Genetic Engineering and Biotechnology (BIOTEC) will also be demonstrated. An increase in plant height, tiller number, total grain number (TGN), filled grain number (FG), percent weight of brown rice, yield per plant and biomass yield per plant were observed. A thorough mechanistic investigation for proper timing of biochar activation for the early flowering rice to benefit from biochar will be further conducted. Intermediate varieties have longer time to accumulate biomass and therefore gained more benefit from the biochar application and then translated into rice yield.

**Keywords:** *Biochar, dMRV, B-Cycle, B-IoT and B-VER*

### Short biography

Dr. Chanchana Thanachayanont holds a Bachelor's and a Ph.D. in Materials Science from Imperial College London, UK. She has contributed her expertise to the National Metal and Materials Technology Center (MTEC) since 1999 and currently serves as a Principal Researcher in the Innovative Ceramics Technology and Environmental Research Group.

Dr. Thanachayanont specializes in the research and development of environmental materials, actively working toward net-zero greenhouse gas emissions. Her work centers on integrating green skills and nature-based solutions with advanced materials technology to mitigate environmental impacts and foster sustainable solutions.

Over the past three years, Dr. Thanachayanont and her MTEC research colleagues have dedicated their efforts to the eco-friendly and traceable production and utilization of biochar. Their primary focus is on developing carbon-negative, biochar-based products to achieve permanent carbon sequestration tailored to the context of Thailand, while promoting biochar carbon credit trading to generate supplementary income for farmers and related enterprises.

**Joram A. Dongus**
Wageningen University & Research (video presentation), Netherlands

**Day 1 · 15:25–15:45**

## Advancing Salt-tolerant Rice with ThermoCas9: an Open-access Gene-editing Toolkit for LMICs

**Joram A. Dongus, Christian Südfeld, Eugenios Bouzetos, William de Martines, Ton Winkelmolen, John van der Oost, Christa Testerink**
Wageningen University & Research, Netherlands

### Abstract

Salt stress reduces crop yield, and soil salinity is expected to worsen with climate change. Although breeding efforts have aimed to improve salt tolerance in rice, success has been limited. One key factor in salt tolerance is the Na+-transporter family HKT1. In rice, OsHKT1;5 promotes salt tolerance, and its expression can be enhanced by reducing the activity of the transcription factor OsWRKY53. Gene editing of OsHKT1;5 and OsWRKY53 could therefore allow breeders to boost OsHKT1;5 expression and improve salt tolerance in rice. However, the CRISPR enzymes SpCas9 and LbCas12a are often impractical for breeding purposes due to high licensing fees, making gene editing inaccessible to small companies and non-profit breeding institutes.

To address this, we aimed to develop an open-source gene-editing approach and, as a proof of concept, are using it to create salt-tolerant rice germplasm. We first improved the mutation efficiency of the CRISPR enzyme ThermoCas9 in *E. coli*. Next, we tested whether this optimised ThermoCas9 can make stable mutations in rice calli. Currently, we are trying to increase OsHKT1;5 expression by targeting the OsHKT1;5 promoter and mutating its repressor, OsWRKY53. Preliminary data indicate that the optimised ThermoCas9 is a cheap, reliable, and robust alternative to SpCas9 for generating gene edits for breeding purposes.



**Kyung Do Kim**
Department of Integrative Biological Sciences and Industry
Sejong University, South Korea

**Day 1 · 15:45–16:05**

## Near-Isogenic Line Genomes Decode Flooding Tolerance in Rice

**Kyung Do Kim [1,2]*, Joong Hyoun Chin [1,2]**
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### Abstract

Flooding is a major climate-driven threat to rice production, damaging the crop both at germination in direct-seeded fields and during vegetative growth under complete submergence. Two loci on chromosome 9, *AG1* (*OsTPP7*) for anaerobic germination (AG) tolerance and Sub1 (Sub1A-1) for submergence tolerance, have been introgressed into elite cultivars such as IR64. However, the complete sequences of these introgressed regions, and the regulatory elements that may govern their expression, remain unresolved in existing reference genomes. Here, by integrating chromosome-level de novo assemblies of the near-isogenic lines IR64-Sub1 and IR64-AG1 with transposable element (TE) annotation, time-series transcriptomics, and co-expression networks, we show that both tolerance loci carry previously hidden structural features linked to stress-responsive transcription. The IR64-Sub1 assembly provides the first complete Sub1 reference and reveals two TEs conserved in tolerant indica varieties: an RIRE2 LTR retrotransposon ~500 bp downstream of Sub1A, inserted ~179,000 years ago, and a ~12-kb CACTA element carrying two genes with Sub1A-1-like expression under submergence, whose promoters are enriched for ERF-binding motifs. The IR64-AG1 assembly delineated a discrete Khao Hlan On-derived introgression harboring *OsTPP7*, which was stably expressed during AG together with energy-metabolism genes; co-expression analysis identified an early OsTPP7-associated module and nominated the structurally divergent cell-wall kinase gene *OsWAK79* as a candidate for coleoptile elongation. These findings demonstrate that genome-resolved comparisons of near-isogenic lines expose TE-derived and introgression-specific regulatory variation invisible to single-reference analyses, advancing rice pan-genomics and providing a basis for haplotype-level markers and combined AG1–Sub1 deployment in flood-resilient rice.

**Keywords:** *Submergence tolerance, Anaerobic germination, Transposable elements, Chromosome-level genome assembly, Near-isogenic lines*

### Short biography

Dr. Kyung Do Kim is an Associate Professor in the Department of Integrative Biological Sciences and Industry at Sejong University, where he leads Genomics and Big Data Laboratory. He is a plant geneticist and biotechnologist developing genomic solutions for agricultural challenges in the era of climate change, with work spanning fundamental genomics to applied crop improvement in rice, soybean, and medicinal crops. A central theme of his research is the discovery and characterization of genes that confer tolerance or resistance to environmental stresses. In rice, his group uses chromosome-level assemblies of near-isogenic lines to dissect loci for submergence tolerance, anaerobic germination, and heat tolerance, revealing how introgressions and transposable elements shape stress-responsive gene regulation. In soybean, he has characterized genes for resistance to soybean cyst nematode and led whole-genome resequencing analyses of more than 2,500 global germplasm accessions to map SNPs, large deletions, and copy-number variants. His laboratory also applies whole-genome sequencing to medicinal crops to decode biosynthetic pathways for valuable phytochemicals, pursues nanomaterial-based genome editing that bypasses conventional tissue culture, and is developing intelligent precision design breeding (IPDB), an agentic AI framework that integrates retrieval-augmented large language models and biological foundation models to support evidence-gated, breeder-accountable decisions. Together, these efforts link genome-resolved discovery of stress-adaptive variation with AI-guided, evidence-based breeding to accelerate the development of climate-resilient crops for sustainable food security.



**Pao-Yang Chen**
Institute of Plant and Microbial Biology
Academia Sinica, Taiwan

**Day 1 · 16:25–16:45**

## DNA Methylation Changes During Long-Term Rice Adaptation

**May Htet Aung [1], Huey Tyng Lee [1], Moe Moe Kyi Win [2], Siwaret Arikit [2]*, Pao-Yang Chen [1]***

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### Abstract

Climate change poses increasing challenges to rice production, highlighting the need to improve rice adaptability to changing environments. Plants respond to environmental changes through acclimation and adaptation. While acclimation involves largely reversible responses, adaptation requires heritable changes that improve fitness across generations. DNA methylation is involved in stress responses, but its contribution to long-term rice adaptation remains unclear. To investigate this, we conducted an eight-generation field experiment in which the Japanese rice cultivar Koshihikari was grown in Thailand. Rice yield increased by approximately 200% between years 2 and 5 and subsequently stabilized. We integrated genome-wide DNA methylation, gene expression, and genetic variation analyses to investigate the underlying molecular changes. We identified distinct methylation patterns during early and late stages of cultivation. Approximately 67% of early differentially methylated regions showed reversed methylation changes, potentially reflecting acclimation, while 33% maintained or reinforced their changes. Persistent methylation changes were associated with genes involved in grain yield, panicle development, and plant growth, whereas reversed changes were more frequently associated with stress-responsive genes. Genetic variants were also identified in genes showing persistent methylation changes. Our findings suggest that genetic and epigenetic changes may jointly contribute to improved rice performance under changing environments, providing insights into rice adaptation and future crop improvement.

**Keywords:** *Rice adaptation, DNA methylation, Epigenetics, Acclimation*

### Short biography

Dr. Pao-Yang Chen received his D.Phil. in Statistics (Computational Biology) from the University of Oxford and completed his postdoctoral training at the University of California, Los Angeles (UCLA). He joined the Institute of Plant and Microbial Biology at Academia Sinica in 2012, where he is currently a Research Fellow. He also holds a joint appointment as Professor at National Taiwan University (NTU). His research focuses on developing bioinformatics tools and computational methods to study epigenetic regulation and genome function. His laboratory has developed several widely used tools for DNA methylation analysis, including BS Seeker, MethGo, and MethGET, as well as QHistone, a machine learning framework for predicting histone modifications. His research integrates statistical and machine learning approaches to analyze large-scale genomic and epigenomic data, including DNA methylation, histone modifications, chromatin accessibility, and gene expression. In plants, his laboratory investigates how epigenetic changes contribute to gene regulation, development, and environmental responses. His rice research focuses on genetic and epigenetic changes during long-term cultivation under different environmental conditions, as well as DNA methylation dynamics during tissue culture, regeneration, and genetic transformation. He welcomes collaborations that combine bioinformatics and experimental approaches to better understand epigenetic regulation in plants and improve crop traits.



**Toru Fujiwara**
Graduate School of
Agricultural and Life Sciences
The University of Tokyo, Japan

**Day 2 · 08:30–08:55**

## Introduction of a Moonshot project "Developing Environmentally Robust Crops based on Crop Design Technology"

**Toru Fujiwara**
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### Abstract

The government of Japan initiated project called Moonshot in 2020. The project for 10 years has currently 9 goals including wide range of sciences to develop challenging technologies. Among them, Goal 5 is defined as "Sustainable Global Food Supply." The Goal 5 aims to establish industries that enables sustainable global food supply by fully exploiting underutilized biological resources by 2050. In response to growing food demand, climate change, resource depletion, and the environmental impacts of conventional agriculture, the program seeks to transform food production and consumption through innovative science and technology.

In this Goal 5, currently 8 projects are running. One of them is our project MS501 entitled "Achieving Zero Food Risks by Improving Crop Resilience Using Cyber-Physical Systems." Global food security is increasingly threatened by climate change, extreme weather events, soil degradation, and the depletion of agricultural resources. Conventional crop breeding often requires many years to develop new varieties adapted to changing environmental conditions. Current rate of environmental changes becomes extreme. Global warming reached already more than 1.5℃ in 2024, which was expected to reach in 2030. This rapid change in the environments exceeds the ability of conventional breeding to cope with the change. MS501 aims to overcome these challenges by establishing innovative technologies for the rapid development of resilient crops.

The project focuses on understanding the mechanisms that enable wild plant species and crop relatives to survive under harsh environmental conditions, including drought, heat, and nutrient deficiency. By identifying the genes and biological mechanisms responsible for these adaptive traits, we seek to apply this knowledge to the development of improved crop varieties. A central feature of the project is the integration of biological research with digital technologies through a cyber-physical system. By combining experimental data, computational modeling, and digital crop design, the project aims to accelerate the breeding process and predict crop performance under diverse environmental conditions. We have successfully generated several stress-tolerant rice lines using resources from wild rice species and omics data/cyber-physical systems. In the present presentation, I would like to present outline of the project, current achievements and future directions. Our project seeks international collaboration, and I hope this presentation will mark a new future collaboration between Thailand and Japan.

**Keywords:** *Rice, Stress Tolerance, Crop Design*

### Short biography

Professor Toru Fujiwara leads the Laboratory of Plant Nutrition and Fertilizers in the Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Japan. He graduated from the Department of Agricultural Chemistry at The University of Tokyo in 1987 and received his Ph.D. from the same university in 1992, with a thesis entitled "Seed Specific Expression of Soybean Seed Storage Protein Genes." From 1989 to 1991, he was a visiting scholar in Professor Roger Beachy's laboratory at Washington University in St. Louis, USA. He served as an Assistant Professor in the Laboratory of Plant Nutrition at The University of Tokyo from 1992 to 2003 and as an Associate Professor at its Biotechnology Research Center from 2003 to 2010. He has held his current professorship since April 2010.



**Erik Murchie**
School of Biosciences
University of Nottingham,
United Kingdom

**Day 2 · 08:55–09:20**

## Photosynthetic Heat Resilience Phenotyping, Scaling from Cell to Field

**Erik H. Murchie**
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### Abstract

Rising temperatures increasingly threaten both the yield and nutritional quality of rice. Heat-induced inhibition of photosynthesis is a key part of the problem, but it must be understood alongside a complex set of traits including tissue tolerance, acclimation, resource partitioning, energy balance and development. Leaf photosynthetic heat tolerance (PHT) itself arises from multiple components spanning gas exchange, carbon assimilation and the thylakoid reactions. We therefore need rapid screening methods that give physiological insight into PHT while being fast enough to link with key yield-forming traits and field validation. Chlorophyll fluorescence offers a rapid, automatable screen for PHT through Tcrit, the critical temperature at which photosystem II stability breaks down. Although the approach originated in classical ecophysiology, its speed and accessibility now make it well suited to breeding-scale phenotyping. I will describe recent work in my group using Tcrit to screen diversity panels at high throughput, showing repeatability and to identify candidate genes through GWAS spanning diverse processes. I will present new data linking Tcrit to whole-plant performance and yield under heat-stress conditions. I will also discuss the likely physical origins of Tcrit and its limitations, and propose a theoretical basis for using it to predict emergent heat tolerance in breeding programmes.

Finally, I will present progress within the UK rice research community and introduce OryzaNet, a new initiative that aims to connect UK rice research and foster productive collaborations.

**Keywords:** *Heat stress, Photosynthesis, Tissue phenotyping, Scaling, Network, Collaboration*

### Short biography

Dr. Erik Murchie is Professor of Applied Plant Physiology in the School of Biosciences at the University of Nottingham, UK. His research has explored how photosynthesis responds to real-world environments and how this knowledge can be used to improve crop yield. Prof Murchie's group has published multiple studies of cereal photosynthesis in collaboration with global partners such as the International Rice Research Institute. Over the last decade his work has focused increasingly on how cereal crops particularly rice copes with heat. His group developed rapid, high-throughput chlorophyll fluorescence methods that predict genotypic variation in photosynthetic heat tolerance using these methods to genetically dissect heat tolerance across diverse Asian (*Oryza sativa*) and African (*O. glaberrima*) rice, and explored how carbon dynamics might stabilise reproductive development under heat stress. He also showed that enhanced photoprotection can increase rice yield and radiation use efficiency, and pioneered 3D canopy reconstruction to resolve dynamic photosynthesis in the field. He helped establish the UK rice research community and contributes to international research on yield potential and night-time warming.



**Inez Slamet-Loedin**
Rice Genetic Design & Validation Unit
International Rice Research Institute (IRRI), Philippines

**Day 2 · 09:20–09:45**

## Harnessing Genome Editing for Healthier and Climate-Resilient Rice

**Inez H. Slamet-Loedin**
International Rice Research Institute (IRRI), Los Baños, Laguna, Philippines
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### Abstract

Rice production faces increasing challenges from climate change, emerging diseases, declining natural resources, and the need for improved nutritional quality. Genome editing offers opportunities to accelerate rice improvement through targeted genetic modifications directly in elite, farmer-preferred varieties.

At the International Rice Research Institute (IRRI), genome editing is integrated into breeding pipelines to develop healthier, more resilient, and resource-efficient rice. Advances in transformation and regeneration have enabled the application of CRISPR-Cas technologies across diverse indica rice varieties from Asia and Africa. Gene knockout, multiplex promoter editing, and prime editing are being applied to address priority traits.

Recent achievements include multiplex editing of *SWEET* gene promoters for bacterial leaf blight resistance; *OsNAS2* promoter editing to increase grain zinc and yield; and prime editing for enhancing fungal disease resistance. Other promising developments include yield increase under very low nitrogen conditions and lowering-glycemic-index rice through targeted modification of starch biosynthesis.

Beyond technical advances, successful deployment requires rigorous molecular characterization, regulatory readiness, accessible intellectual property arrangements, and partnerships with national research systems. Integrating genome editing into public-sector breeding program offers a promising pathway to accelerate the delivery of healthier, climate-resilient rice varieties for farmers and consumers.

**Keywords:** *Genome editing, CRISPR-Cas, Rice improvement, Climate resilience, Nutritional quality*

### Short biography

Dr. Inez H. Slamet-Loedin is Principal Scientist at the International Rice Research Institute (IRRI), where she leads the Genetic Design and Validation Unit and serves as Global Lead of the CGIAR Genome Editing Initiative. With over three decades of experience in plant biotechnology and crop improvement, she specializes in genetic transformation and genome editing.

She began her scientific career at the Indonesian Institute of Sciences (LIPI), earned her PhD from the University of Nottingham, UK, and completed postdoctoral research at Leiden University, the Netherlands. At IRRI, she has pioneered research in genetic transformation and genome editing of elite indica rice varieties.

Her work advances rice nutritional quality, disease resistance, climate resilience, and resource-use efficiency. She has published extensively in international journals such as Nature, Nature Biotechnology, Nature Plants, Nature Genetics, Nature Communications, and PNAS. She is also recognized for strengthening global research partnerships and capacity development, particularly across Asia and Africa.

Dr Slamet-Loedin is an Adjunct Professor at the University of the Philippines Los Baños and a Fellow of The World Academy of Sciences (TWAS). Recently elected to the TWAS Council (2027–2028) representing East and Southeast Asia, she is committed to advancing scientific innovation and sustainable agriculture.



**Takeshi Izawa**
Department of Agricultural and Environmental Biology
The University of Tokyo, Japan

**Day 2 · 10:05–10:30**

## From Molecular Mechanisms to Applications: Understanding and Controlling Flowering Time in Rice

**Takeshi Izawa**
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### Abstract

Flowering time is a key determinant of rice adaptation to diverse environments and various traits including grain yields and quality. My research has focused on elucidating the molecular mechanisms underlying photoperiodic flowering in rice, a short-day plant.

In this presentation, I will first summarize our previous studies on the molecular mechanisms that enable rice to perceive day length and precisely regulate flowering through the transcriptional control of florigen genes. I will then introduce recent advances in transcriptome analysis and promoter dissection to investigate the regulatory networks and cis-regulatory elements controlling flowering-related gene expression. In addition, I will present a newly developed genome-wide association study (GWAS) approach designed to improve the detection of genes underlying complex traits by addressing the problem of false-negative loci.

Finally, I will discuss our ongoing efforts to develop rice cultivars for whole-crop silage (WCS) production using florigen mutants. By connecting fundamental research on flowering-time regulation with genomic approaches and cultivar development, this presentation will highlight the potential of molecular plant science to address emerging challenges in rice production and agricultural sustainability.

**Keywords:** *Rice, Short-day plant, Photoperiodic flowering, GWAS, Whole crop silage*

### Short biography

Dr. Takeshi Izawa is a Professor in the Graduate School of Agricultural and Life Sciences at The University of Tokyo, Japan. His research focuses on the molecular mechanisms of photoperiodic flowering in rice, a short-day plant, and the genetic and molecular basis of flowering-time regulation.

After contributing to the establishment of rice transformation technology in the late 1980s at Plantech Research Institute (1988-1994), he conducted research at NAIST (1994-2001) and subsequently at NIAS (2001-2016) before joining The University of Tokyo as a professor in 2016. His research has revealed key genetic components and regulatory mechanisms controlling rice flowering, including the roles of photoperiod perception and florigen genes. His work has contributed significantly to establishing rice as a model system for understanding the molecular basis of flowering in short-day plants.

Beyond elucidating fundamental biological mechanisms, Dr. Izawa is committed to translating molecular insights into innovative approaches to crop improvement. His research explores the genetic basis of flowering-time variation, the evolution of gene function during rice domestication, and the development of strategies to manipulate flowering time under different environmental conditions. By integrating molecular genetics, genomic analyses, and field-based research, he aims to bridge fundamental plant science and practical applications in agriculture.



**Nese Sreenivasulu**
International Rice Research Institute (IRRI), Philippines
**Day 2 · 10:30–10:55**

## Artificial Intelligence aided precision breeding approaches to breed next generation high-quality nutritious rice varieties

**Nese Sreenivasulu**
International Rice Research Institute, Los Banos, Laguna 4030, Philippines
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### Abstract

The world is grappling with a triple burden of malnutrition, characterized by the simultaneous rise in non-communicable diseases, undernutrition, and hidden hunger, especially in low- and middle-income countries with significant income inequality. Coincidentally, a significant portion of the population affected by these health-threatening conditions relies heavily on rice as a staple food. This underscores the vital role that rice can play in addressing the global malnutrition crisis and combating diet-related conditions. We systematically explored the diverse gene bank collections for phenotypic plasticity in seed metabolism for multi-nutritional properties and low glycemic index (GI) properties. We performed comprehensive genomics and metabolomics complemented with modeling analyses emphasizing the importance of OsSBEIIb along with additional candidate genes whose variations allowed us to produce target rice lines with lower GI and high PC (14-16%) in a high-yielding background. By integrating genetic techniques with classification models, this comprehensive approach identified candidate genes on chromosome 2 (qGI2.1/qAC2.1 spanning the region from 18.62 Mb to 19.95 Mb), exerting influence on low GI and high amylose. Notably, the phenotypic variant with high value was associated with the recessive allele of the starch branching enzyme 2b (sbeIIb). The genome-edited sbeIIb line confirmed low GI phenotype in milled rice grains. Comprehensive metabolomic analysis further revealed a metabolic shift in superior rice lines, favoring peptides and specific flavonoids, while high glycemic index rice lines showed an enrichment of certain triglycerides. The metabolite genome-wide association study (mGWAS) conducted on the whole grain rice collection revealed genetic variants influencing various metabolic traits during seed development and maturation. Further analysis linked genetic variants on chromosome 7 (6.06–6.43 Mb region) with complex epistatic interactions affecting multiple nutritional targets, including carbohydrate starch quality, glycemic index, antioxidant catechin levels, and grain pigmentation. This multi-omics approach identified rare gene bank accessions carrying variants in bHLH and IPT5 genes, associated with low glycemic index, increased catechin and total flavonoid content, and enhanced antioxidant activity. These accessions also exhibited strong anti-cancer properties in cell line assays. The metabolomic-driven insights from this study provide valuable information for breeding rice varieties with low glycemic index, improved nutritional profiles, and potential health benefits. Deploying this genetic knowledge we have introgressed low GI and high protein traits into multiple mega-varieties exhibiting high yielding attributes without compromising texture. These healthier rice varieties have been scaled in India and Philippines to more than 1400 hectares and a dedicated processing plant being set up to scale the low GI and high protein milled rice and low GI food products for domestic and international markets.

### Short biography

Dr. Nese Sreenivasulu is an internationally renowned principal scientist who provides leadership for grain quality and nutrition research program at the International Rice Research Institute (IRRI) in the Philippines. His team developed and deployed enabling technologies with far-reaching implications in the fields of biochemistry, food science, genetics and genomics.

From 2013 to 2017, Dr. Sreenivasulu led the program for full integration of grain quality and nutrition research with IRRI's varietal improvement programs towards creating product-oriented breeding pipelines that meet the demand of rice farmers, millers, processors, and consumers. He served as IRRI-India Research Coordinator to streamline the ICAR-IRRI research program.



**Zhang Guangheng**

China National Rice Research Institute, China

**Day 2 · 10:55–11:20**

## NLSS3 Protects SHM1 from ATG8d-Mediated Autophagic Degradation to Regulate Leaf Morphology and Salt Tolerance in Rice

**Abstract:** printed with the oral abstracts as OS3-10, page 77.



**Fangjie Zhao**

College of Resources and Environmental Sciences Nanjing Agricultural University, China

**Day 2 · 11:20–11:45**

## Strategies to Reduce Heavy Metal Accumulation in Rice

**Fang-Jie Zhao**

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### Abstract

Rice is a staple food for about half of the global population, for whom rice is also a major dietary source of the toxic metal cadmium (Cd) and metalloid arsenic (As). Contamination of paddy soils with Cd and As is a common problem in some areas of Asian countries, resulting in elevated dietary exposure to Cd and As and significant health risk for the local residents. It is therefore imperative to develop strategies to limit Cd and As accumulation in rice. Substantial progress has been made in recent years on understanding of the biogeochemistry of As and Cd in paddy soils, providing a basis for controlling their bioavailability in soil. There are large variations in As and Cd accumulation among rice germplasm. Genes for some of the grain Cd accumulation QTLs have been cloned and characterized. Strategies have also been developed to limit the uptake or translocation of Cd and As by rice through plant breeding or biotechnology, based on recent progress on understanding the molecular mechanisms of their uptake, translocation and detoxification. These progresses and future research needs will be discussed in the presentation.

**Keywords:** *Arsenic, Cadmium, Heavy metals, Rice*

### Short biography

Dr. Fang-Jie Zhao is a Professor at Nanjing Agricultural University, China. He obtained his PhD at the University of Newcastle Upon Tyne, U.K. in 1992 and worked at Rothamsted Research, U.K. for over 20 years. He has been a group leader at Nanjing Agricultural University since 2012, focusing on the nexus between soil-plant nutrition-human health. His research interests include the biogeochemistry of trace elements in soil-plant systems, molecular mechanisms of trace element uptake by plants, biofortification of essential micronutrients and bioremediation of contaminated soils. His research group adopts a multidisciplinary approach, employing research tools and methodologies in environmental chemistry, soil microbiology, plant genetics and molecular biology. He has published 460 peer-reviewed papers with a H-index of 136. He is a Highly Cited Researcher (Web of Science) and received the World Academy of Sciences TWAS Award in Agricultural Science (2024) and the IFA Norman Borlaug Plant Nutrition Award by the International Fertilizer Association (2022).



**Nitsara Karoonuthaisiri**

National Center for Genetic Engineering and Biotechnology (BIOTEC), NSTDA, Thailand

**Day 2 · 11:45–12:10**

## Mycotoxins in Rice: Occurrence, Detection, and Mitigation Strategies

**Nitsara Karoonuthaisiri [1,2,3]*, Umaporn Uawisetwathana [1,2], Prae Noppakuadrittidej [1,2], Nazmi Waesoh [2,4], Awanwee Petchkongkaew [2,3,4], Christopher Elliott [3,4], Christina Vlachou [5], Thanit Praneenararat [6], Thanasat Sooksimuang [2,7], Waraporn Panchan [2,7], Wannee Sukbangnop [2,7], Grit Pichayaway-tin [2,8], Armote Somboonkaew [2,8]**

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### Abstract

Mycotoxin contamination in rice represents a critical threat to global food safety, international trade, and public health. As climate change accelerates environmental stress, shifting fungal dynamics have increased the occurrence of not only known mycotoxins such as aflatoxins, ochratoxin A, and fusarium toxins, but also emerging mycotoxins across both pre-harvest and post-harvest stages of the rice supply chain. A comprehensive analysis of mycotoxins in Thai rice, along with its exposure assessment and health risk evaluation, will be reported.

Addressing these exposure risks relies on robust, multi-tiered detection frameworks. For rapid, on-site monitoring, mycoSMART (Mycotoxin Strip based on MicroARray Technology) was developed as a field-deployable, high-throughput lateral flow platform capable of simultaneously detecting multiple regulated mycotoxins within minutes without complex laboratory infrastructure. To complement rapid field screening, advanced Liquid Chromatography–Mass Spectrometry (LC-MS/MS) techniques enable high-sensitivity, super-multiplex quantification of both regulated mycotoxins and newly emerging or modified forms in complex rice matrices.

To effectively lower risk, diagnostic data must be paired with actionable mitigation strategies across the entire value chain. Several potential mitigation strategies will be discussed to safeguard the future of rice safety and security.

**Keywords:** *Mycotoxins, Rice, mycoSMART, Detection, Mitigation*

### Short biography

Dr. Nitsara Karoonuthaisiri is a biotechnology innovator based at the National Center for Genetic Engineering and Biotechnology (BIOTEC) in Thailand. Her research focuses on advancing food safety and security by translating complex laboratory science into field-deployable biosensors, microarrays, and diagnostic platforms.

A pioneer in multiplex diagnostic technologies, Dr. Karoonuthaisiri led the development of mycoSMART (Mycotoxin Strip based on MicroARray Technology), an innovative diagnostic platform designed for rapid mycotoxin monitoring and surveillance in agricultural commodities such as rice. Her multidisciplinary work bridges key gaps between early contaminant detection, risk management, and practical mitigation strategies across agricultural and food systems.

Dr. Karoonuthaisiri serves as a founding Co-Director of the International Joint Research Center on Food Security (IJC-FOODSEC) and an Honorary Professor at Queen's University Belfast, UK. Internationally recognized for her leadership in global scientific policy, she was also a founding Co-Chair of the Global Young Academy and a Young Global Leader with the World Economic Forum. Throughout her career, she has authored over 90 peer-reviewed scientific publications (h-index of 34), holds more than 40 patents, and has delivered over 15 field-ready prototypes to strengthen regional and global food safety.



**Lianxing Yang**
HC Scientific Bio (Chengdu) L.L.C., China
**Day 2 · 14:10–14:25**

## Intelligent Automation in Rice Breeding: From Genomics to Phenomics

**Lianxing Yang**
HC Scientific Bio (Chengdu) L.L.C., Chengdu, China
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### Abstract

Driven by global initiatives to enhance agricultural productivity and sustainability, crop breeding has entered a transformative era that integrates conventional methods, biotechnology, and artificial intelligence (AI) into a multidisciplinary, systematic framework. This presentation introduces the end-to-end intelligent automation solutions developed by HC Scientific, built upon two interconnected core technology pillars: genomics and phenomics. The genomics platform enables high-throughput, cost-effective genotyping to achieve precise dissection of complex crop genomes. Complementarily, the phenomics platform leverages advanced sensors and AI-powered computer vision for the automated, high-throughput acquisition of key agronomic traits. Together, these platforms establish a robust, data-driven closed loop bridging genetic screening, functional validation, and phenotypic integration.

As a leading life science technology provider, HC Scientific addresses the bottlenecks of modern AgTech through proprietary automation platforms and interdisciplinary R&D. Key innovations highlighted in this session include:

Genomics & Molecular Breeding Solutions: The HyperGeno system for automated ultra-high-throughput genotyping, delivering a testing capacity of 153,600 reactions per 8 hours at a 50% reduction in consumable costs; versatile throughput options including the GeneMathematica Pro and GeneMatrix Lite series, and the TechCycler 480 real-time PCR system with interchangeable 96/384 blocks; the MagC9600 and MagC384 automated nucleic acid extraction workstations.

Phenomics & Trait Evaluation Platforms: PhenoFlex II (Handheld Field Phenotyping System), an all-weather portable field terminal utilizing multi-dimensional ranging and machine vision algorithms for intelligent trait data management; and RootBiScan (Automated Dual-Sided Root Scanning Platform), a high-throughput system capable of rapid dual-sided imaging (<10 seconds per root) coupled with deep learning algorithms for deep architecture and nodule analysis of complex root systems.

By seamlessly embedding genomic insights and phenomic data within fully automated workflows, HC Scientific provides critical tools and systematic architecture to transition crop breeding from experience-based selection to precision design, empowering the global agricultural community to scale breeding programs with unprecedented reproducibility and efficiency.

**Keywords:** *Intelligent Rice Breeding, High-Throughput Genotyping, Crop Phenomics.*

### Short biography

Dr. Lianxing Yang brings over 15 years of cross-functional expertise in molecular diagnostics, nucleic acid chemistry, and global business development. Currently serving as Regional Sales Manager at HC Scientific, he not only focuses on revenue growth but also provides scientific and technical consultation for key accounts and distributors, driving commercial adoption of high-throughput automation solutions in modern molecular breeding. He works closely with breeding institutions and agricultural genomics labs to align HC Scientific's platform capabilities with real-world workflow needs, ensuring that sales success is built on sound science and customer trust. He holds a PhD in Biology from Philipps University Marburg, Germany.



**Bui Tan Yen**
International Rice Research Institute (IRRI), Philippines
**Day 2 · 14:10–14:30**

## Potential Mitigation Measures in Rice Cultivation

**Bui Tan Yen**
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### Abstract

Rice cultivation is a significant source of greenhouse gas (GHG) emissions, particularly methane ($CH_4$) generated under flooded soil conditions and nitrous oxide ($N_2O$) associated with nitrogen fertilizer application and soil processes. Reducing emissions from rice production requires an integrated approach combining improved land and crop management, irrigation water management, residue management, and more efficient fertilizer use. The International Rice Research Institute (IRRI) conducted several studies to examine potential GHG mitigation measures and their applicability and scaling potential across rice-growing countries.

The potential GHG mitigation options include reducing the area and duration of flooded rice cultivation, land laser leveling, minimum tillage, adoption of short-duration and low-emission rice varieties, and dry direct seeding. Improved irrigation practices, particularly Alternate Wetting and Drying (AWD) and Mid-season Drainage (MSD), offer substantial mitigation potential by creating aerobic soil conditions that suppress methane production, with reported reductions of up to 45% in $CH_4$ emissions and 30% in water use without yield penalties. Rice residue management provides further opportunities through mechanized straw collection, composting, mushroom production, biochar, organic fertilizer, and other value-added products, thereby reducing methane emissions from straw incorporation and emissions associated with open-field burning. In addition, improved fertilizer management, including optimized nitrogen application, site-specific nutrient management, deep placement, and slow-release fertilizers, can enhance nutrient-use efficiency and reduce $N_2O$ emissions.

To assess the potential for scaling these measures, spatial analysis can integrate rice extent and cropping calendars derived from remote sensing with climate, soil, topographic, flood and drought risk, and irrigation infrastructure data. For mechanized straw collection, soil conditions, terrain, accessibility, and field trafficability are important factors in identifying suitable areas. Emerging solutions, including low-emission rice varieties and microbial seed and seedling treatments, also show promising initial results, although further research and validation are required.

Overall, combining agronomic, water, residue, and fertilizer management interventions offers opportunities to reduce the GHG emission and footprint of rice production while improving resource-use efficiency and supporting more sustainable rice value chains. Spatially explicit assessment of mitigation potential and implementation constraints is essential for prioritizing suitable technologies and developing effective strategies for scaling low-emission rice production.

**Keywords:** *Rice cultivation, low-emission practices, climate change mitigation*

### Short biography

Dr. Bui Tan Yen is a Climate Change Scientist at the International Rice Research Institute (IRRI), based at the IRRI Cambodia Office in Phnom Penh. He specializes in climate change mitigation and adaptation in agriculture, with particular expertise in greenhouse gas (GHG) mitigation in rice production, monitoring, reporting and verification (MRV) systems, and digital solutions for climate change management.

He has over two decades of experience in agricultural research and development, combining expertise in soil science, land-use planning, geospatial analysis, and integrated natural resource management. He has worked extensively across Southeast Asia, coordinating multidisciplinary research initiatives and collaborating with national governments, research institutions, and development partners to promote climate-smart and low-emission agricultural practices. His work focuses on developing and strengthening rice-sector MRV frameworks, integrating digital technologies into GHG monitoring, and applying spatial modelling to assess climate risks and identify suitable areas for scaling mitigation interventions.

Dr. Yen has contributed to the development of several digital tools supporting rice-sector GHG monitoring and mitigation assessment, including RiceMoRe, MapAWD, CF-Rice, SECTOR, and LUSET. He has also been actively involved in research on rice carbon footprints, methane emission assessment, climate risk mapping, and the implementation of climate change adaptation and mitigation measures in national agricultural policies and strategies.

He holds a PhD in Wageningen University, the Netherlands, an MSc in Soil Science, and a Bachelor's degree in Agronomy from Hanoi Agricultural University, Vietnam. He has authored and co-authored numerous scientific publications on climate-smart agriculture, GHG mitigation, land-use planning, and sustainable rice production.



**Chatchawan Jantasuriyarat**
Kasetsart University, Thailand
**Day 2 · 14:10–14:30**

## Strain-Specific Thermotolerance in *Pyricularia oryzae* Is Associated with Temperature-Dependent Appressorium Development and Pathogenicity

**Thanathip Sutthiphai [1], Sayuki Hiraiwa [2], Pattavipha Songkumarn [3], Hitoshi Nakayashiki [2], Kenichi Ikeda [2]*, Chatchawan Jantasuriyarat [1,4]***
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2 Department of Agrobioscience, Faculty of Agriculture, Kobe University, Hyogo, Japan
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### Abstract

Rice blast, caused by *Pyricularia oryzae*, poses a major threat to rice production worldwide. Understanding pathogen responses to elevated temperatures is increasingly important under climate warming. This study investigated strain-specific thermotolerance through phenotypic characterization, pathogenicity assays, chemical complementation, and transcriptomic analysis. Ten strains were evaluated for appressorium development at 25, 30, and 35°C. All strains exhibited high appressorium maturation (>85%) at 25°C, whereas development was nearly inhibited at 35°C. At 30°C, five thermotolerant strains maintained >90% mature appressoria, while five thermosensitive strains showed reduced maturation (approximately 6–44%). Pathogenicity assays revealed that thermotolerant strains maintained pathogenicity, whereas thermosensitive strains exhibited contrasting responses. PL61017 showed significantly reduced pathogenicity, while MSN61005 maintained pathogenicity despite impaired appressorium maturation at 24 h. Time-course experiments revealed delayed rather than permanently inhibited appressorium development in MSN61005. Chemical complementation with 1,16-hexadecanediol partially restored appressorium formation in MSN61005 but had little effect on PL61017, suggesting differential responses to surface-associated cues. Comparative transcriptomic analysis of representative thermotolerant (PL61001) and thermosensitive (MSN61005) strains identified 32 and 365 strain-specific differentially expressed genes, respectively, with 44 shared genes. The thermosensitive strain exhibited broader transcriptional responses involving metabolism, transport, and secondary metabolism. Together, these findings demonstrate strain-specific variation in thermal responses and highlight the importance of developmental timing and transcriptional responses in understanding rice blast pathogenicity under elevated temperatures.

**Keywords:** *Rice blast, Thermotolerance, Appressorium development, Pathogenicity, Transcriptomics*

### Short biography

Dr. Chatchawan Jantasuriyarat is an Associate Professor in the Department of Genetics, Faculty of Science, Kasetsart University, Thailand. He received his Bachelor of Science degree in Biology from Kasetsart University, Thailand, a Master of Science degree in Crop Science from Oregon State University, USA, and a Ph.D. in Plant Pathology from The Ohio State University, USA.

His research focuses on rice genetics, molecular plant pathology, and rice–pathogen interactions, particularly the interactions between rice and the rice blast fungus, *Magnaporthe oryzae*. His research interests include the identification and characterization of genes associated with rice blast resistance, genetic diversity and population structure of rice blast pathogen populations, molecular marker development, and the application of molecular and genomic approaches to rice improvement. He also investigates the molecular mechanisms underlying rice defense responses against fungal pathogens and explores innovative molecular diagnostic tools for the rapid detection of rice blast disease.

Through an integrated approach combining genetics, molecular biology, and plant pathology, his research aims to improve the understanding of rice–*Magnaporthe oryzae* interactions and support the development of rice varieties with enhanced disease resistance, contributing to sustainable rice production and food security.



**Pornpoj Pramyothin**
Faculty of Medicine Siriraj Hospital, Mahidol University, Thailand

**Day 2 · 14:10–14:30**

## Rice as a Clinically Proven Dietary Strategy Against Obesity and Diabetes

### Short biography

Associate Professor, Division of Clinical Nutrition, Department of Medicine, Faculty of Medicine Siriraj Hospital, Mahidol University (2024–present).

Doctor of Medicine with First Class Honors, Faculty of Medicine Siriraj Hospital, Mahidol University (2004). Internal Medicine Residency, University of Hawaii at Manoa (2006–2009). Fellowship in Endocrinology, Diabetes and Nutrition (2009–2011) and Fellowship in Clinical Nutrition (2011–2012), Boston University School of Medicine.

American Board of Internal Medicine (2009); American Board of Endocrinology, Diabetes, and Metabolism (2011); National Board of Physician Nutrition Specialist (2011).



**Sunee Chotineeranat**
National Center for Genetic Engineering and Biotechnology, Thailand

**Day 2 · 14:30–14:50**

## Unlocking the Health Potential of Thai Rice: From Biodiversity to Processing Innovation

**Sunee Chotineeranat [1*], Usa Yonkoksung [1], Rungtiwa Wansuksri [1], Pathama Chatakanonda [2]**

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2 Biomass and Bioenergy Technology Division, Kasetsart Agricultural and Agro-Industrial Product Improvement Institute (KAPI), Kasetsart University, Bangkok, Thailand

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### Abstract

Thailand is recognized as one of the world's richest sources of rice biodiversity, encompassing a wide range of varieties with unique nutritional and functional characteristics. Beyond its role as a staple food, rice contains valuable bioactive components, including resistant starch, dietary fiber, antioxidants, γ-oryzanol, and GABA, which have been associated with health benefits such as improved glycemic control, gut health, and chronic disease prevention.

This presentation explores how the genetic diversity of Thai rice contributes to variations in grain composition, starch structure, and nutritional quality. The results highlight the relationship between rice biodiversity and health-promoting traits, with particular emphasis on starch digestibility. The lecture also discusses how innovative processing technologies, including germination, heat-moisture treatment, parboiling, and fermentation, can enhance the functional properties of rice and unlock its full health potentials.

By integrating rice biodiversity with processing innovation, Thailand has a unique opportunity to develop next-generation functional rice products that address emerging consumer demands for healthier and more sustainable foods. The presentation also provides insights into current research trends and future directions for creating value-added rice products that support both human health and agricultural competitiveness.

**Keywords:** *Thai Rice Biodiversity, Functional Rice, Resistant Starch, Processing Innovation, Health-Promoting Foods*

### Short biography

Dr. Sunee Chotineeranat is a Senior Researcher at the National Center for Genetic Engineering and Biotechnology (BIOTEC), National Science and Technology Development Agency (NSTDA), Thailand. She received her Ph.D. in Agro-Industrial Product Development from Kasetsart University and has more than 25 years of experience in food science, starch technology, and agro-industrial research. Her work focuses on starch structure and functionality, rice and cassava processing and modification, resistant starch development, and the application of innovative processing technologies to enhance the nutritional and functional properties of starch-based food products. Throughout her career, she has led and participated in numerous research projects aimed at adding value to agricultural commodities and supporting the development of functional foods and bio-based products. She has collaborated with researchers, academic institutions, government agencies, and industry partners in Thailand and internationally to advance research and innovation in the food and agricultural sectors. Her current research interests include utilizing rice biodiversity, starch modification, and sustainable processing technologies to develop healthier starch-based products with improved nutritional quality and potential health benefits, contributing to Thailand’s bioeconomy and sustainable food systems.

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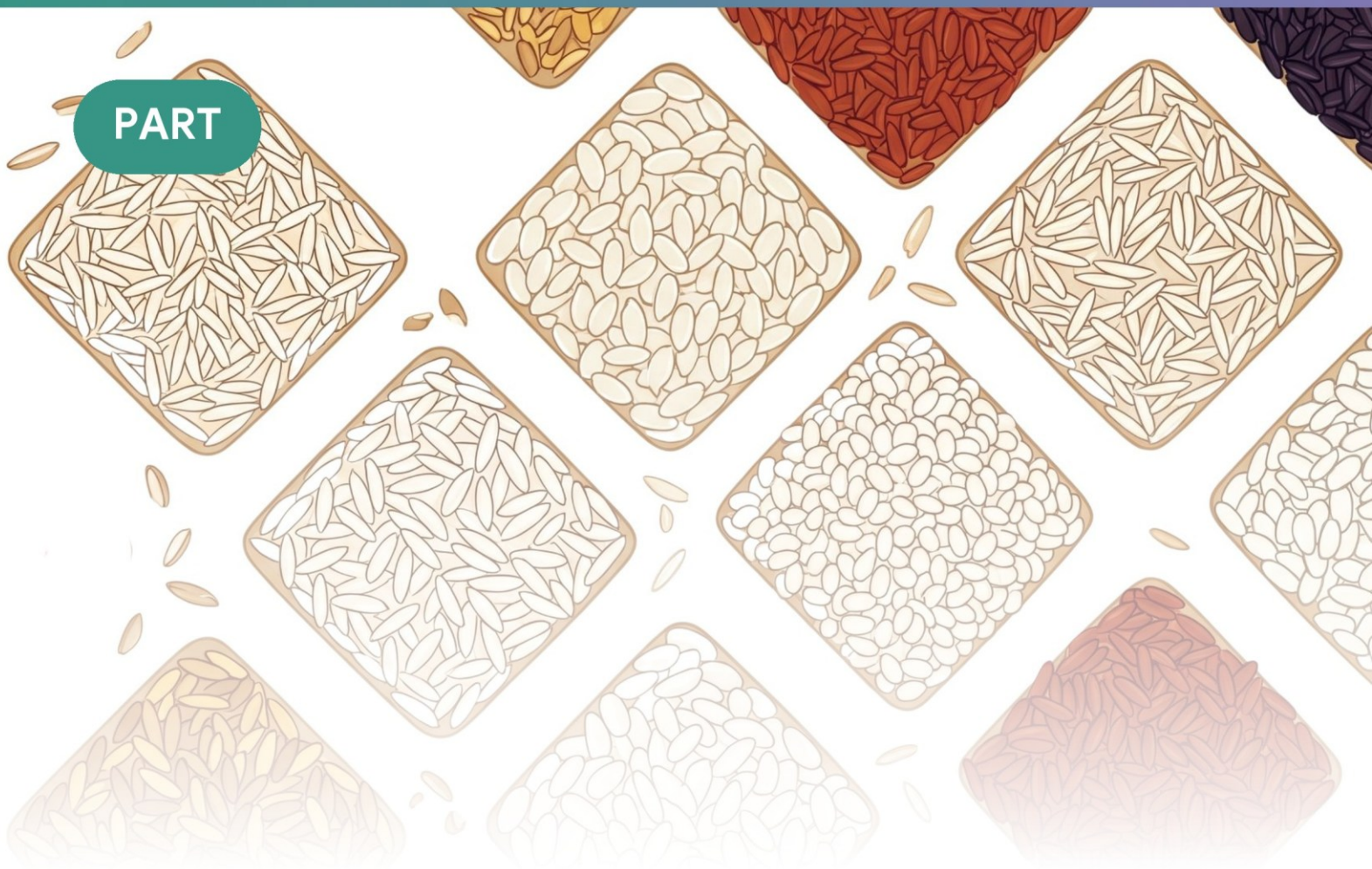

PART

# ORAL

## Oral Presentations

Abstracts of oral presentations, arranged by topic (codes OS1-OS6)

Abstracts 49



SECTION

# OS1

## Rice Genomics / Rice-omics

Genomics, genetics, breeding and multi-omics of rice

Oral 9

# Methylation Heterogeneity as an Indicator of Epigenetic Regulation and Gene Expression in Rice

**Pei-Yu Lin [1], HueyTyng Lee [1], and Pao-Yang Chen [1*]**
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## Abstract

Methylation heterogeneity captures the degree of variation in DNA methylation at specific loci among cells, whereas conventional methylation level represents their average methylation state. In rice, DNA methylation is associated with gene expression in a context- and region-dependent manner, but whether methylation heterogeneity provides regulatory information beyond methylation level remains unclear. Here, we developed the MeH bioinformatic framework, derived from biodiversity-based mathematical models, to quantify genome-wide methylation heterogeneity in rice. We found that transposable elements exhibited high heterogeneity across methylation contexts, whereas CG heterogeneity was enriched in promoters and gene bodies. Importantly, methylation heterogeneity showed stronger associations with gene expression than methylation level in several genomic regions, suggesting that cell-to-cell variation in methylation states captures regulatory information not represented by average methylation alone. In particular, gene-body non-CG heterogeneity showed a stronger negative association with expression, while promoter CG and CHG heterogeneity also showed greater predictive value than their corresponding methylation levels. These differences suggest that heterogeneity and methylation level capture distinct aspects of epigenetic regulation. Developmental and tissue-specific changes in gene-body heterogeneity further suggest dynamic remodelling of methylation states associated with transcriptional changes. Together, our findings establish methylation heterogeneity as a complementary measure to conventional methylation levels for understanding epigenetic regulation and gene expression in rice.

**Keywords:** *DNA methylation, Methylation heterogeneity, Epigenetic regulation, Gene expression, Rice, Bioinformatics*

# Uncovering the Transcriptomic Signatures Associated with Arbuscular Mycorrhizal Responsiveness in Rice.

**Alessandra Learmount [1,2*], Emily Servanté [2], Mignon Natividad [3], Shalabh Dixit [3], Anton Enright [1], and Uta Paszkowski [2]**

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## Abstract

Arbuscular mycorrhizal fungi (AMF) are ubiquitous soil fungi that form associations with around 80% of land plants, including rice. AMF can improve resilience to biotic and abiotic stresses, increase crop yields and reduce micro- and macronutrient deficiencies, supplying up to 100% of a plant's phosphorus and up to 40% of its nitrogen in exchange for carbon. However, substantial genetic variation in plant response to AMF has been identified across many species, including rice, with some genotypes benefiting significantly and others showing limited or even negative effects of colonisation. The molecular mechanisms underpinning this "mycorrhizal responsiveness" remain poorly understood.

This research is particularly relevant to direct-seeded rice (DSR), in which seeds are sown directly into the field rather than transplanted as seedlings, an increasingly adopted lower-emission alternative to conventional flooded rice. As flooding limits AMF colonisation, the more aerobic conditions of DSR offer greater potential to harness this symbiosis, which could help offset DSR yield penalties and reduce fertiliser requirements. This PhD project is designed to elucidate the mechanisms underpinning mycorrhizal responsiveness in DSR.

Using a ~250-genotype DSR breeding panel from IRRI, grown in field-like conditions, we will integrate transcriptome-wide (TWAS) and genome-wide (GWAS) association analyses to identify molecular signatures that distinguish highly responsive from poorly responsive lines. We anticipate these signatures will inform marker-assisted breeding and gene-editing strategies to enhance AMF responsiveness, reducing synthetic input requirements and supporting more resilient, higher-yielding, sustainable DSR systems.

**Keywords:** *Arbuscular mycorrhizal fungi, Mycorrhizal responsiveness, TWAS, GWAS*

# Genomic Selection for Culm Strength-Related Traits in Rice (*Oryza sativa* L.)

**Jyothi Badri [1*], and Swargam Vaishnavi [1,2]**
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## Abstract

Culm strength is a key breeding target for improving lodging resistance and sustaining yield stability in rice, with breaking resistance (BR) serving as an important measure of culm mechanical strength. As BR is a complex trait with relatively low heritability, genomic selection (GS) can improve selection efficiency and accelerate genetic gain by integrating phenotypic performance with genome-wide marker information. A panel of 156 rice genotypes was subjected to multi-environment evaluation during 2022-2025 for 11 traits including days to 50% flowering (DFF), plant height (PH), culm thickness (CT), culm diameter (CD), section modulus (SM), culm leaf sheath weight (CLSW), breaking resistance (BR), tiller number (TN), bending stress (BS), test weight (TW) and plot yield (PY). Based on their moderate positive correlations with BR (r = 0.572-0.677), SM, CD and CLSW were selected as secondary traits, with BR designated as the primary trait for genomic prediction. Genotyping-by-sequencing (GBS) generated approximately 36,000 SNPs, of which 16,415 high-quality SNPs were retained after quality filtering and curation. Genomic prediction was evaluated using 20 repetitions of five-fold cross-validation by comparing single-trait and multi-trait approaches for BR. The inclusion of these correlated secondary traits provided complementary information for multi-trait prediction. Single-trait models showed relatively low predictive ability, whereas incorporation of secondary traits substantially improved prediction. Among the pairwise models, BR+CLSW showed the strongest performance, while the Bayesian multi-trait model combining BR, SM, CD and CLSW achieved the highest prediction accuracy (0.678) and the lowest prediction error. The Bayesian multi-trait and FA(2) models showed complete agreement among the top 20 selected genotypes, indicating high consistency in genomic ranking across multi-trait approaches. Among these, RMS 2097, JBB 5952, JBB 6436, JBB 6443 and JBB 451 recorded the highest genomic merit for BR. At the genetic-group level, the indica-tropical japonica (ITrJ-D) group showed the most favourable BR GEBV distribution, with 67% of genotypes exhibiting positive breeding values. The identified elite genotypes and favourable genetic background provide useful breeding material for improving culm strength and lodging resistance. Overall, multi-trait genomic selection improved BR prediction and supported more efficient identification of superior breeding lines.

**Keywords:** *Genomic selection, Breaking resistance, Multi-trait prediction, Genomic estimated breeding value, Rice*

# Elucidating Genetic Variation Underlying Beneficial Responses to Arbuscular Mycorrhizal Fungi in Aerobic Rice

**Emily Kate Servante [1*], Rayko Halitschke [2], Meng Li [3], Dmytro Chebotarov [4], Ian T. Baldwin [2], Uta Paszkowski [1*], and Ruairidh Sawers [3*]**

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## Abstract

Arbuscular mycorrhizal fungi (AMF) form widespread symbioses with plants and can enhance nutrient acquisition, yet crop genotypes vary widely in the growth benefits they derive from symbiosis. Understanding the genetic basis of this variation could help identify rice varieties that make more effective use of AMF, particularly under aerobic cultivation systems such as dry direct seeded rice (DDSR) and alternate wetting and drying (AWD) irrigation, where nutrient and water availability differ from flooded systems. Here, we investigated the genetic basis of mycorrhizal responsiveness (MR) in a globally diverse panel of 187 indica rice varieties from the 3K Rice Genomes Project. Plants were grown under DDSR and phosphorus-limiting conditions with and without AMF inoculation, and we assessed biomass, root traits, foliar elemental concentrations and blumenol-based indicators of AMF colonisation. We found that AMF inoculation had minimal effects on biomass at the population level but generated substantial variation among genotypes.

Using a genotype-by-environment genome-wide association approach, we identified 17 loci associated with biomass and nutrient traits whose effects depended on AMF status. The strongest biomass-associated locus, qTDW5.2, was linked to differences in root development and biomass allocation. Across the wider panel, fungal colonisation itself was only weakly related to host performance. Together, these findings suggest that mycorrhizal responsiveness is determined less by the extent of fungal colonisation than by how effectively individual rice genotypes integrate AMF-derived nutrient acquisition with their existing root developmental and resource-allocation strategies. These findings highlight genetic variation that could be explored to enhance the contribution of AM symbiosis to nutrient-efficient, low-input aerobic rice production.

**Keywords:** *Arbuscular mycorrhizal fungi, GWAS, Plant–microbe interactions, Genetic variation; Nutrient acquisition*

# Mining and Breeding Utilization of Salt Tolerance Gene *qSL7* in Rice

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## Abstract

Global food security and climate warming are common challenges that we face. Rice is one of the important grain crops in China, Thailand and the world, so we need to take on the important task of food security. However, rice production is affected by many environmental factors of drought, saline-alkali land and low-nutrient, which seriously affect food security. So, it is of great significance to explore new gene resources for salt-tolerant and other abiotic tolerant rice, and breeding improvement of new rice varieties for food security and environmental security. On the basis of previous exchanges and cooperation with Indonesia, we have mined some excellent genes and regulatory factors of salt tolerance in rice and analyzed their functions and allelic variation. We have just created some new rice germplasm or variety with high salt tolerance using molecular marker selection and gene editing techniques, combining with hybridization and backcross breeding. Also, we functionally characterized a candidate gene of the salt-responsive locus *qSL7* (LOC_Os07g43530) that we previously reported encodes a putative basic helix-loop-helix (bHLH) transcription factor and showed variable expression levels in different organs. Using CRISPR/Cas9-mediated genome editing in the japonica rice cultivar Nipponbare (wild type, WT), we generated two independent homozygous knock-out (KO) lines with frameshift mutations and evaluated their response to salinity stress. Compared to WT, the two KO lines reduced chlorosis and tissue senescence, and markedly increased survival under prolonged salt stress. *qSL7* expression increased with salinity intensity and stress duration in WT but not in the KO lines, leading to significantly lower accumulation of reactive oxygen species (ROS) and higher redox stability. Our findings revealed that qSL7 was a negative regulator of salinity tolerance by modulating ROS homeostasis and imply it is a promising target for simultaneous improving rice salt tolerance and yield.

# Distal *Cis*-Regulatory Elements Mediate Morning Light Activation and Circadian Gating of the Rice Flowering Repressor *Ghd7*

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## Abstract

Rice is a short-day plant with a pronounced critical day-length response. The transcriptional regulator *Grain number, plant height, and heading date 7* (*Ghd7*) represses the flowering promoter *Ehd1* and the florigen genes *Hd3a* and *RFT1* under long-day conditions. *Ghd7* transcription is acutely induced after dawn by phytochrome-mediated red-light signaling and repressed at night by the Evening Complex (EC). However, the *cis*-regulatory elements required for these responses remain poorly understood. Using CRISPR/Cas9, we generated a series of 2–25-kb deletions covering a 65-kb region upstream of the *Ghd7* transcription start site (TSS), extending to the nearest upstream gene. This survey identified a critical region for light-responsive *Ghd7* expression, located approximately 30 kb upstream of the TSS. Further fine-scale deletion analysis revealed two adjacent regions with opposing regulatory functions. Lines carrying a 600-bp or 200-bp deletion 28 kb upstream of *Ghd7* flowered about three weeks earlier than the wild type, similar to the *ghd7* mutant, and exhibited severely reduced morning *Ghd7* induction. In contrast, a 7-bp deletion at the end of the 600-bp and 200-bp deletion intervals delayed flowering by about three weeks. In addition, deletion of adjacent LUX-binding-site-like motifs resulted in nighttime derepression of *Ghd7*. The timing of this derepression coincided with that observed in a loss-of-function mutant of *OsELF3-1*, which encodes an EC component, suggesting a role for this region in EC-associated repression. Together, these findings support a model in which adjacent distal *cis*-regulatory regions integrate morning light activation and nighttime repression to regulate *Ghd7* transcription and photoperiodic flowering in rice.

**Keywords:** *cis-regulation, Ghd7, Photoperiodic flowering, Rice*

# Production of Rice Zygote *in vitro*: For Investigating Basic Plant Biology and Establishing New Breeding Technology

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## Abstract

As developing zygotes and embryos are deeply embedded in ovular tissues, direct investigation of the developmental profile and molecular events during early embryogenesis of angiosperm is highly difficult. To overcome this difficulty, *in vitro* fertilization (IVF) system using isolated rice gametes has been established and enabling direct observations of various cytological and molecular machineries in early rice zygotes and embryos, including reactive oxygen species (ROS) homeostasis and *de novo* transcriptional dynamics during early embryogenesis. As for breeding science, electrofusion of isolated gametes has overcome the fertilization barriers of interspecific and intergeneric hybridization, and that the hybrids of rice with other species and genera via IVF have been produced. Due to spontaneous genome doubling, interspecific rice hybrids between cultivated and wild species produced by IVF exhibited allopolyploidy and stable transmission of hybrid traits, offering a chance for introgression of alleles from wild to cultivated rice. In addition, fertilization-independent reproduction, *in vitro* parthenogenesis (IVP) using unfertilized rice egg cells, can be induced by transient exposure to cold stress and histone deacetylase inhibitor. The subsequent haploid egg-derived embryos produced by IVP developed into doubled haploid rice plants, thereby enabling the generation of fertile homozygous DNA or selectable marker-free genome-edited rice plants via CRISPR-Cas9-based mutagenesis and instant allele fixation in a progeny possessing desirable agronomic traits. Micromanipulation of isolated gametes through IVF and IVP will provide new horizons for future rice breeding technology.

**Keywords:** *In vitro Fertilization, Reactive oxygen species, in vitro parthenogenesis, Interspecific / intergeneric hybrid, CRISPR-Cas9*

# Beyond a Single Reference: A Graph-Based Pan-Genome Framework for Exploring Thai Rice Genomic Diversity

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## Abstract

Thailand possesses extensive rice genetic diversity that is valuable for crop improvement, conservation, and adaptation to changing environments. However, genomic analyses derived from variant calling on a single linear reference may introduce reference bias and fail to represent divergent haplotypes present in diverse germplasm. This study aims to construct a graph-based pan-genome framework for genomic analysis of 300 accessions from the Thai Rice Diversity Panel. The initial graph combines seven publicly available assemblies chosen to represent genetic backgrounds relevant to the panel: Khao Yai Guang as the coordinate and annotation anchor; Nipponbare as the most typical rice standard; Ketan Nangka representing *tropical japonica* and closely related glutinous germplasm; IR64 representing *indica* rice; Gobol Sail providing divergent *indica* landrace diversity; ARC 10497 representing *aromatic* germplasm and serving as a proxy for KDML105 Thai Hom Mali rice; and N22 representing *aus* diversity and stress-tolerance-associated genomic regions. Alignment of short-read data from the 300 accessions to the graph achieved consistently high mapping rates, with overall alignment rates of 98–99%. Notably, 30–35% of mapped reads represent genuine structural variations and alternative ancestral haplotypes, eliminating reference bias by resolving non-linear segments through their true biological paths rather than an artificial linear template. Analysis of the complete 300-accession panel identified approximately 2.7 million high-quality SNPs and 1.0 million small indels, together with tens of thousands of structural variants and presence–absence variations. The seven-assembly graph is also expected to contain approximately 40–60 Mb of sequence that is absent from, or poorly represented by, the Nipponbare reference. This graph-based framework provides a foundation to improve the representation of divergent Thai rice haplotypes, provide greater genetic resolution for genome-wide association studies, facilitate the discovery of favorable alleles and donor accessions, and support the development of trait-specific markers for precision breeding.

**Keywords:** *Thai rice, Graph-based pan-genome, Genomic diversity*

# Genome-Wide Association Study of Rice Vegetative Growth Under Ammonium or Nitrate Nutrition

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## Abstract

Rice is the most important source of daily calories in human diets and second only to wheat as the most important protein source. Rice is generally exposed to high ammonium ($NH_4^+$) levels in the rhizosphere but may employ both $NH_4^+$ and nitrification-derived nitrate ($NO_3^-$) as major sources of nitrogen. However, the genetic basis underlying rice adaptation to different nitrogen forms remains poorly characterized. Here, we assessed biomass under either $NH_4^+$ or $NO_3^-$ as a sole nitrogen source in 390 accessions from the USDA Rice Diversity Panel 1. Rice effectively used either form of nitrogen to support early growth. Tolerance to a high-$NH_4^+$ exposure was correlated with biomass under $NO_3^-$ and lower $NH_4^+$ levels. Both genotype and nitrogen source strongly influenced biomass accumulation and partitioning between shoot and root. Root showed the greatest biomass variability and sensitivity to nitrogen source. Genome-wide analyses identified 176 single nucleotide polymorphism (SNP) markers associated with biomass across the full diversity panel and individual populations. The majority of the associations were unique to the individual nitrogen source. We compiled a list of candidate genes, including putative genes involved in nitrogen metabolism, located within 150 kb of 112 most significant SNPs, each with at least 3 adjacent markers detected under the same combination of population and nitrogen source. A flexible consumer, rice may employ distinct genetic mechanisms to use different nitrogen sources, making the species more resilient to fluctuations in soil nitrogen. These insights can guide matching rice genotypes with fertilizer management to improve nitrogen-use efficiency.

**Keywords:** *Nitrogen, Oryza sativa, Genetic, Nutrient, Fertilizer, Indica, Japonica*



SECTION

# OS2

## Climate Change

Climate-smart rice, low-emission production and resilient systems

Oral 8

# Cultivating Livelihood Survival: The Direct Impact of Entrepreneurial Competencies on Rice Farm Resilience

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## Abstract

As agricultural disruptions become increasingly frequent and severe, building long-term resilience is essential for the survival of rice farming communities. This study investigates the role of human capital by exploring how a farmer's individual entrepreneurial competencies, specifically risk-taking, opportunity-finding, innovativeness, decision-making, and market orientation, directly contribute to agricultural resilience. Using a quantitative research design, the study collected survey data from a sample of 335 experienced rice farmers in Sakon Nakhon Province, Thailand. Partial Least Squares Structural Equation Modelling (PLS-SEM) was employed to evaluate the structural relationships and measure how these entrepreneurial competencies influence the multi-dimensions of resilience, including adaptability, transformability, and robustness. The PLS-SEM analysis statistically supported that entrepreneurial competencies exert a strong, direct positive impact on overall farm resilience ($\beta = 0.256$, $p < 0.001$). The findings indicate that these competencies are not just tools for daily economic transactions, but function as foundational dynamic capabilities that allow farmers to adapt their cropping patterns, restructure land use under stress, and manage market volatility. These results suggest that top-down agricultural aid and physical resource relief are insufficient if implemented without parallel investments in human capital. For policymakers and development agencies, fostering grassroots self-reliance through targeted training programs that build practical entrepreneurial competencies is a fundamental strategy to empower farmers to navigate environmental shocks on their own terms and secure the future of sustainable rice production.

**Keywords:** *Entrepreneurial competencies, Resilience, PLS-SEM*

# Agronomic and Yield Performance of Two Rice (*Oryza sativa* L.) Azucena Bi-parental Mutant Populations Grown Under Conventional and Field Rapid Generation Advance Conditions in Los Baños, Laguna, Philippines

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## Abstract

Rice breeding is constrained by prolonged generation cycles, limiting the rapid development of improved cultivars. To accelerate breeding, the Field Rapid Generation Advance (FRGA) approach was employed. This study assessed and compared the agronomic traits, yield performance, and associated costs of Azucena bi-parental mutants under conventional and FRGA setups. In the $F_2$ generation, MON 329 × Azucena (P1) and Azucena × MON 329 (P2) headed at 81 days and matured at 104 days, with P1 producing taller plants, more tillers, and higher yield, while P2 had longer panicles. In the $F_3$ generation under conventional conditions, P1 headed earlier at 75.68 days, matured at 105.18 days, produced more tillers and longer panicles, and yielded 2,840.89 kg $ha^{-1}$. Under FRGA, plants matured 5–10 days earlier but showed reduced height, tiller number, panicle length, and yield, with P1 producing 977.08 kg $ha^{-1}$ and P2 587.09 kg $ha^{-1}$. Correlation analysis showed a strong relationship between heading and maturity and identified tiller number as the trait most associated with yield. Scatter plots indicated wider trait dispersion under FRGA, reflecting stronger environmental influence. Selected lines P1 (C-11784-3, C-11784-30) and P2 (C-11785-30, C-11785-6) showed stable expression for advancement. Although FRGA shortened the generation cycle, partial budget analysis indicated higher costs and lower yield, resulting in a net loss of ₱193,849.12. Thus, FRGA is not economically feasible under the evaluated conditions but provides technical advantages for rapid line assessment and functions as a breeding acceleration platform rather than a cropping system.

**Keywords:** *Azucena mutants, FRGA, Conventional, Partial budget analysis, Breeding*

# Climatic Elasticities of Rice Yield under Irrigated and Rainfed Production Systems in Selected Visayan Provinces, Philippines

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## Abstract

Climate variability influences rice productivity, particularly in production systems with differing dependence on rainfall. This study was conducted to assess the climatic elasticities of rice productivity with respect to rainfall, maximum temperature (Tmax), and minimum temperature (Tmin) in irrigated and rainfed rice systems across the three provinces in the Visayas, namely Bohol, Cebu, and Negros Oriental, Philippines, from 1991 to 2020. Log-log regression models were employed to estimate the elasticities of rice productivity with respect to climatic variables in both irrigated and rainfed rice systems. Province–production-system fixed effects and system-specific temporal trends were considered to account for unobserved spatial heterogeneity and long-term changes in rice productivity. To examine whether climatic responses differed between irrigated and rainfed rice, interaction terms between production system and climatic variables were used. Sensitivity analyses were also performed to evaluate the robustness of the estimates. Rainfall showed the clearest positive association with rice productivity, with estimated elasticities of 0.161 for rainfed rice and 0.150 for irrigated rice. In contrast, Tmax showed negative point estimates, while Tmin showed positive point estimates; however, both temperature responses were characterized by wide uncertainty intervals and were not sufficiently robust for definitive interpretation. A significant difference in the estimated climate–productivity responses between irrigated and rainfed systems was not detected. Furthermore, results showed persistent temporal increases in rice productivity across the three provinces in both irrigated and rainfed systems. Generally, the findings indicate that rainfall availability is an important climatic correlate of rice productivity.

**Keywords:** *Climatic Elasticities, Rice Yield, Temperature, Rainfall*

# Projecting Spatiotemporal Shifts in Phenology of Southeast Asian Commodity Crops Through A Simple Growing Degree Day Model for Near and Midterm Climate Change Scenarios

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## Abstract

Understanding the impacts of climate change on crop phenology is vital for regional agricultural planning. This is especially pertinent to agricultural regions like Southeast Asia (SEA) dominated by small-holder modes of production. This study projected the Days to Maturity (DTM) trends for the key commodity crops of rice, coffee, and sugarcane in the region over different future emission scenarios. A simple Growing Degree Day (GDD) model was used with data from ERA5 and CMIP6 projections (2026 - 2045, 2046 - 2065) in order to estimate trends in crop phenology until the mid century. The results demonstrate that crop maturity across the region has already begun advancing due to rising temperatures, a trend projected to accelerate into the future. The magnitude of these shifts exhibits significant spatial heterogeneity and varies considerably based on crop species as well as seasonal timing. The majority of SEA will experience varying degrees of phenological acceleration, while some special sub-regions will remain unaffected. These findings underscore the necessity of continued emission mitigation and adaptation strategies. The gradual onset of temperature-driven shifts provides a critical temporal window to implement measures such as climate control technologies, agroforestry, and resilient crop varieties. Ultimately, urgent action is imperative to safeguard the smallholder-dominated agricultural systems that form the agricultural backbone of SEA.

**Keywords:** *Phenology, Agriculture, Climate Change, Southeast Asia, CMIP6*

# Sustainable Rice Platform Performance Indicators as a Framework for Farmer-centered Extension and Sector Monitoring

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## Abstract

Rice is the staple food, basis of rural livelihoods, main irrigation water user and a substantial methane source. Investment in the sector focuses heavily on a limited set of mitigation interventions, notably alternate wetting and drying and straw management. While beneficial where technically and economically feasible, they are not suitable in all regions or seasons, and this narrow focus can limit adoption and climate mitigation by overlooking farmers' main constraints.

The Sustainable Rice Platform (SRP) Performance Indicators quantify farm-level profitability and production efficiency, and social and environmental outcomes. We propose using them as a standardized framework for benchmarking, identifying and prioritizing problems, planning and measuring impact from farm to regional scale. Benchmarking shows farmers where they stand and what to prioritize. Aggregated, benchmarking provides an evidence base to target and sequence extension.

At the field level, a phased approach would first identify locally relevant solutions targeting immediate income, labor and yield constraints that can still achieve broader environmental and social co-benefits before progressing towards community and consumer safety and wider environmental outcomes. We expect this to increase the rate and ceiling of adoption. Benchmarking also exposes needs beyond agronomy, such as financial literacy, business skills, policy realignment and value chain support.

Governments and programs could adopt this standardized framework, supported by open data collection and shared extension and capacity development approaches and resources. This would support national climate and SDG reporting, buyer ESG reporting, deliver direct benefits to farmers, and lower the barrier to entering Verified supply chains.

**Keywords:** *Sustainable Rice Platform, Performance indicators, Benchmarking, Agricultural extension, Climate-smart agriculture*

# Life Cycle Assessment of Rice Cultivation in China

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## Abstract

Rice is a vital agricultural commodity worldwide, with China as one of its major producers and consumers. However, rice cultivation contributes substantially towards greenhouse gas emissions, heavy water consumption, and agrochemical-induced pollution. This study, therefore, used Life Cycle Assessment (LCA) to evaluate the environmental impacts of three rice cultivation systems in China: transplanting rice (TR), dry direct-seeded rice (DR), and organic rice (OR). Using a cradle-to-gate approach with 1 tonne of paddy rice as the functional unit, the life cycle impact assessment (LCIA) was conducted via SimaPro 9.6.0.1 using the ReCiPe 2016 Midpoint (H) method, supported by regional foreground data and Ecoinvent 3 background data. Normalized results indicated that human carcinogenic toxicity was the most significant impact across all systems, followed by water consumption and freshwater ecotoxicity. Hotspot analysis revealed that TR impacts were driven by electricity, irrigation water, and machinery; DR impacts by machinery, electricity, nitrogen fertilizer, and OR impacts by irrigation water and manure-derived N and $P_2O_5$. Comparative results showed that DR and OR effectively mitigated global warming impacts relative to TR, with DR also reducing irrigation water use. Conversely, DR exhibited higher stratospheric ozone depletion and terrestrial ecotoxicity than TR, driven by higher seed, chemical fertilizer, and pesticide inputs needed to maintain yields. Similarly, substituting chemical fertilizers with manure in OR increases marine eutrophication and land use impacts. This study therefore suggests that precision fertilizer management, efficient irrigation and efficient machinery adoption are essential to enhance the environmental sustainability of rice production.

**Keywords:** *Life Cycle Assessment (LCA), Environmental impact, Global warming, Rice cultivation*

# Driving the BCG Model via Multi-Technology to Mitigate Heavy Metal Pollution Risks and Upgrade Sustainable Rice Production (SRP): A Case Study of Rice Innovation Community in Baan Dai Sub-district, Mae Sai District, Chiang Rai Province

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## Abstract

This research evaluated the application of multi-technologies under the Bio-Circular-Green Economy (BCG) Model to upgrade a rice-producing community toward the Sustainable Rice Platform (SRP) standard and manage environmental risks. The study was conducted in Baan Dai Sub-district, Mae Sai District, Chiang Rai Province—a key rice-growing area requiring active surveillance for heavy metal contamination risks (Arsenic, Cadmium, Lead, and Chromium) in soil and water resources. Consequently, farmers previously faced market price deductions and an average net loss of -679 THB/rai/crop. A tailor-made SRP technology package was implemented with 31 pilot farmers covering 884 rai, including: 1) Soil and water bioremediation innovations using biochar, vetiver grass bio-filters, and quick test kits; 2) Alternate Wetting and Drying (AWD) paired with solar-powered water pumping systems; 3) Azolla cultivation and field application (442 rai) for biological nitrogen fixation; and 4) Microbial straw decomposition for zero-burning practices, biopesticide production (*Metarhizium anisopliae*), and personal protective equipment (PPE) support.

The results demonstrated that the average SRP compliance score increased significantly from 65% (Level C - Non-compliant) to 94% (Level A - Sustainable Rice Production). Laboratory analyses confirmed 100% compliance with heavy metal safety standards across grain, soil, and water samples. Economically, despite a yield transition adjustment from 798.2 kg/rai/crop to 688.2 kg/rai/crop, reduced chemical input costs and avoided price penalties successfully reversed net farm profitability to +456.2 THB/rai/crop. Environmentally, methane emissions were reduced by 34.1% (from 7.28 to 4.8 Mg $CO_2$eq/ha), nitrous oxide emissions decreased by 11.0% (from 1.91 to 1.7 Mg $CO_2$eq/kg rice), and straw burning was 100% eliminated. Furthermore, Food Safety (PI9) reached a full score of 50 points, and Labor Health and Safety (PI10) improved to 100 points. The findings confirm that multi-technology BCG interventions under the SRP standard effectively mitigate heavy metal pollution risks, restore farm economic viability, and enhance environmental sustainability

**Keywords:** *BCG model, Sustainable Rice Platform (SRP), Alternate wetting and drying (AWD), Greenhouse gas reduction*

# Developing an Advanced Rice Cultivation Model to Produce High Quality Rice, and Improve Soil Health for the Climate Resilience and Mitigation in the Vietnamese Mekong Delta Region

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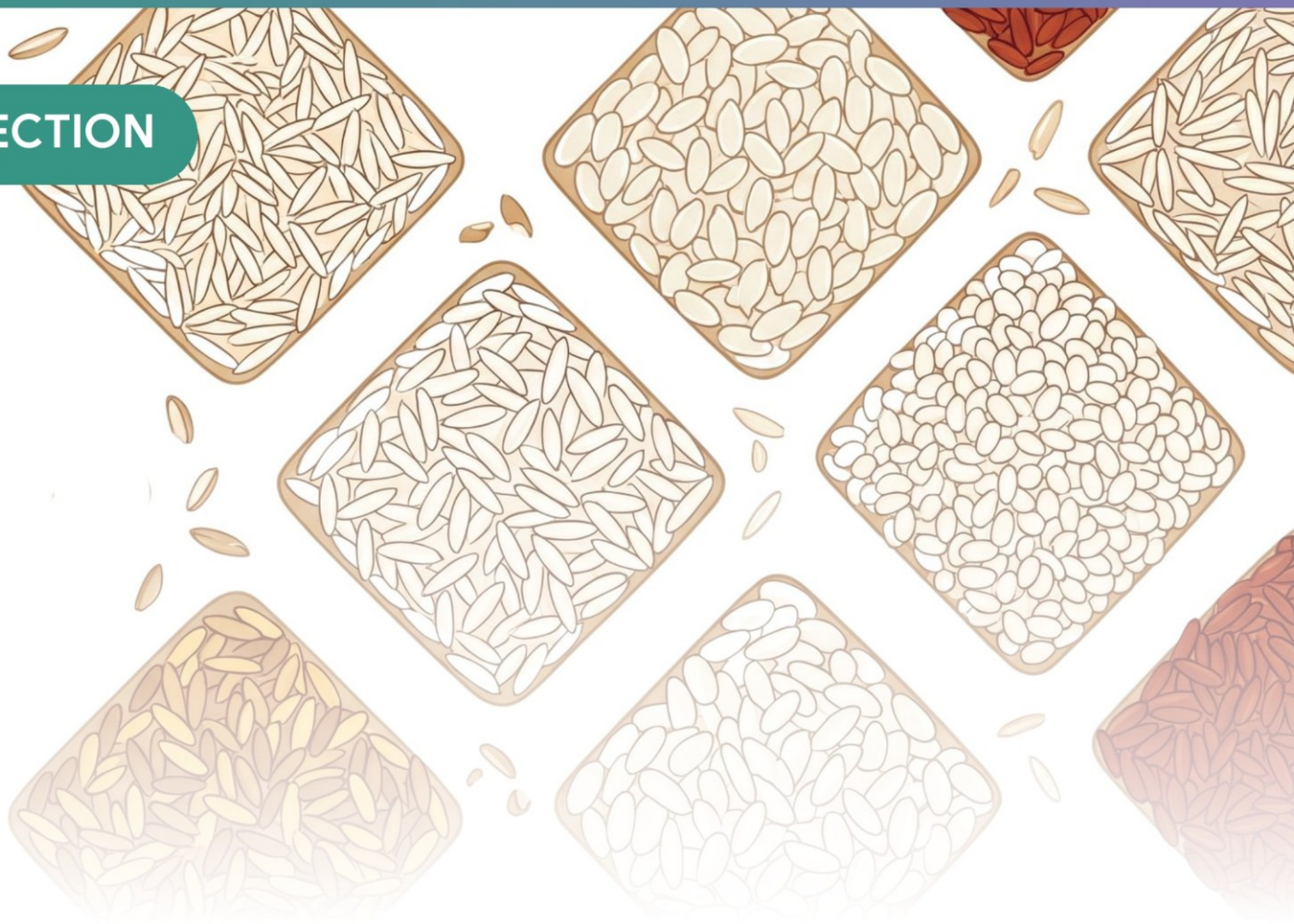
## Abstract

The advanced rice model in Hon Dat district, Kien Giang province of the Vietnamese Mekong Delta for 5 consecutive crops with DS1 rice variety from 2023 to 2025 was conducted by applying a comprehensive set of measures: no-till system; the use of the salt-tolerant microbial inoculant NPKISi to supply and release soil nutrients to the rice plants; *Aspergillus oryzae* fungus to decompose rice straw in the field; lactic acid bacteria and a garlic-chili extract for pest and disease management; organic fertilization; the application of Alternate Wetting and Drying (AWD) irrigation; and a 50% reduction in chemical NPK fertilizers. These practices maintained rice yields comparable to traditional farming methods while enhancing grain quality, improving soil health, and potentially reducing greenhouse gas emissions from the rice fields. The results showed that the advanced rice model provided yields equivalent or even higher than the farmers' farming practices (6.71 - 9.52 tons/ha versus 5.96 – 9.28 tons/ha, respectively). Soil health was significantly restored by increasing organic matter (OM) content, essential nutrients ($NH_4^+$, $P_2O_5$, $K_2O$, Zn), looser soil structure, and a strong increase in beneficial bacterial and nematode populations. The rice product was completely free of toxic chemical residues. Economically, the model helped reduce production costs by 20-32%, boosting the net profit margin by 4.80% to 84.50% (cumulative profit was 20.3% higher over 5 cropping seasons). Our findings provide evidence that advanced rice cultivation model can be scaled up for other floodplain provinces in the VMD and beyond.

**Keywords:** *Advanced rice model, AWD, Bio-fertilizer, Soil health, Climate change, Mitigation*

SECTION



# OS3

## Abiotic and Biotic Stresses

Tolerance and resistance to environmental stress, pests and diseases

Oral 17

# Promoter Architecture and Transcriptional Regulation of Genes Upregulated in Germination and Coleoptile Elongation of Diverse Rice Genotypes Tolerant to Submergence

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## Abstract

Rice is unique in its ability to germinate and elongate its coleoptile in response to submergence stress compared to other crops that fail to germinate under such conditions. However, the rate of germination and coleoptile elongation varies from genotype to genotype. Therefore, to elucidate the unique transcriptional mechanism that regulates differences in coleoptile elongation, an ab initio approach was used to reveal the promoter architecture and possible transcriptional regulation of rice genotypes from diverse backgrounds which have different rates of coleoptile elongation to reach the surface of water for shoot and root initiation in response to submergence tolerance. The putative *cis*-elements and their associated transcription factors provide useful information on the crosstalk between transcription factors and phytohormones. The results suggest that the endogenous ABA level could be acting as an on-off switch regulating in a spatio-temporal manner to activate/repress other TFs and hormonal signaling pathways during germination and coleoptile elongation. Co-ordination of both auxin-BR responses could be regulating coleoptile elongation. TFs such as MYB3Rs, TSO1, TCX2/SOL2, TCX3/SOL1 and ASHR1 could potentially be involved in epigenetic regulation of coleoptile elongation. The information derived from the current *in silico* analysis can potentially guide in developing new emerging rice genotypes for direct seeding.

**Keywords:** *Rice germination, Submergence, Promoter cis-elements, Transcription factors, Gene regulation*

# Rice Seedlings Respond to Phosphorus Deficiency in a Manner Comparable to Shading: Evidence from Leaf Pigmentation, Anatomy, and Hyperspectral Profiles

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## Abstract

While phosphorus (P) deficiency commonly induces chlorosis and leaf senescence in rice, our previous studies revealed a contrasting response in KDML105 seedlings at the early stage. P deficiency increases leaf greenness through enhanced chlorophyll accumulation, yet reduces photosynthetic efficiency (Phi2) owing to deformation of chloroplast structures with abundant starch granules. Moreover, transcriptomic analyses indicated that this response involves galactolipid biosynthesis, suggesting thylakoid membrane remodeling. In this study, we hypothesize that the increase in leaf greenness under P deficiency is associated with the adaptation of rice seedlings to shading. To examine changes in leaf greenness in response to different P availability and light conditions, rice seedlings were grown under high- and low-P conditions combined with high- and low-light conditions. We found that low-P and/or low-light treatments increased chlorophyll and carotenoid accumulation. Furthermore, P-deficient leaves were morphologically and anatomically similar to low-light-treated leaves, regardless of environmental P status. Hyperspectral imaging confirmed that, within the 540–560 nm and 620–680 nm ranges, P-deficient rice leaves exhibited hyperspectral patterns comparable to those of leaves grown under low light, irrespective of P supply. These findings indicate that rice modifies its leaves under P deficiency in a manner comparable to its response to shading. Further analyses, including chloroplast characteristics and carbohydrate metabolism in the leaves of rice seedlings subjected to the four treatments, will be conducted to clarify the shared cellular mechanisms underlying the responses of rice leaves to P and light deficiencies.

**Keywords:** *Phosphorus deficiency, Low light, Leaf greenness, Chlorophyll accumulation, Hyperspectral imaging*

# Optimizing Artificial Screening of Salinity–Drought Tolerance in $M_2$ Mutant Rice Utilizing Rapid Generation Advance and Image-Based Plant Phenotyping

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## Abstract

Drought and salinity stresses reduce crop productivity by disrupting plant water relations, ion homeostasis, and photosynthesis, causing yield losses in major crops like rice. While developing stress-tolerant varieties is a crucial adaptation strategy, most breeding efforts focus on single-stress traits. However, drought and salinity frequently co-occur in fields, necessitating multi-stress tolerance. Although mutation breeding can generate genetic variability to address this problem, conventional screening methods remain slow and inefficient for identifying genotypes that perform well under combined stresses. To overcome this limitation, this study seeks to optimize the selection process for M2 mutant rice under combined drought and salinity stress by incorporating Rapid Generation Advance (RGA) and Image-Based Plant Phenotyping (IBP). Conducted at the Plant Phenomic Studio and Experimental Farm Hasanuddin University, the research utilized an Augmented Design with 1,950 M2 mutant seeds and controls. The RGA treatment involved limiting root space and applying NPK fertilizer at half the recommended rate, followed by 14 days of drought stress and incremental salinity levels (6–18 dS/m). Plant images were analyzed using ImageJ and evaluated with Spearman analysis, factor analysis, PCA, and Gradient Boosting Machine (GBM) modeling. The findings revealed that RGA and IBP approach effectively identified 148 mutant lines that were tolerant to multiple stresses, with GBM classification accuracy reaching 91.67% for training and 75% for testing. The combination of RGA and IBP proved to be an efficient method for quickly and accurately selecting and identifying rice lines with multi-stress tolerance.

**Keywords:** *Image-based plant phenotyping, Multi-tolerance, Mutation breeding, Rapid generation advance*

# Spray-Induced RNA Silencing for Sustainable Control of Rice Blast in Thai Rice

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## Abstract

Rice blast disease caused by *Pyricularia oryzae* is a major constraint to sustainable rice production, highlighting the need for effective alternatives to conventional disease management. This study evaluated spray-induced RNA silencing as a non-transgenic strategy for controlling rice blast in the susceptible Thai rice cultivar Khao Dawk Mali 105. Six double-stranded RNA (dsRNA) candidates targeting genes associated with fungal growth, development, and pathogenicity were evaluated at 20 and 40 ng/µL using detached-leaf and greenhouse assays. RNAi efficacy is varied with target gene, dsRNA concentration, and application timing. In detached-leaf assays, several dsRNAs suppressed disease development, with *MoVps41*-R1 targeting dsRNA at 40 ng/µL resulting in a disease index of 0 when applied either before or after pathogen inoculation. Greenhouse evaluation further identified *MoVps41*-R1 and *MoVps41*-R2 as the most promising targets. Pre-inoculation application at 40 ng/µL reduced disease severity scores to 0.3 and 0.2, respectively, compared with 9.0 in the pathogen control. Notably, *MoVps41*-R2 dsRNA also reduced disease severity to 0.2 at 20 ng/µL. To increase the efficiency of dsRNA delivery, *MoVps41*-R1 has been chosen to be entrapped with LDH-ZnAl for stability study. Pre-treatment with the ZnAl-dsVPS41-R1 for 24 hours before inoculation with *P. oryzae* reduced rice blast disease symptoms than the spraying naked dsVPS41-R1. This study demonstrates the potential of nanotechnology to enhance the development of RNAi-based formulations into an effective product. These findings identify promising RNAi targets against rice blast and prove the potential of foliar dsRNA application as a non-transgenic, sequence-specific strategy for sustainable disease management in Thai rice.

**Keywords:** *RNA interference (RNAi), Spray-induced gene silencing (SIGS), Pyricularia oryzae, Double-stranded RNA (dsRNA), dsRNA Deliverys*

# Multi-Trait-Based Identification of Putative Drought–Heat Tolerant Rice Mutants Through Artificial Screening at The Seedling Stage

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## Abstract

Rice is vulnerable to drought and heat stress, and may result in seedling mortality. Restricted genetic diversity impedes breeding for dual stress adaptation. Mutation breeding has been suggested to induce variability into rice genomes. This study aimed to identify rice mutants tolerant to drought and heat using screening and multi-trait index analysis. Experiments conducted from April to August 2025 at Hasanuddin University in two phases: seedling screening in a controlled stress chamber, followed by pot evaluation under semi-controlled conditions. Mutants were derived from seeds of the double haploid (DH) rice line HS1-28-1-5, developed through anther culture and showing potential for abiotic stress adaptation. DH seeds were subjected to gamma irradiation (200–1000 Gy) to generate the M1 population. Based on radiosensitivity assessments, 200 and 400 Gy were selected for the current study as M2 populations. Evaluation of M2 rice revealed that 200 Gy irradiation increased variability with improved performance, whereas 400 Gy produced broader but less stable variation. Yield components were associated with weight per clump; panicle length was the primary contributor, and weight per panicle influenced indirect effects. Principal component analysis accounted for 89.13% of the total variation, driven by yield traits. The integrated weighted average absolute score–tolerance score analysis classified genotypes into groups, identifying 33 tolerant mutants; M2 200 Gy mutants showed superior adaptability to drought-heat stress. These findings suggest that moderate irradiation and multi-trait index selection provide a method to identify drought-heat-tolerant rice candidates at early stages while maintaining relevance to future yield recovery.

**Keywords:** *Artificial screening, Drought-heat stress, Multi-trait selection, Rice mutants, Seedling stage screening*

# Silicon-Mediated Suppression of Brown Planthopper in Rice: A Sustainable Approach to Enhance Plant Health

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## Abstract

Brown planthopper (BPH), *Nilaparvata lugens* (Stål), is a major insect pest of rice and a serious threat to sustainable rice production in Asia. Excessive dependence on chemical insecticides can disrupt ecological balance and increase production costs. Silicon (Si) supplementation offers a promising and environmentally sound approach to strengthen rice plants and reduce pest pressure. This study evaluated the effect of soil-applied silicon on Si accumulation, plant physiological responses, and BPH performance in rice. A pot experiment was conducted using BRRI dhan29 with four soil silicon levels equivalent to 0, 100, 200, and 300 kg $SiO_2$ $ha^{-1}$. Silicon accumulation in rice plants was quantified under different treatments. Plant soluble protein content was measured at different intervals following BPH infestation. BPH feeding activity and nymph survival were also evaluated. Silicon supplementation substantially increased Si accumulation in rice plants. The highest Si treatment resulted in markedly greater Si accumulation than the untreated plants. Silicon application also altered soluble protein content following BPH infestation. BPH feeding activity declined with increasing silicon levels, as indicated by reduced honeydew excretion. Nymph survival was also reduced in silicon-treated plants. The strongest suppression of BPH performance was observed at the highest silicon level. These findings demonstrate that soil silicon supplementation can enhance rice plant tolerance to BPH and reduce pest performance. Silicon-based crop management could therefore complement integrated pest management and reduce reliance on insecticides. Integrating silicon nutrition with sustainable pest management may contribute to healthier rice plants, resilient production systems, and the One Health Rice vision.

**Keywords:** *Silicon supplementation, Brown planthopper, Rice plant health, Pest management*

# Brown Planthopper Survival on Rice Treated with Nanosilica Through Different Application Routes

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## Abstract

Nanosilica application to rice offers a potential approach to managing the brown planthopper (*Nilaparvata lugens*) or BPH, but the choice of application route requires evaluation. This study compared BPH survival and development on rice treated with nanosilica through seed soaking, root dipping, and foliar spraying. A factorial experiment was conducted using rice cultivar IR 42, three application routes, and seven nanosilica concentrations (0, 100, 200, 300, 400, 500, and 600 ppm), with four replicates per treatment combination. Each experimental unit contained five rice seedlings infested with 15 third-instar nymphs. Mortality, adult emergence, adult normality, and nymphal development were assessed. Data were analyzed using analysis of variance followed by the least significant difference test at the 5% level. The results showed that there was no significant interaction between application route and concentration for these variables. Averaged across application routes, mortality of BPH reached 72.22% and 73.33% at 500 and 600 ppm, respectively. Correspondingly, survival to adulthood declined from 100% in the control to 27.78% and 26.67%. These two concentrations did not differ significantly in mortality or adult emergence. Averaged across concentrations, root dipping resulted in higher mortality and lower adult emergence than foliar spraying, while seed soaking showed intermediate responses. Application route did not significantly alter nymphal stage duration, whereas concentration influenced development. These findings identify root dipping as a promising application route and 500–600 ppm as a concentration range for further evaluation of nanosilica-based BPH management under field conditions.

**Keywords:** *Concentration, Foliar spraying, Nilaparvata lugens, Root dipping, Seed soaking*

# The Potential of Endophytic Bacteria from West Sumatra Local Rice Seed Varieties to Suppress *Xanthomonas oryzae* pv. *oryzae* Growth and Enhance Rice Seedling Growth

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## Abstract

*Xanthomonas oryzae pv. oryzae (Xoo)* causes bacterial leaf blight, one of the major diseases affecting rice production. The use of endophytic bacteria as biocontrol agents and biofertilizers is a promising strategy for disease management and sustainable rice production. This study aimed to isolate endophytic bacteria from local rice seed varieties in West Sumatra, Indonesia, and evaluate their potential to suppress *Xoo* growth and promote rice seedling growth. Endophytic bacteria were isolated from five local rice varieties: Junjuang, Bujang Marantau, Caredek Merah, Cisokan, and Batang Piaman. The isolates were evaluated for biocontrol activity against *Xoo* in vitro and for their potential to promote rice seedling growth. A Completely Randomized Design was used with 15 selected endophytic bacterial isolates. Sixty-one endophytic bacterial isolates were obtained, and 15 were selected as potential biological agents based on hypersensitive reaction, pathogenicity, and hemolysis tests. Isolates BM07, CS03, CM01, and JJ06 suppressed *Xoo* growth in vitro, producing inhibition zones of 12.25, 11.25, 10.75, and 10.00 mm, respectively. Four isolates produced siderophores and protease enzymes, while seven isolates were capable of phosphate solubilization and nitrogen fixation. Isolates CM01, BM07, JJ06, and CS03 showed the best performance in promoting seedling height, root length, and fresh and dry weights. These four isolates demonstrated potential as biocontrol agents against *Xoo* and biofertilizers for rice through multiple plant-beneficial traits, including siderophore and protease production, phosphate solubilization, and nitrogen fixation. The results support further evaluation of these promising isolates under greenhouse and field conditions for sustainable rice disease management and production systems.

**Keywords:** *Bacterial blight disease, Biocontrol, Endophytic bacteria, Rice*

# Cytokinin Strengthens Antioxidant Defense and Restructures Metabolomic Landscape to Rescue Rice Growth Under Arsenic and Cadmium Stress

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## Abstract

Arsenic (As) and cadmium (Cd) contamination in agricultural soils poses a serious threat to rice productivity and food safety. The present study investigated the potential of cytokinin (CK; 6-benzylaminopurine, 6-BAP, 2 µM) in mitigation of As (50 mg $kg^{-1}$ soil) and Cd (200 mg $kg^{-1}$ soil) stress in rice. *Oryza sativa* cv. DRR Dhan 42 was used for experimentation based on screening of sixteen high-yielding rice genotypes for As and Cd stress tolerance. The CK biosynthesis inhibitor uniconazole (Uni; 200 µM) was co-applied to confirm the CK-dependency of the observed responses. As and Cd stress significantly increased oxidative damage, impaired photosynthetic pigment production and carbon metabolism, disrupted proline and nitric oxide signaling and elevated secondary metabolite accumulation in addition to increased shoot metal translocation. CK supplementation markedly reduced these effects as evinced by strong recovery in growth and tolerance indices, photosynthetic pigment content, carbon partitioning and strengthened antioxidative defenses encompassing enzymatic (SOD, APX, MDHAR, DHAR, GR, GST) and non-enzymatic (AsA, GSH) components of the ascorbate-glutathione cycle and glyoxalase system (Gly-I, Gly-II). GC-MS based metabolomics profiling further revealed CK-mediated restoration of membrane lipid pools disrupted by As and Cd stress, alongside reorganization of secondary metabolite and volatile organic compound profiles, thereby depicting metabolomic reprogramming for stress adaptation. Uni co-treatment partially reversed these benefits, confirming CK-dependency. Collectively, these findings showcase the potential of CK supplementation as a sustainable strategy to combat heavy metal toxicity in rice and secure grain safety in As- and Cd-contaminated agricultural landscapes.

**Keywords:** *Arsenic, Cadmium, Cytokinin, Rice, Metabolomics*

# NLSS3 Protects SHM1 from ATG8d-Mediated Autophagic Degradation to Regulate Leaf Morphology and Salt Tolerance in Rice

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## Abstract

The inherent trade-off between optimal plant architecture and robust stress resilience represents a fundamental challenge in the breeding of high-yielding rice cultivars. Overcoming this antagonistic relationship requires identifying master regulatory genes that can coordinately modulate both growth and stress response pathways. *NLSS3 (Narrow Leaf and Salt sensitive 3*) was identified as a pleiotropic regulator governing both leaf morphogenesis and salinity tolerance in rice. NLSS3 physically interacts with SHM1 (serine hydroxymethyltransferase), preventing it from being targeted for ATG8d-mediated autophagic degradation and thus maintaining its protein stability. The loss of *NLSS3* function causes *SHM1* depletion, resulting in serine deficiency and heightened salt sensitivity. Strikingly, *SHM1* overexpression not only restored salt tolerance in the *nlss3* mutant but also significantly increased grain yield in wild-type plants. Moreover, the superior *NLSS3* haplotype Hap1, which is predominant in japonica accessions, shows high expression and enhanced salinity tolerance. These findings establish NLSS3 as a central "autophagy guardian" that integrates plant development and environmental adaptation through the regulation of protein homeostasis. This work positions *NLSS3* as a promising target for precision breeding to engineer high-yielding and stress-resilient rice varieties.

**Keywords:** *Rice, Leaf morphogenesis, Salinity tolerance, Autophagic degradation, Pleiotropic regulation.*

# From Weed to Resource: Weedy Rice as a Source of Heat and Submergence Tolerance for Climate-Resilient Rice

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## Abstract

Climate change is increasing the frequency and intensity of heat and flooding events threatening rice production and global food security. Although weedy rice is one of the most problematic weeds in rice production, its high genetic and phenotypic diversity provides valuable traits for improving crop resilience. This study evaluated diverse weedy rice germplasm for tolerance to prolonged heat and complete submergence stress. Fifty-four weedy rice accessions, along with cultivated rice and breeding lines, were screened at the 3–4 leaf stage. Seedlings were exposed separately to 38°C heat or complete submergence for 21 days, followed by a recovery period in which plant height and biomass were evaluated. Considerable variation in stress response was observed among weedy rice accessions. Following heat stress, accession S108 showed only 6% reduction in plant height at 28 days after treatment, while B83 and S124 showed no biomass reduction. Frontiers Following complete submergence, 40% of surviving weedy rice accessions had less than 20% height reduction, 27% showed no biomass reduction, and 67% had less than 20% biomass reduction at 28 days after treatment. Several accessions recovered rapidly after de-submergence, while selected cultivated and breeding lines remained substantially stunted. Accessions including S21 and B28 exhibited tolerance to both heat and submergence stresses. These findings demonstrate that weedy rice is not only a major production challenge but also a potentially valuable reservoir of adaptive traits. Characterizing and utilizing this diversity may provide new opportunities for developing climate-resilient rice and strengthening sustainable rice production under increasingly variable environmental conditions.

**Keywords:** *Weedy rice, Heat stress, Submergence tolerance, Climate resilience, Rice improvement.*

# Can Stomatal Density Predict Photosynthetic Performance and Drought Resilience in Rice?

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## Abstract

Stomata regulate the trade-off between carbon assimilation and water loss, making stomatal traits promising physiological targets for improving rice productivity under water-limited environments. This study investigates whether natural variation in stomatal density is associated with photosynthetic performance, water-use strategy, and drought resilience across diverse rice germplasm.

More than 300 indica rice accessions were characterized across multiple field seasons for stomatal, gas-exchange, agronomic, and UAV-derived traits. Substantial genotypic variation was observed, and integration of physiological phenotyping with genome-wide association analysis identified genetic variation associated with photosynthetic performance. These results highlighted diverse stomatal and photosynthetic strategies within indica germplasm and provided candidate materials for further stress evaluation.

To extend these findings toward drought adaptation, breeding lines from the IRRI irrigated rice program and traditional Thai rice varieties were evaluated during the 2024 and 2025 dry and wet seasons. Consistent genotypic variation was observed in photosynthetic rate, stomatal conductance, flowering time, biomass, and grain yield, with several IRRI breeding lines maintaining relatively high photosynthetic capacity across seasons. In 2026, ten selected genotypes with contrasting stomatal density and photosynthetic capacity are being evaluated under well-watered and managed-drought conditions in parallel rain-shelter field experiments at IRRI and greenhouse experiments in Thailand. By integrating stomatal density, gas exchange, biomass, and yield responses, this work aims to determine whether contrasting stomatal phenotypes can explain variation in productivity under water limitation and support physiology-based selection for drought-resilient rice.

**Keywords***: Stomatal density, Photosynthesis, Water-use efficiency, Drought tolerance, Rice*

# Exploring Arbuscular Mycorrhizal (AM) symbiosis in Rice

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## Abstract

Arbuscular Mycorrhizal fungi (AMF) form beneficial symbiotic relationships with over 80% of land plants, including rice. Through their extensive hyphal networks, they support plant nutrient acquisition and resilience to environmental stress. Mycorrhizal pathways have been shown to supply a substantial proportion of phosphate acquired by rice. In return, plants supply AMF with photosynthesis-derived carbon, establishing a mutually beneficial exchange of resources. This association has the potential to improve crop nutrient-use efficiency, making it an important target for sustainable agriculture research.

The establishment of symbiosis relies on a complex exchange of signals between plants and fungi, enabling the recognition and establishment of symbiosis. By investigating the genetic mechanisms involved in regulating fungal colonisation of plant roots, we can gain a deeper understanding of plant-fungal interactions and identify opportunities to improve nutrient-use efficiency to promote more sustainable agriculture.

I will introduce the complementary molecular biology and microscopy approaches we undertake to study this symbiosis. Our work aims to characterise rice lines exhibiting advantageous phenotypic traits associated with AMF symbiosis. Microscopy enables us to visualise and quantify fungal colonisation of the roots, while molecular biology techniques provide quantitative insights into the expression of symbiosis-associated genes. Combining these approaches allows rice lines to be compared in their ability to establish and maintain AMF associations, alongside differences in fungal colonisation and plant growth and development. While controlled-environment studies provide valuable insights into these intricate interactions, future work hopes to apply these findings into field conditions to evaluate their potential in sustainable rice production.

**Keywords:** *AMF, Biotic, Symbiosis, Sustainability*

# Identification of Leaf Structural Changes and Candidate Genes for Rice Drought Tolerant Physiology and Yield

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## Abstract

Drought has profound effect on rice yield, cutting down global rice productivity ~8% each year predicted to reach up to 13% in future. Achieving drought tolerant physiology is important to retain rice yield under water deficit conditions. To study how rice physiology, especially the photosynthetic traits, behave under water deficit conditions, we have screened around 1000 indica rice accessions from 3K rice genome panel in a field drought-like environment in two dry seasons. These genotypes were phenotyped for several leaf morphological characters together with UAV-based HTP measurements of canopy temperature (CT) and NDVI, leaf water potential ($\psi_{Leaf}$), photosynthetic traits like, $A$, $g_s$ $E$ and $Ci$. The relations of these traits with the drought response index (DRI) were derived from > 600 indica genotypes in two field dry seasons. The performance of all these characters under managed drought stress (MDS) was compared against the performance in well-watered (WW) conditions has revealed drought-induced leaf morpho-functional interactive changes determine grain yield under drought. Onset of drought caused ~35 – 56% reduction in $A$ depending on the severity of the stress causing serious loss in yield. Correlation analyses revealed that the combination of initially broader leaves capable of increasing leaf thickness in response to drought, as evidenced by changes in SLA, along with maintenance of high $\psi_{Leaf}$ and high $A_{net}$, can collectively drive a higher DRI. Genome-Wide Association Studies (GWAS) identified seven QTLs for DRI which include known drought-responsive aquaporin, dehydrin, and heat shock protein genes, which coincide with the GWAS interval identified for CT on chromosome 7. From our study, we have predicted a functional inaction of our identified loci to manage water balance, leaf development, and photosynthesis-related performance to achieve higher yield under drought. Our results provide deep understanding about how to improve grain yield of rice under drought and provide opportunities to select the best-performing rice genotypes to aid drought breeding efforts by selecting optimal haplotype combinations for gene edits.

**Keywords:** *Rice, Drought, Leaf, Photosynthesis, 3K rice genomes, Leaf water potential, GWAS, High throughput drone images*

# Fungicide-Compatible *Trichoderma* sp. Suppresses Three Rice Diseases and Outyields Chemical Control in '*Morkhor 60-1*'

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## Abstract

Bakanae (*Fusarium fujikuroi*), brown spot (*Bipolaris oryzae*), and dirty panicle (*Fusarium verticillioides*) are seed-borne fungal diseases that threaten rice yield, grain quality, and food safety worldwide. Under sustainable integrated disease management, effective biocontrol agents should also be compatible with agrochemicals. This research aimed to screen *Trichoderma* spp. compatible with Mancozeb and copper hydroxide and evaluate their efficacy in controlling Bakanae, brown spot, and dirty panicle disease in the rice variety '*Morkhor 60-1*' under greenhouse conditions. Three *Trichoderma* isolates, TRB1, TRQ7, and TRQ15, tolerated Mancozeb and copper hydroxide via the poisoned food technique and suppressed three fungal pathogens in vitro. Each isolate was applied alone or in combination with either chemical to evaluate disease suppression and yield promotion under the greenhouse on '*Morkhor 60-1*' rice. For each *Trichoderma* isolate, all *Trichoderma* treatments showed significantly lower incidence and severity of all three diseases than respective pathogen-inoculated controls. Trichoderma applied alone produced significantly higher grain yield than either chemical alone or chemical–*Trichoderma* combinations for each disease inoculation experiment. Moreover, individual *Trichoderma* isolates were recovered from 75% of collected cultivated soil samples after chemical application, showing that they persist under fungicide exposure. Indigenous *Trichoderma* sp. therefore offers a dual benefit by remaining compatible with chemical fungicides. These findings support reduced fungicide inputs in sustainable, integrated management of multiple rice diseases.

**Keywords:** *Biological control, Copper hydroxide, Mancozeb, Integrated disease management, Antagonist persistence*

# Dose-Dependent Alleviation of Salinity Stress in Rice Seedlings by Salicylic Acid: Growth, Water Relations, and Membrane Integrity

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## Abstract

Salinity stress threatens rice establishment during the critical early seedling stage, while the effectiveness of salicylic acid (SA) as a stress-protective elicitor may depend strongly on its concentration, salinity level, and the trait evaluated. This study determined how exogenous SA modulates germination, early growth, water relations, membrane integrity, and osmotic adjustment in rice (*Oryza sativa* L. cv. Ciherang) under increasing salinity. A 4 × 4 factorial completely randomized design with four replications was used, comprising SA concentrations of 0, 1, 2, and 3 mM and salinity levels of 0, 4, 6, and 8 dS $m^{-1}$. Germination, seedling establishment, growth, biomass, photosynthetic pigments, relative water content (RWC), electrolyte leakage, and proline accumulation were measured and analyzed using two-way ANOVA followed by Duncan's multiple range test. Although all treatments reached 100% final germination, higher SA concentrations delayed initial germination. Increasing salinity reduced seedling growth and RWC while increasing electrolyte leakage. Under severe salinity at 8 dS $m^{-1}$, 3 mM SA increased shoot length from 3.20 to 14.77 cm and RWC from 20.56 to 50.99%, while reducing electrolyte leakage from 75.8 to 35.1% relative to the untreated control. Photosynthetic pigments and proline showed dose-specific responses, indicating that improvement in one physiological trait did not necessarily correspond with improvement in others. Overall, the response to SA was governed by an interaction among SA dose, salinity intensity, and trait type. Application of SA at 3 mM provided the most consistent post-germination protection against severe salinity, suggesting its potential as a practical seedling-stage intervention; however, validation at later growth stages and under field conditions is needed before wider application.

**Keywords:** *Electrolyte leakage, Osmotic adjustment, Photosynthetic pigments, Proline, Salicylic acid, Salinity stress*

# Epigenetic Plasticity and Transcriptional Reprogramming During Rice Regeneration and Transformation

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Plant regeneration and genetic transformation are fundamental to crop improvement, yet their impacts on the plant epigenome remain incompletely understood. DNA methylation is a key regulator of genome stability and gene expression, and its dynamic remodeling may contribute to variation in regeneration efficiency and transformation outcomes. Here, we investigated genome-wide DNA methylation changes associated with tissue culture, regeneration, and genetic transformation in rice. Comparative analyses of japonica (TNG67) and indica (IR64) cultivars revealed distinct epigenetic responses during callus induction and regeneration. TNG67 exhibited greater epigenetic plasticity, characterized by early promoter demethylation and transcriptional activation of stress- and hormone-responsive pathways, potentially contributing to its higher regeneration capacity. We further examined the epigenomic consequences of individual transformation procedures and identified widespread DNA methylation perturbations, particularly CHH hypo-methylation at promoter regions enriched for miniature inverted-repeat transposable elements (MITEs). Interestingly, promoter hypo-methylation was not consistently associated with transcriptional activation, suggesting complex relationships between DNA methylation and gene regulation. Moreover, binary vector exposure induced substantial transcriptional changes even without T-DNA transfer, indicating that transformation-associated molecular responses can occur independently of transgene integration. Together, these findings reveal distinct yet interconnected epigenetic responses during rice regeneration and transformation. Our study highlights the importance of epigenomic regulation in plant biotechnology and provides insights that may contribute to improving regeneration efficiency and minimizing unintended molecular alterations during genetic transformation.

**Keywords:** *DNA methylation, Rice, Epigenetics, Callus regeneration, Genetic transformation*



SECTION

# OS4

## Novel Rice Processing and Product Innovation

From grain to food: processing technology, quality and new products

Oral 7

# Cluster-based Characterization of Thermomechanical Structuring in Rice Bran Oil Oleogels Fabricated by Winterized Rice Bran Wax and Surfactants

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## Abstract

This study characterizes the thermomechanical structuring of rice bran oil (RBO) oleogels fabricated using winterized rice bran wax (RBW) and two low-hydrophile-lipophile-balance (HLB) surfactants—mono- and di-acylglycerol (MDG) and sucrose palmitate (SP)—through cluster-based analysis. The monounsaturated and polyunsaturated fatty acids in triacylglycerols (TAG) give RBO its naturally liquid behaviour, while the wax–surfactant mixtures act as oleogelators responsible for immobilizing the oil. Thermal and thermomechanical measurements provided the dataset for clustering, which identified non-linear relationships among RBW and surfactants within the structured RBO and grouped the formulations into four distinct structural regimes. SP-containing systems exhibited low onset crystallization temperatures and narrow melting ranges, indicating facilitated nucleation but weak network formation, consistent with their short structure-holding times or instantaneous melting at 22 °C. In contrast, MDG-containing systems showed markedly enhanced stability, with the 1.3% RBW + 1% MDG formulation maintaining its oleogel structure at 22 °C for over 1,440 min (24 h). These contrasting behaviors align with differences in head-group geometry: MDG's compact glycerol head promotes closer molecular packing and denser crystallite aggregation, whereas SP's bulky sucrose head sterically hinders network development. Cluster analysis effectively distinguished SP-driven, RBW-dominant, MDG-enhanced, and unstructured RBO systems, highlighting how wax–surfactant mixed oleogelator govern oleogel formation in RBO. Overall, the findings underscore the potential of rice-derived co-products to create structured RBO oleogels suitable for healthier fat replacement.

**Keywords:** *Oleogel, Rice Bran Oil, Surfactants, Wax, Winterizing Process*

# Development of Gluten-Free Macaroni-Type Pasta from Sago Starch and Annealed White and Pigmented Rice Flours: Physicochemical and Dietary Fiber Characteristics

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## Abstract

Conventional pasta is commonly made from refined wheat flour and may contain relatively limited amounts of dietary fiber. This study aimed to develop gluten-free macaroni-type pasta using sago starch and annealed white, red, and black rice flours and to evaluate its physicochemical characteristics and dietary fiber content. Seven formulations were prepared: C (100% sago starch), WR1 (50% white rice flour:50% sago starch), WR2 (100% white rice flour), RR1 (50% red rice flour:50% sago starch), RR2 (100% red rice flour), BR1 (50% black rice flour:50% sago starch), and BR2 (100% black rice flour). The evaluated parameters included color (L*, a*, b*, and hue angle), hardness, moisture, ash, fat, protein, carbohydrate, and dietary fiber contents. Rice flour type and substitution level significantly affected the physicochemical characteristics and dietary fiber content of the macaroni. Red and black rice flours produced darker-colored pasta, while rice flour substitution generally reduced hardness compared with the control. Protein and fat contents tended to increase, whereas carbohydrate content decreased with increasing rice flour proportions. Dietary fiber content ranged from 5.83 to 11.80 g/100 g, with the highest value observed in BR2. According to the high-fiber criterion of BPOM Regulation No. 1 of 2022 (at least 6 g/100 g for solid foods), all rice flour-containing formulations qualified as high-fiber, with values of 6.51–11.80 g/100 g, whereas the control contained 5.83 g/100 g. These findings demonstrate the potential of white, red, and black rice flours combined with sago starch to produce gluten-free macaroni-type pasta enhanced nutritional value and high dietary fiber content from locally available ingredients.

**Keywords:** *Gluten-free pasta, Macaroni-type pasta, Sago starch, Nutrient-enriched pasta, Pigmented rice flour*

## Introduction

Macaroni is a popular pasta product due to its convenience, affordability, and long shelf life (da Silva et al., 2024). Pasta is commonly produced from wheat-based ingredients and water, with eggs and other ingredients used depending on the product type (Abdo et al., 2024). Indonesia imported approximately 11.71 million tons of wheat in 2024 (Mahayani, 2024). Furthermore, wheat-based pasta has limited dietary fiber content and is unsuitable for individuals with celiac disease due to its gluten content (Pasini et al., 2025). Therefore, developing gluten-free macaroni-type pasta from local food ingredients offers an opportunity to diversify staple food sources and reduce dependence on wheat-based ingredients.

White, red, and black rice are local commodities with potential as raw materials for gluten-free macaroni-type pasta, given their distinct physicochemical characteristics and bioactive profiles. Red and black rice contain bioactive compounds such as anthocyanins, polyphenols, flavonoids, and γ-oryzanol, which offer potential antioxidant activity (Huang & Lai, 2016). In addition to rice flour, sago starch characterized by its high starch content can serve as a base for gluten-free macaroni-type pasta and contribute to the product's structural

formation (Lesse et al., 2026). However, the functional and technological properties of rice flour may require modification to obtain desirable characteristics for pasta processing.

Annealing is a physical hydrothermal modification technique that involves heating starch in excess water (over 60%) at a temperature below its gelatinization temperature for an extended period (Fonseca et al., 2021). This treatment can promote molecular rearrangement and improve the organization of starch chains, thereby altering starch crystallinity, water absorption capacity, gelatinization behavior, swelling capacity, and pasting properties. Annealing is a physical starch modification technique that can promote the formation of resistant starch (RS) (Anugerah et al., 2022). Resistant starch (RS), a fraction of starch that resists digestion in the small intestine and can be fermented by gut microbiota in the large intestine to produce short-chain fatty acids, which may support colonic health and help regulate postprandial blood glucose levels (Han et al., 2023). Previous research by Sulistyawati et al. (2024) investigated the physicochemical and functional properties of vermicelli produced from annealed white, red, and black rice flour. Nevertheless, findings from vermicelli cannot automatically be generalized to macaroni-type pasta because differences in product formulation and processing may influence the properties of the resulting products. The application of annealed rice flour in macaroni-type pasta formulated with sago starch therefore warrants further investigation.

Research on rice-based gluten-free macaroni-type pasta remains limited regarding comparisons between white, red, and black rice varieties, particularly when combined with sago starch and utilizing annealed rice flour. Variations in rice flour type and proportion are expected to influence nutritional and dietary fiber content of the gluten-free macaroni-type pasta. Therefore, this study aimed to develop gluten-free macaroni-type pasta based on sago starch and white, red, and black rice flour modified by annealing, as well as to evaluate the influence of rice flour type and proportion on physicochemical characteristics and dietary fiber. The findings are expected to support the utilization of local food sources as alternatives to wheat flour and provide insights into the role of annealing-modified rice flour in the development of gluten-free macaroni-type pasta.

## Materials and Methods

### Materials

The primary materials used to produce this starch-modified rice flour included three types of rice (white, red, and black) were obtained from local markets in Surakarta, Java, Indonesia. White rice refers to polished rice from a non-pigmented variety, whereas red and black rice refer to pigmented rice varieties. The rice samples were milled into flour before undergoing annealing modification. The ingredients for gluten-free macaroni-type pasta production were rice flour, sago starch (Pati Sagu Metro Brand, Pondok Sagu Metro, Bogor, Indonesia), chicken eggs, water, Carboxymethyl Cellulose (CMC; Koepoe-Koepoe brand, PT. Gunacipta Multirasa, Tangerang, Indonesia), and salt (obtained from a marketplace and TipTop Grocery in Ciputat, South Tangerang, Indonesia). Chemicals used for analysis were of analytical grade.

### Annealing Modification of Rice Flour

Rice flour modification by the annealing method was performed following the procedure described by Sulistyawati et al. (2024). A total of 300 g of rice flour was mixed with 240 mL of distilled water. The mixture was allowed to stand for 24 hours at room temperature. Subsequently, the mixture was incubated at 50°C for 24 hours using a shaking water bath. The sample was centrifuged in 2000 xg for 15 minutes, and the supernatant was discarded. The resulting sample was then dried at 30°C (±5 hours) and sieved using an 80-mesh sieve.

## Gluten-Free Macaroni-Type Pasta Production

Gluten-free macaroni-type pasta production was based on the method of Thomas et al. (2022) with modifications. Pasta production was carried out using a cold extrusion technique with a pasta machine (Oxone OX356, PT. Octa Utama, Jakarta, Indonesia) with a capacity of 400 g/batch. A macaroni-shaped die was used. For each treatment (Table 1), the flour ingredients were placed into the extrusion machine's hopper. All ingredient ratios were calculated based on 100 g of flour blend. While the machine was running, water (20 mL/100 g) and egg (28 mL/100 g) were added to form a 400 g batch of dough. Prior to this, the CMC (2 g/100 g) was mixed with hot water and stirred until a thick mixture formed. This mixture and the salt (2 g/100 g) were added to the dough, which was then mixed for approximately 10 minutes before the machine automatically switched to extrusion mode. The gluten-free macaroni-type pasta was manually cut into pieces approximately 2.5 cm in length. The cut pasta was then steamed in boiling water for 15 minutes, followed by oven-drying at 50°C for 5 hours.

**Table 1. Sample code for treatment combinations for gluten-free macaroni-type pasta based on sago starch and different types of rice flour**

| Sample no | Treatment code | Blends of flour materials (g/100 g) |
|---|---|---|
| 1 | C | SS100 |
| 2 | WR1 | WR50:SS50 |
| 3 | WR2 | WR100:SS0 |
| 4 | RR1 | RR50:SS50 |
| 5 | RR2 | RR100:SS0 |
| 6 | BR1 | BR50:SS50 |
| 7 | BR2 | BR100:SS0 |

C: control; SS: sago starch; WR: white rice; RR: red rice; BR: black rice; 1: 50% rice flour : 50% SS; 2: 100% rice flour : 0% SS.

## Physical Property Analysis of Uncooked Pasta

Color analysis was performed using a Minolta CR-300 Chromameter (CIELAB color system) for L*, a*, b*, and hue* [h° = arctan(b*/a*)], and uncooked gluten-free macaroni-type pasta hardness was analyzed using the Texture Profile Analysis (TPA) method with a TA-TX21 analyzer (Stable Microsystems, UK), following the procedure described by Rismaya et al. (2022).

## Chemical Property Analysis of Uncooked Pasta

Proximate analysis was performed on uncooked gluten-free macaroni-type pasta following the Association of Official Analytical Chemists methods (AOAC, 2006). Carbohydrate content was calculated by difference [carbohydrate (% dry basis, %db) = 100 – (ash + protein+ fat) % db]. Dietary Fiber (TDF) analysis refers to AOAC 991.43 total, soluble, and insoluble dietary fiber in foods, enzymatic-gravimetric method using the enzymatic-gravimetric method.

## Data Analysis

Each treatment was performed in triplicate. Data for all observed parameters were analyzed using One-Way ANOVA at a significance level of 5% ($p<0.05$). If the ANOVA results indicated a significant effect of the treatment on the observed parameters, the analysis proceeded with Duncan's Multiple Range Test (DMRT) at the 5% level. Statistical analysis was performed using SPSS software version 22.

## Results and Discussion

### Physical Characteristics

The research results show that rice flour substitution had a significant effect ($p<0.05$) on the color characteristics of the gluten-free macaroni-type pasta, including L*, a*, and b* values and the hue angle (Table 2). WR2 exhibited the highest lightness (L* = 62.01), yellowness (b* = 29.12), and hue angle (88.93°), indicating a lighter color with a predominantly yellow hue. In contrast, BR1 showed the lowest lightness (L* = 18.52), while BR2 had the lowest yellowness (b* = 5.65) and hue angle (46.58°). RR1 exhibited the highest redness (a* = 10.21), followed by RR2 (a* = 9.78). These differences may be associated with variations in the natural color and pigment composition of the rice flours (Figure 1). These findings align with studies by Sulistyawati et al. (2024) and Kusumawati et al. (2022), which reported that the use of colored rice yields products with lower L* and b* values and a tendency for higher a* values compared to white rice.

**Table 2. Physical properties of uncooked gluten-free macaroni-type pasta based on sago starch and different types of rice flour**

| Parameter | L* | a* | b* | (h°) | Hardness (N) |
|---|---|---|---|---|---|
| C | 54.21±6.88$^{b}$ | 3.29±0.48$^{d}$ | 20.91±0.61$^{b}$ | 81.07±1.26$^{b}$ | 7.03±1.67$^{a}$ |
| WR1 | 60.81±2.62$^{a}$ | 0.82±0.11$^{e}$ | 16.87±0.24$^{c}$ | 87.22±0.36$^{a}$ | 4.20±0.26$^{bc}$ |
| WR2 | 62.01±2.16$^{a}$ | 0.54±0.17$^{e}$ | 29.12±0.62$^{a}$ | 88.93±0.36$^{a}$ | 1.13±0.15$^{d}$ |
| RR1 | 31.07±3.05$^{c}$ | 10.21±0.20$^{a}$ | 17.04±0.32$^{c}$ | 59.05±0.98$^{c}$ | 5.17±0.15$^{b}$ |
| RR2 | 27.00±1.33$^{cd}$ | 9.78±0.26$^{a}$ | 14.42±0.06$^{d}$ | 55.87±0.41$^{d}$ | 0.10±0.02$^{d}$ |
| BR1 | 18.52±0.62$^{e}$ | 4.52±0.15$^{c}$ | 6.78±0.06$^{e}$ | 56.29±0.88$^{d}$ | 3.23±0.20$^{c}$ |
| BR2 | 21.70±1.79$^{de}$ | 5.65±0.49$^{b}$ | 5.65±0.49$^{f}$ | 46.58±2.88$^{e}$ | 1.37±0.55$^{d}$ |

C: control; SS: sago starch; WR: white rice; RR: red rice; BR: black rice; 1: 50% rice flour : 50% SS; 2: 100% rice flour : 0% SS; N: newton.



C WR1 WR2 RR1 RR2 BR1 BR2

**Figure 1. Visual appearance of uncooked gluten-free macaroni-type pasta based on sago starch and different types of rice flour.** C = control; SS = sago starch; WR = white rice; RR = red rice; BR = black rice; 1 = 50% rice flour: 50% SS; 2 = 100% rice flour: 0% SS.

These changes are attributed to the presence of natural pigments in colored rice such as proanthocyanidins contribute red color in red rice and anthocyanins contribute black color in black rice (Goufo & Trindade, 2014). Theoretically, as the concentration of anthocyanin pigments within the food matrix increases, leading to a decrease in lightness and hue angle values, correlating with higher a* values (Karaoglan et al., 2019; Lembo et al., 2025). The low brightness values of red and black rice macaroni were influenced not only by the natural color of the raw materials but also by pigment changes occurring during processing. These results are consistent with Jiamyangyuen et al. (2019) who reported that after cooking and oven drying, the brightness of black glutinous rice increased, whereas the brightness of non-glutinous black

rice decreased. This difference was attributed to the high anthocyanin content of black glutinous rice, which resulted in greater anthocyanin release. Variations in the color of rice-based pasta are also influenced by its chemical composition. Kraithong & Rawdkuen (2021) reported that higher ash content in rice flour is associated with lower noodle brightness.

Different types of rice flour substitution had a significant effect ($p<0.05$) on gluten-free macaroni-type pasta hardness. In general, increasing rice flour substitution reduced gluten-free macaroni-type pasta hardness compared to the control based on 100% sago starch. Treatment C exhibited the highest hardness value (7.03 N), whereas RR2 shows the lowest value (0.10 N), which did not differ significantly from WR2 and BR2. These findings align with those of Makdoud & Rosentrater (2017) and Axentii et al. (2026) who reported that altering ingredient composition in gluten-free pasta can result in a less dense or less cohesive and more brittle matrix, more fragile and less elastic, exhibited higher fracturability, requiring less force for deformation. The texture profile of different rice-based macaroni products is influenced by the amylose content of the raw materials. The high amylose content of Guichao rice (23.91%) produced rice noodles with greater elasticity, whereas rice varieties with moderate amylose content produced softer noodles (Wei et al., 2022). The amylose content of rice flour ranged from 22.83-26.66% (Sulistyawati et al., 2024), while the amylose content in sago starch is 21–31% (Moshawih et al., 2025). To address this issue, Chillo et al. (2007) incorporated CMC and a pre-gelatinization treatment into the production of oat pasta. In the production of gluten-free pasta, an egg protein emulsifier can also be added to enhance cooking quality, cohesiveness or binding within the dough, thereby improving the structural integrity of the pasta's texture (Padalino et al., 2016).

**Proximate Properties and Dietary Fiber**

The results show that the different types of rice flour substitution had a significant effect ($p<0.05$) on moisture, ash, fat, protein, carbohydrate and dietary fiber of uncooked gluten-free macaroni-type pasta (Table 3). Analysis results show that the moisture content of uncooked gluten-free macaroni-type pasta ranged from 8.37% to 10.36%. The moisture content of all samples met the SNI 01-3777-1995 standard (maximum 12.5%) (Rahma et al., 2024). This may be due to the water-binding capacity of hydroxyl groups in dietary fiber and protein limiting moisture removal during drying process (Rismaya et al., 2018). Fiber with a high water-binding capacity can retain more water, thereby reducing water availability (Aydogdu et al., 2018). Although the fiber content in red and black rice might theoretically enhance water binding and reduce moisture content, these results show a different trend. Fluctuating water content results may also be caused by several factors, such as thick layer drying and an initial moisture content. The drying rate decreases exponentially as the number of stacked layers increases due to greater airflow resistance and reduced convective water vapor transport (Guo et al., 2023). In this study, the molded macaroni was steamed before drying, which may have affected its initial moisture content. Initial moisture content and temperature significantly influence effective moisture diffusivity and the convective mass transfer coefficient (Baidhe et al., 2025).

Regarding ash content, the values ranged from 1.45% to 1.66%, with the highest value in BR2 (1.66%), reflecting the mineral contribution from the rice flour. These findings align with reports by Hatta et al. (2025) and Sulistyawati et al. (2024) that the addition of rice flour (red and black rice) can increase the product's ash content. The ash content of a food sample reflects its total mineral content (Pradipta et al., 2023). Red rice contained $9.26 \pm 1.01$ mg/100 g calcium and $451.68 \pm 4.43$ mg/100 g potassium, while black rice was particularly rich in

potassium (1,032.91 ± 19.26 mg/100 g) and contained 1.26 ± 0.01 mg/100 g zinc (Winarti et al., 2023).

**Table 3. Proximate properties and dietary fiber of uncooked gluten-free macaroni-type pasta based on sago starch and different types of rice flour.**

| Samples | Parameter | | | | | |
|---|---|---|---|---|---|---|
| | Moisture (%wb) | Ash (%db) | Fat (%db) | Protein (%db) | Carbohydrate (%db) | Dietary fiber (%db) |
| C | 10.25±0.14$^{ab}$ | 1.45±0.03$^{b}$ | 1.78±0.02$^{e}$ | 2.66±0.06$^{f}$ | 94.12±0.01$^{a}$ | 5.83±0.14$^{g}$ |
| WR1 | 8.52±0.19$^{e}$ | 1.45±0.01$^{b}$ | 3.33±0.08$^{c}$ | 6.27±0.11$^{e}$ | 88.96±0.04$^{b}$ | 6.51±0.04$^{f}$ |
| WR2 | 9.22±0.19$^{d}$ | 1.60±0.04$^{a}$ | 3.58±0.06$^{b}$ | 10.81±0.23$^{c}$ | 84.02±0.12$^{c}$ | 7.04±0.04$^{e}$ |
| RR1 | 8.37±0.19$^{e}$ | 1.58±0.03$^{a}$ | 3.03±0.05$^{d}$ | 6.89±0.13$^{d}$ | 88.51±0.06$^{b}$ | 9.44±0.06$^{d}$ |
| RR2 | 9.60±0.19$^{cd}$ | 1.66±0.03$^{a}$ | 4.88±0.12$^{a}$ | 11.51±0.29$^{b}$ | 81.97±0.13$^{d}$ | 10.11±0.09$^{b}$ |
| BR1 | 9.83±0.21$^{bc}$ | 1.60±0.04$^{a}$ | 2.81±0.05$^{d}$ | 7.05±0.13$^{d}$ | 88.55±0.04$^{b}$ | 9.67±0.11$^{c}$ |
| BR2 | 10.36±0.20$^{a}$ | 1.65±0.03$^{a}$ | 4.93±0.18$^{a}$ | 12.00±0.30$^{a}$ | 81.43±0.49$^{e}$ | 11.80±0.03$^{a}$ |

C = control; SS = sago starch; WR = white rice; RR = red rice; BR = black rice; 1 = 50% rice flour: 50% SS; 2 = 100% rice flour: 0% SS; %wb (wet basis); %db (dry basis).

Fat content ranged from 1.78% to 4.93%, while protein content ranged from 2.66% to 12.00%, with the highest value of fat and protein observed in BR2. The increase may be attributed to the relatively higher protein and lipid contents of pigmented rice flour compared with sago starch. The pigmented rice has protein content of 5-10%, higher amino acid composition, and better fatty acid composition (Sontakke et al., 2026; Zhai et al., 2023). Conversely, carbohydrate content decreased from 94.12% in control to 81.97% in BR2. This decrease was also influenced by the "by difference" method, as increases in protein, fat, moisture, and ash content automatically resulted in a lower calculated proportion of carbohydrates (Bala et al., 2020). Sago starch contains approximately 90% carbohydrates per 100 g, and considerably higher than white rice (34%) (Setiawan et al., 2022).

The dietary fiber content of the gluten-free macaroni-type pasta ranged from 5.83% to 11.80% and differed significantly among treatments ($p<0.05$). The control sample had the lowest content, while BR2 (100% black rice) had the highest. Treatments rice flour (white, red, black) were classified as high fiber, as they exceeded 6 g/100 g, in accordance with BPOM (2022) regulations. The increase in dietary fiber content may be attributed to the higher fiber content of rice flour compared with sago starch, particularly in pigmented rice, which contains approximately 9–10% to 34% dietary fiber (Das et al., 2025; Savitha & Singh, 2011), whereas sago starch contains only about 3.48% fiber (Budiyanto et al., 2026).

## Conclusion

In conclusion, rice flour substitution significantly influenced the physical, proximate, and dietary fiber characteristics of gluten-free macaroni-type pasta. White rice flour produced lighter-colored pasta, whereas red and black rice flours resulted in darker products, with RR1 exhibiting the highest redness (a* = 10.21). Rice flour substitution generally reduced hardness compared with the control (7.03 N), with RR2 showing the lowest value (0.10 N). In terms of nutritional composition, BR2 exhibited the highest protein (12.00%), fat (4.93%), and dietary fiber (11.80%) contents, while RR2 also showed relatively high protein (11.51%), fat (4.88%), and dietary fiber (10.11%) contents. All rice flour-substituted formulations met the high-fiber criterion of more than 6 g/100 g. Overall, black rice flour is

a promising ingredient for enhancing the nutritional value of gluten-free macaroni-type pasta, particularly its protein and dietary fiber contents. However, the low hardness values observed in rice flour-based formulations suggest that the products may be too fragile and prone to breakage. Therefore, further formulation optimization is needed to improve textural properties and structural integrity while maintaining the nutritional benefits and desirable sensory characteristics of the final product.

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## References

[BPOM]. (2022). *Peraturan Badan Pengawas Obat dan Makanan Nomor 1 Tahun 2022 tentang Klaim pada Label dan Iklan Pangan*.

Abdo, E. M., Darwish, A. M. G., Hussein, M. M. E., & Mansour, H. M. M. (2024). Pasta enriched with de-oiled sesame and yellow pepper flours: Evaluation of physicochemical properties, protein quality, and antioxidant potential. *Applied Food Research*, *4*(2), 100602. https://doi.org/10.1016/j.afres.2024.100602

Anugerah, M. P., Faridah, D. N., Afandi, F. A., Hunaefi, D., & Jayanegara, A. (2022). Annealing processing technique divergently affects starch crystallinity characteristic related to resistant starch content : a literature review and meta-analysis. *International Journal of Food Science and Technology*, *57*(4), 2535–2544. https://doi.org/10.1111/ijfs.15628

AOAC. (2006). *Official Methods of Analysis of The Association of Official Analytical Chemists 16th edition. Virginia (US)*. Association of Official Analytical Chemists Washington, DC.

Axentii, M., Codină, G. G., Andrade Laborde, J. E., & Rotaru, A. (2026). Rapeseed protein–fiber concentrate as a novel ingredient for pasta production: technological and quality characteristics. *Gels*, *12*(560), 1–21. https://doi.org/10.3390/gels12070560

Aydogdu, A., Sumnu, G., & Sahin, S. (2018). Effects of addition of different fibers on rheological characteristics of cake batter and quality of cakes. *Journal of Food Science and Technology*, *55*(2), 667–677. https://doi.org/10.1007/s13197-017-2976-y

Baidhe, E., Clementson, C. L., Hellevang, K., & Zhulu, L. (2025). Comprehensive analysis of drying kinetics, heat and mass transfer, and thermodynamic properties in high-temperature drying of high-moisture corn. *Journal of Food Process Engineering*, *48*(6), e70159. https://doi.org/10.1111/jfpe.70159

Bala, M., Handa, S., D, M., & Singh, R. K. (2020). Physicochemical, functional and rheological properties of grass pea (*Lathyrus sativus* L.) flour as influenced by particle size. *Heliyon*, *6*(11), e05471. https://doi.org/10.1016/j.heliyon.2020.e05471

Budiyanto, A., Risfaheri, R., Winarti, C., Widaningrum, W., Kailaku, S. I., Sulistyaningrum, A., Jamal, I. B., Hidayat, T., Hendriadi, A., & Arif, A. Bin. (2026). Fortification of sago starch with egg powder: impacts on starch and noodle properties. *The Scientific World Journal*, *2026*(1), 1–18. https://doi.org/10.1155/tswj/3631288

Chillo, S., Laverse, J., Falcone, P. M., & Del Nobile, M. A. (2007). Effect of carboxymethylcellulose and pregelatinized corn starch on the quality of amaranthus spaghetti. *Journal of Food Engineering*, *83*(4), 492–500. https://doi.org/10.1016/j.jfoodeng.2007.03.037

da Silva, L. M., Santos, M. F., da Silva, B. L., Francisco, C. L., de Paula, S. C. S. E., Pereira, N. R., Saraiva, S. H., Teixeira, L. J. Q., & Filho, A. M. M. (2024). Influence of drying method on the shelf life of artisanal pasta. *Food and Humanity*, *3*(100431), 1–9. https://doi.org/10.1016/j.foohum.2024.100431

Das, S., Kumari, T., Babu, S., C, N., Kumar, S., & Deka, S. C. (2025). Bioactive compounds, functional properties,

health benefits, and food applications of black rice: a comprehensive review. *Food Chemistry Advances*, *7*(June), 101028. https://doi.org/10.1016/j.focha.2025.101028

Fonseca, L. M., Lisie, S., El, M., Renato, A., Dias, G., & Zavareze, R. (2021). Physical modification of starch by heat-moisture treatment and annealing and their applications : A review. *Carbohydrate Polymers*, *274*(118665), 1–15. https://doi.org/10.1016/j.carbpol.2021.118665

Goufo, P., & Trindade, H. (2014). Rice antioxidants: Phenolic acids, flavonoids, anthocyanins, proanthocyanidins, tocopherols, tocotrienols, γ-oryzanol, and phytic acid. *Food Science and Nutrition*, *2*(2), 75–104. https://doi.org/10.1002/fsn3.86

Guo, W., Tong, L., Yang, L., Zhao, S., Yin, S., & Liu, C. (2023). A thick-layer drying kinetic model and drying characteristics of moisture-containing porous materials. *International Communications in Heat and Mass Transfer*, *149*(107133), 1–13. https://doi.org/10.1016/j.icheatmasstransfer.2023.107133

Han, J., Wu, J., Liu, X., Shi, J., & Xu, J. (2023). Physiological effects of resistant starch and its applications in food : a review. *Food Production, Processing and Nutrition*, *5*(48), 1–8. https://doi.org/10.1186/s43014-023-00156-x

Hatta, W., Ningrum, E. M., Yuliati, F. N., & Syawal, S. (2025). Antioxidant activities, physicochemical and sensory quality attributes of steam milk dodol using red rice flour. *Jurnal Ilmu-Ilmu Peternakan*, *35*(2), 209–219. https://doi.org/10.21776/ub.jiip.2025.035.02.4

Huang, Y. P., & Lai, H. M. (2016). Bioactive compounds and antioxidative activity of colored rice bran. *Journal of Food and Drug Analysis*, *24*(3), 564–574. https://doi.org/10.1016/j.jfda.2016.01.004

Jiamyangyuen, S., Nuengchamnong, N., & Ngamdee, P. (2019). Changes of anthocyanins in black rice flours prepared by cooking and pregelatinization. *Natural and Life Science Communications*, *18*(4), 534–552. https://doi.org/10.12982/CMUJNS.2019.0035

Karaoglan, H. A., Keklik, N. M., & Develi Isıklı, N. (2019). Degradation kinetics of anthocyanin and physicochemical changes in fermented turnip juice exposed to pulsed UV light. *Journal of Food Science and Technology*, *56*(1), 30–39. https://doi.org/10.1007/s13197-018-3434-1

Kraithong, S., & Rawdkuen, S. (2021). Quality attributes and cooking properties of commercial Thai rice noodles. *PeerJ*, *9*(e11113), 1–19. https://doi.org/10.7717/peerj.11113

Kusumawati, R., Palupi, N. S., & Budijanto, S. (2022). Aktivitas antioksidan makaroni beras hitam dan kacang-kacangan berpigmen metode cold extrusion. *AgriTECH*, *42*(3), 195–205.

Lembo, M., Eramo, V., Riggi, R., Forniti, R., Bellincontro, A., & Botondi, R. (2025). Destructive and non-destructive evaluation of anthocyanin content and quality attributes in red kiwifruit subjected to plant spray treatment with cis-3-hexenyl butyrate. *Foods*, *14*(3), 1–15. https://doi.org/10.3390/foods14030480

Lesse, C., Lusiana, S. A., Kristanto, B., Sarmpumpwain, A., & Mado, J. E. (2026). Optimization of the sensory and nutritional properties of sago-based wet noodles fortified with red fruit oil. *Journal of Indonesia Applied Nutrition (JIAN)*, *1*(1), 32–39. https://doi.org/10.56303/jian.v1i1.1305

Mahayani, N. M. H. (2024). Tata kelola kebijakan pengurangan ketergantungan impor gandum dalam perspektif ketahanan pangan Indonesia. *GOVERNANCE: Jurnal Ilmiah Kajian Politik Lokal Dan Pembangunan*, *10*(3), 67–68.

Makdoud, S., & Rosentrater, K. A. (2017). Development and testing of gluten-free pasta based on rice, quinoa and amaranth flours. *Journal of Food Research*, *6*(4), 91–110. https://doi.org/10.5539/jfr.v6n4p91

Moshawih, S., Pei, J., Kong, T., Goh, B. H., Renganathan, E., Goh, H. P., Goh, K. W., & Ming, L. C. (2025). Exploring the nutritional, cultural, and industrial significance of Metroxylon sagu. *Discover Food*, *5*(337), 1–19. https://doi.org/10.1007/s44187-025-00638-6

Padalino, L., Conte, A., & Nobile, M. A. Del. (2016). Overview on the general approaches to improve gluten-free pasta and bread. *Foods*, *5*(4), 1–18. https://doi.org/10.3390/foods5040087

Pasini, G., Arp, C. G., de Leo, S., Brandolini, A., Estivi, L., & Hidalgo, A. (2025). Technological and nutritional characteristics of gluten-free pasta enriched with tomato and linseed by-products. *Food Science and Nutrition*, *13*(10), 1–11. https://doi.org/10.1002/fsn3.71105

Pradipta, S., Siswoyo, T. A., & Ubaidillah, M. (2023). Nutraceuticals and bioactive properties of local Java pigmented rice. *Biodiversitas*, *24*(1), 571–582. https://doi.org/10.13057/biodiv/d240166

Rahma, C., Apriani, L., Harahap, H., Budijanto, S., Kurniati, Y., & Lubis, F. (2024). Innovation macaroni pasta of based lumi-lumi fish- endemic and effect of boiling method process on nutritional content. *Media Teknologi Hasil Perikanan*, *12*(2), 121–127.

Rismaya, R., Syamsir, E., & Nurtama, B. (2018). Pengaruh penambahan tepung labu kuning terhadap serat pangan, karakteristik fisikokimia dan sensori muffin. *Jurnal Teknologi Dan Industri Pertanian*, *29*, 58–68. https://doi.org/10.6066/jtip.2018.29.1.58

Rismaya, R., Syamsir, E., Nurtama, B., & Tohyeng, N. (2022). Effects of water addition and baking time on the production process optimization of pumpkin muffins: Pilot plant study. *Canrea Journal: Food Technology, Nutritions, and Culinary Journal*, *5*(2), 183–207. https://doi.org/10.20956/canrea.v5i2.711

Savitha, Y. S., & Singh, V. (2011). Status of dietary fiber contents in pigmented and non-pigmented rice varieties before and after parboiling. *LWT*, *44*(10), 2180–2184. https://doi.org/10.1016/j.lwt.2011.06.004

Setiawan, B., Fetriyuna, F., Letsoin, S. M. A., Purwestri, R. C., & Jati, I. R. A. P. (2022). A sago positive character: a literature review. *Jurnal Ilmiah Kedokteran Wijaya Kusuma*, *11*(2), 145–155. https://doi.org/10.30742/jikw.v11i2.2443

Sontakke, M., M, M. A., Shams, R., Dash, K. K., Shaikh, A. M., & Béla, K. (2026). Processing effects on the nutritional and phytochemical properties of pigmented rice products: A comprehensive review. *Food Chemistry Advances*, *12*(101363), 1–15. https://doi.org/10.1016/j.focha.2026.101363

Sulistyawati, E. Y. E., Mustofa, A., Rismaya, R., & Suhartatik, N. (2024). Physicochemical and functional properties of vermicelli made of modified white rice, brown rice, and black rice. *International Journal on Advanced Science Engineering Information Technology*, *14*(3), 1042–1048.

Thomas, B., Sudheer, K. P., Saranya, S., Kothakota, A., Pandiselvam, R., & Joseph, M. (2022). Development of protein enriched cold extruded pasta products using hybrid dried processed mushroom powder and defatted flours: A study on nutraceutical, textural, colour and sensory attributes. *LWT*, *170*(113991), 1–11. https://doi.org/10.1016/j.lwt.2022.113991

Wei, P., Fang, F., Liu, G., & Zhang, Y. (2022). Effects of composition, thermal, and theological properties of rice raw material on rice noodle quality. *Frontiers in Nutrition*, *9*(1003657), 1–13. https://doi.org/10.3389/fnut.2022.1003657

Winarti, C., Widaningrum, Widayanti, S. M., Setyawan, N., Qanytah, Juniawati, Suryana, E. A., & Widowati, S. (2023). Nutrient composition of Indonesian specialty cereals: rice, corn, and sorghum as alternatives to combat malnutrition. *Preventive Nutrition and Food Science*, *28*(4), 471–482. https://doi.org/10.3746/pnf.2023.28.4.471

Zhai, J., Li, X., Svensson, B., Jin, Z., & Bai, Y. (2023). Increasing protein content of rice flour with maintained processability by using granular starch hydrolyzing enzyme. *Molecules*, *28*(8), 1–18. https://doi.org/10.3390/molecules28083522

# Effect of Hydrothermal and Dry Heat Treatment on the Quality Improvement of Dried Rice Noodles from Freshly Harvested Rice

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## Abstract

The production of quality rice noodles conventionally requires rice aged more than 6 months because using of freshly harvested rice caused high cooking loss and excessive surface stickiness. However, the natural aging process demands prolonged storage, incurring substantial inventory holding costs. Generally, rice accelerated aging methods are mainly used dry heat or hydrothermal, but their application to noodle processing remains limited. In this study, effect of hydrothermal and dry heat treatment on the quality of rice noodles were investigated. Freshly milled rice was subjected to either hydrothermal treatment (HT) at 100°C for 30 and 60 min or dry heat treatment (DH) at 70°C and 110°C for 3 h before making rice noodles. Noodles from HT-treated rice exhibited a marked reduction in cooking loss and superior textural firmness compared to those prepared from 6-month naturally aged grains. Furthermore, the cooked strand length was significantly increased, with longer HT durations conferring greater improvements in cooking and textural properties. For DH, milled rice treated at 70°C had noodles with superior cooking quality relative to the naturally aged control, characterized by lower cooking loss, increased firmness, reduced surface adhesiveness, and higher cooked strand length. In contrast, noodles from rice treated with DH at 110°C could not maintain their shape and exhibited a mushy texture. HT-treated rice noodles had lower cooking loss and higher number of long length cooked strands than DH-treated rice noodles. Therefore, HT, especially at 100°C for 60 min, was more suitable for improving the quality of dried rice noodles from freshly harvested rice.

**Keywords:** *Rice noodles, Accelerated aging, Cooking quality, Texture*

# Engineering Shelf-Stable Ready-to-Eat Adobo Rice: Process Optimization and Thermal Validation

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## Abstract

Urban consumers are shifting to a more convenient rice options suited to their modern lifestyle while also addressing their preference and quality of food choices. In this regard, this research used a novel rice variety from IRRI in the development of ready-to-eat adobo flavored rice. The study optimized processing parameters for a safe, shelf-stable, ready-to-eat (RTE) adobo meal using the novel rice variety. Using a Box-Behnken Design under Response Surface Methodology (RSM), the ideal parameters were established: 70-minute soak time, 1:2 rice-to-water ratio, and 25-minute cook time. Thermal validation using Bigelow's General Method confirmed commercial sterility with a lethality (F0) of 8.58 minutes. Texture Profile Analysis indicated that the optimized RTE grain was significantly softer (10.75 N) and more adhesive (-0.55 N) than a freshly cooked control. Instrumental and sensory evaluations revealed significant changes to the rice matrix resulting from the processing conditions. The optimized RTE adobo rice exhibited a significantly softer and more adhesive texture compared to freshly cooked rice, driven by the intense thermal load, high moisture availability, and the acidic adobo formulation. While the optimized product achieved 100% consumer acceptability, preference testing heavily favored the freshly cooked control. The thermal degradation of volatile compounds and the potential generation of Maillard-derived "processed" off-flavors during retorting resulted in lower taste scores, highlighting a common sensory challenge in thermally sterilized convenience meals.

**Keywords:** *Canned rice, Retort sterilization, Response surface methodology, Flavored rice, Adobo rice*

# Enhancing the Convenience of Whole-Grain Nutrition: Retort Processing of Unpolished Low-Amylose NSIC Rc218 SR Rice

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## Abstract

This study established the thermal processing parameters for unpolished NSIC Rc218 SR (Mabango 3) rice packaged in flexible stand-up retort pouches to develop a convenient, shelf-stable, and highly nutritious ready-to-eat (RTE) product. Physicochemical evaluation of the raw brown rice revealed a moisture content of 12.03 ± 0.36%, an optimum cooking time of 45 min, and a water uptake ratio of 2.18 ± 0.07. To optimize product quality, twelve formulation treatments were evaluated, combining rice-to-water ratios (1:4 and 1:5), pre-boiling durations (5, 7, and 10 min), and vinegar concentrations (0.00%, 0.25%, and 0.50% w/w). Pre-boiling duration and rice-to-water ratio significantly influenced moisture retention and hardness ($p < 0.05$), whereas vinegar incorporation significantly decreased pH ($p < 0.05$) and altered starch retrogradation. Sensory evaluation by 32 semi-trained panelists identified the formulation with a 1:5 rice-to-water ratio, a 7-min pre-boiling duration, and 0.00% vinegar as optimal, achieving the highest overall acceptability score (5.57 ± 1.24). Thermal validation at a target retort temperature of 121.1 °C yielded a come-up time of 12 min, an operator process time of 20 min, and a total process time of 90 min. Heat penetration analysis demonstrated a cumulative lethality ($F_0$) value of 12.40 min (with $F_0 = 6.53$ min achieved at the 30-min mark), substantially exceeding the commercial sterility requirement ($F_0 = 3.0$ min). These findings confirm that retort-processed unpolished NSIC Rc218 SR rice provides a microbiologically safe, convenient, and consumer-acceptable ready-to-eat brown rice product.

**Keywords:** *Commercial sterility, Heat penetration testing, Ready-to-eat brown rice, Thermal processing*

# Fungal Control and Quality Responses of Electron Beam-Irradiated Riceberry Rice during Storage

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## Abstract

Pigmented rice is increasingly valued for its nutritional composition and bioactive compounds with potential health benefits. However, fungal contamination has been reported in commercially available pigmented rice, raising concerns about product quality and food safety. Electron beam irradiation (EBI) offers a promising approach for fungal decontamination of cereal grains, but its effectiveness must be considered alongside its potential effects on the nutritional and technological quality of pigmented rice during storage. This study investigated the effects of EBI at doses of 0, 1, 3, and 5 kGy on fungal contamination, nutritional and bioactive characteristics, and pasting properties of Riceberry rice during 16 weeks of storage. Irradiation treatment and storage time significantly affected fungal contamination and inactivation efficiency ($p < 0.001$). The highest inactivation efficiency was observed at 5 kGy after 4 weeks of storage, reaching 97.11 ± 1.47%. EBI had limited effects on nutritional and bioactive characteristics, whereas storage significantly influenced several quality attributes ($p<0.05$). Pasting properties were more responsive to irradiation, with peak viscosity at week 16 decreasing from 498.21 RVU in the control to 293.25 RVU at 5 kGy, indicating changes in starch functionality. Overall, EBI provided effective fungal control while largely maintaining the nutritional and bioactive characteristics of Riceberry rice; however, the observed changes in pasting behavior indicate a trade-off between fungal control and technological functionality, particularly at higher irradiation doses.

**Keywords:** *Electron beam irradiation, Pigmented rice, Fungal contamination, Nutritional quality, Bioactive compounds*

# Scalable Production, Bioactive Profiling, and Industrial Applications of Rice Malt Extract Powder

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## Abstract

This study presents an optimized pilot-scale bioprocess for manufacturing gluten-free rice malt extract powder from local Thai rice cultivar Phitsanulok 80. Controlled malting (48 h steeping, 60 h germination) coupled with a two-stage enzymatic hydrolysis (protease/β-amylase at 50 °C for 60 min followed by α-amylase at 75 °C for 60 min) yielded a high-quality fermentable extract. Pilot-scale validation in a 1,500 L stainless-steel system produced a free-flowing powder rich in maltose sugars (47.10 g/100g), γ-aminobutyric acid (GABA, 252.55 mg/100 g), and thiamine (0.65 mg/100 g). Toxicological and microbiological evaluations confirmed the complete absence of gluten (<0.85 mg/kg gliadin), aflatoxins, and heavy metals, meeting international safety standards. Application trials established that the rice malt extract powder successfully replaced commercial barley malt in Yeast and Mold (YM) agar for microbial cultivation. Furthermore, trial formulations of a gluten-free malt beverage demonstrated favorable nutritional profiles. This standardized bioprocessing framework provides a validated, non-infringing template easily adaptable to another alternative Thai rice cultivars.

**Keywords:** *Rice malt extract powder, Enzymatic saccharification, Gluten-free ingredient, Bioactive GABA, Pilot-scale bioprocess*

## Introduction

Malt extracts represent foundational functional ingredients in food processing, beverage manufacturing, and industrial biotechnology. Historically, barley malt extract has dominated global supply chains; however, reliance on barley poses substantial economic and technical hurdles for tropical regions where barley cannot be cultivated locally (Gusain, 2022). In Southeast Asia, importing barley malt incurs supply chain vulnerabilities and elevated production overheads. Concurrently, the accelerating global prevalence of celiac disease and non-celiac gluten sensitivity—affecting 1–6% of the population—has driven market expansion for certified gluten-free alternatives (Global Market Insights, 2025). Developing sustainable malt extract substitutes from indigenous cereal crops is therefore both an economic imperative and an innovation opportunity.

Thailand's vast agricultural capacity provides an ideal foundation for grain-based bioprocessing. Thai rice cultivars possess favorable starch architectures (78–82% total starch) and moderate protein levels suitable for enzymatic transformation (Farooq and Yu, 2025). While previous research demonstrated the feasibility of grain malting, low endogenous diastatic power and limited free amino nitrogen (FAN) in rice grains frequently hindered full saccharification (Guimaraes et al., 2024). To overcome these metabolic constraints, strategic malting combined with exogenous food-grade enzyme supplementation (exopeptidases, β-amylase, and endo-α-amylase) is required to unlock fermentable sugars and functional bioactives.

This study establishes a comprehensive pilot-scale framework (1,500 L system) for manufacturing gluten-free rice malt extract powder. Utilizing Chainat 1 rice as a benchmark non-glutinous rice cultivar (Puangwerakul et al,2025), we systematically optimized malting parameters, validated a two-stage enzymatic extraction scheme, characterized physicochemical and safety profiles, evaluated packaging stability, and demonstrated application in microbiological media and functional beverages. Crucially, the standardized bioprocessing workflow developed herein serves as a modular prototype designed for straightforward adaptation to other prominent Thai rice cultivars, Phitsanulok 80 in this research.

## Materials and Methods

### Grain Preparation and Controlled Malting

Certified paddy rice (Phitsanulok 80, harvested at 12.08% initial moisture content) was cleaned to eliminate debris and light grains. Malting was conducted in accordance with European Brewery Convention standards (EBC, 1987). Steeping was performed in distilled water at 30 °C for 48–72 h with 12 h water refreshes to maintain grain oxygenation. Germination proceeded on trays under dark conditions at 30 °C and 95–100% relative humidity for 120 h until acrospires reached 2/3 to 3/4 of kernel length. Moisture content, germination energy (GE), and diastatic power (DP) were recorded at 12 h intervals. Germinated grains were kilned at 50–60 °C for 18–24 h to fix enzymatic activity and milled into fine malt flour.

### Two-Stage Enzymatic Extraction Optimization

Enzymatic extraction was conducted in accordance with Puangwerakul et al. (2025). The method was optimized in bench-scale slurry reactors (1:4 w/v flour-to-water ratio). The bioprocess comprised two sequential thermal phases: (1) Protease and β-Amylase Rest: Slurries were treated with commercial protease (0.1% w/w, 50,000 U/g) and β-amylase (0.1% w/w, 2,500 U/g) at 50 °C for 30–60 min to promote protein solubilization and maltose release; (2) α-Amylase Saccharification Rest: Following proteolysis, α-amylase (0.1% w/w, 3,000 U/g) was added, and the mixture was heated to 75 °C for 30–60 min to accomplish thorough starch liquefaction. Enzymes were thermally inactivated at 85 °C for 15 min.

### Pilot-Scale Production and Spray Drying

Industrial scale-up was conducted in accordance with Puangwerakul et al. (2025). The method was executed in a 1,500 L stainless-steel extraction plant. Milled malt flour was homogenized with water (1:4 w/v) and processed under the optimized sequential enzyme regimen. The clarified mash was isolated via mechanical filtration and dried using a rotary spray dryer (inlet temperature 150 °C, outlet temperature 50 °C). The resulting powder was sieved and sealed in laminated foil pouches and high-density polyethylene (HDPE) containers.

### Analytical Protocols and Safety

Sugar profiles (maltose, glucose, sucrose) and bioactive thiamine (vitamin B1) were analyzed using HPLC-UV (Liu, 2002). Gamma-aminobutyric acid (GABA) was determined spectrophotometrically at 630 nm (Kamjijam et al., 2021). Microbiological safety (total plate count, pathogen screening) and toxicological contaminants (aflatoxins B1/B2/G1/G2 via AOAC 991.31; gliadin gluten content via ELISA; heavy metals Pb/Cd/As/Hg via ICP-MS) were accredited by ISO/IEC 17025 facilities..

### Industrial Application Testing

### Microbiological Media Suitability in YM Agar Formulations

To determine the viability of Phitsanulok 80 rice malt extract powder as a functional substitute in culture media, its performance was benchmarked against a commercial-grade reference ("Malt Extract for Microbiology," Merck Chemicals). The pilot-produced rice malt powder was integrated into yeast and mold (YM) agar media at identical concentration levels to enable direct comparative analysis.

The baseline YM agar medium was prepared per liter of distilled water containing 3.0 g malt extract, 3.0 g yeast extract, 5.0 g peptone, 10.0 g dextrose, and 15.0 g agar. Evaluation was conducted across eight representative fungal strains: *Candida albicans* ATCC 10231, *Saccharomyces cerevisiae* ATCC 9763, *S. cerevisiae* ATCC 9080, *Geotrichum candidum* DSM 1240, *Rhodotorula mucilaginosa* DSM 70403, *Penicillium commune* ATCC 10428, *Aspergillus brasiliensis* ATCC 16404, and *Trichophyton ajelloi* ATCC 28454. Test strains were inoculated at $10^2$-$10^3$CFU and maintained aerobically at 28 °C for a 7-day incubation cycle. Microbial growth kinetics and medium efficiency were quantitatively and qualitatively appraised by evaluating colony density, morphology, and proliferation rates relative to the control medium formulated with commercial barley malt extract.

### Wort Preparation and Production of Low-Alcohol Beer Utilizing Rice Malt Powder

Wort featuring low sugar concentration was formulated using a modified protocol adapted from Puangwerakul et al. (2025). Rice malt extract powder was reconstituted in water at a 1:11 (w/v) ratio, achieving an initial gravity of 8°Plato. Fermentation was conducted at 30 °C for 14 days following inoculation with *Saccharomyces cerevisiae* RSU No. 10 a strain chosen from the Rangsit University Culture Collection for its controlled ethanol output and advantageous metabolic characteristics. To lower the final ethanol level below the 0.5% (v/v) non-alcoholic threshold, thermal vacuum evaporation was executed at 80 °C for 2 hours. The dealcoholized beverage was characteristic analyzation.

## Results and Discussion

### Grain Malting Kinetics and Bioactive Enhancement

Steeping dynamics established that kernel moisture reached equilibrium (25.11 ± 0.25%) within 48 h, triggering embryonic activation. Germination energy reached 98.0 ± 1.0%, exceeding the EBC benchmark minimum of 95.0%. Diastatic power peaked at 134.0 ± 11.5 WK units at 60 h of germination. Malting induced profound compositional changes: crude protein increased from 7.15 g/100 g to 8.88 g/100 g, total reducing sugars surged from 0.03 g/100 g to 4.08 g/100 g, and bioactive GABA expanded over 8-fold (from 2.02 mg/100 g to 16.88 mg/100 g), corroborating germination-induced glutamate decarboxylase activity as summarized in Table 1.

**Table 1 Compositional transformation of raw vs. malted rice grain (dry basis).**

| Parameter | Raw Paddy Grain | Malted Grain (60 h) |
|---|---|---|
| Moisture Content (%) | 12.08 ± 0.20a | 5.17 ± 0.43b |

| | | |
|---|---|---|
| Crude Protein (g/100 g) | 7.15 ± 0.25b | 8.88 ± 0.05a |
| Total Reducing Sugars (g/100 g) | 0.03 ± 0.00b | 4.08 ± 0.16a |
| GABA Content (mg/100 g) | 2.02 ± 0.02b | 16.88 ± 0.34a |
| Diastatic Power (WK units) | Not Detected | 134.0 ± 11.5 |

**Note:** Values are expressed as mean ± standard deviation (n=3). Different letters within the same row indicate significant differences ($p \leq 0.05$).

## Enzymatic Saccharification Efficiency

Bench-scale trials demonstrated that relying solely on endogenous grain enzymes yielded incomplete starch cleavage (Table 2). Incorporating exopeptidases and β-amylase at 50 °C for 60 min doubled soluble protein release (3.10 mg/mL) and elevated maltose yield to 16.73 g/100 g. Subsequent α-amylase treatment at 75 °C for 60 min maximized starch breakdown, driving glucose and sucrose sugar concentration in the wort mash to 5.21 and 1.14g/100 g, respectively. This verified that a sequential 50 °C → 75 °C enzyme regime is vital for high extract recovery.

**Table 2 Hydrolysis efficiency under sequential enzymatic extraction treatments.**

| Parameter | Control Hydrolysis | Full Hydrolysis |
|---|---|---|
| Soluble Protein (mg/mL) | 1.52 ± 0.11b | 3.10 ± 0.24a |
| Maltose (g/100 g) | 5.08 ± 0.25b | 16.73 ± 0.22a |
| Glucose (g/100 g) | 1.42 ± 0.10b | 5.21 ± 0.25a |
| Sucrose (g/100 g) | Not Detected | 1.14 ± 0.10a |

**Note:** Values are expressed as mean ± standard deviation (n=3). Different letters within the same row indicate significant differences ($p \leq 0.05$).

## Pilot Powder Quality and Safety Compliance

Spray drying of clarified pilot extract yielded a golden, free-flowing powder with 3.55% moisture content and 78.41 g/100 g total carbohydrates (Table 3). Sugar profiling revealed high fermentability: 47.10 g/100 g maltose. The powder retained high levels of functional bioactives, including GABA (252.55 mg/100 g) and thiamine (0.65 mg/100 g). Crucially, toxicological screening confirmed complete safety: gliadin gluten was non-detectable (<0.85 mg/kg), aflatoxins B1/B2/G1/G2 were absent, and heavy metals (Pb < 0.015 mg/kg, Cd < 0.010 mg/kg, As and Hg non-detectable) satisfied stringent food safety limits.

**Table 3 Physicochemical, bioactive, and safety profile of pilot-scale powder.**

| Quality Attribute | Measured Value | Safety / Standard Limit |
|---|---|---|
| Total Carbohydrates (g/100 g) | 78.41 ± 5.25 | Major Component |
| Maltose Content (g/100 g) | 47.10 | Fermentable sugar |
| GABA Bioactive (mg/100 g) | 252.55 ± 10.15 | Functional Bioactive |
| Thiamine / Vitamin B1 (mg/100 g) | 0.65 ± 0.08 | Essential Micronutrient |
| Gluten Allergen (Gliadin) | ND (<0.85 mg/kg) | <20 mg/kg (Gluten-Free) |

| | | |
|---|---|---|
| Aflatoxin ($B_1$,$B_2$,$G_1$,$G_2$) | ND (<0.25 μg/kg) | Codex Alimentarius Safe |
| Heavy Metals (Pb, Cd, As, Hg) | Pass / < LOD | Codex Alimentarius Safe |

**Performance Evaluation as a Fungal Growth Substrate**

The nutritional efficacy of the rice malt extract powder was investigated by supporting the growth of diverse fungal organisms, using a premier commercial product ("Malt Extract for Microbiology," Merck) as a reference control. Eight fungal strains *Candida albicans*, two distinct strains of *Saccharomyces cerevisiae*, *Geotrichum candidum*, *Rhodotorula mucilaginosa*, *Penicillium roquefortii*, *Aspergillus niger*, and *Trichoderma harzianum* were cultured on solid agar media formulated with either the rice-derived or commercial malt extract. Agar plates were inoculated with $10^2$-$10^3$CFU and incubated under aerobic conditions at 28 °C for seven days.

The experimental outcomes summarized in Table **4** revealed that for the eight fungal species, colony formation rates on the rice malt media were statistically equivalent to those on the commercial reference, confirming that the rice malt extract effectively substitutes commercial media in supporting fungi proliferation.

**Table 4 Comparison of fungal colony proliferation on media formulated with rice malt extract versus a commercial benchmark.**

| Fungal Strain | Colony Count (CFU/mL) on Medium NS | |
|---|---|---|
| | Rice Malt Extract | Commercial Malt Extract |
| *Candida albicans* TISTR5554 | (2.44±0.22) x$10^2$ | (2.52±0.25) x$10^2$ |
| *Saccharomyces cerevisiae*TISTR5774 | (2.52±0.25) x$10^2$ | (2.64±0.20) x$10^2$ |
| *Saccharomyces cerevisiae*TISTR5240 | (2.81±0.23) x$10^2$ | (2.93±0.25) x$10^2$ |
| *Geotrichum candidum* TISTR3422 | (2.40±0.20) x$10^2$ | (2.68±0.21) x$10^2$ |
| *Rhodotorula mucilaginosa*TISTR5864 | (2.50±0.20) x$10^2$ | (2.96±0.26) x$10^2$ |
| *Penicillium roquefortii* TISTR3511 | (2.10±0.25) x$10^3$ | (2.42±0.20) x$10^3$ |
| *Aspergillus niger* TISTR1867 | (2.15±0.20) x$10^3$ | (2.85±0.25) x$10^3$ |
| *Trichoderma harzianum* TISTR3553 | (2.12±0.15) x$10^3$ | (2.25±0.22) x$10^3$ |

Note: Values represent mean ± standard deviation (n = 3). NS indicates no statistically significant difference between values in this row ($p > 0.05$).

**Development of Non-Alcoholic, Beer-Style Beverage Derived from Rice Malt Powder**

We assessed the commercial potential of utilizing rice malt extract powder to produce a gluten-free, alcohol-free beverage mimicking traditional beer profile. The production workflow commenced with the dissolution of rice malt powder in distilled water (1:11 w/v ratio) to yield a low-sugar wort with an initial gravity of 10°Plato. Primary fermentation was executed with *Saccharomyces cerevisiae* RSU No. 10 at 30 °C for a 14-day cycle. Thermal vacuum processing was subsequently applied to reduce the ethanol content below the mandated non-alcoholic ceiling (<0.5% ABV), followed by bottling and pasteurization prior to analytical evaluations (Kreimeyer et al., 2025) Table 5 outlines the key physicochemical parameters determined for both the wort and the processed beer.

Table 5 summarizes the physicochemical attributes of the unfermented wort and the resulting malt beverage. The wort and final beer exhibited light pale color values on the EBC scale (1.74 ± 0.05 and 2.82 ± 0.15, respectively), aligning with standard pale commercial lagers and offering a visually desirable appearance for traditional beer consumers. Turbidity dropped markedly from 4.42 ± 0.26 to 2.00 ± 0.22 EBC Helm post-fermentation, demonstrating effective liquid clarification. The final product displayed a specific gravity of 1.0110 ± 0.0010 and a residual extract level of 2.5 ± 0.15 °Plato, reflecting unfermented or partially converted sugars (Table 15) that imparted a characteristic sweetness and body to the beverage.

While the fermentation verified the viability of rice malt extract as a gluten-free substrate, the process produced a low-alcohol beverage (2.58% ABV) rather than a non-alcoholic one (<0.5% ABV). Consequently, refining the vacuum evaporation parameters or implementing secondary dealcoholization techniques remains essential to achieve true non-alcoholic compliance.

Post-fermentation acidification reduced the wort pH from 5.76 ± 0.14 to 4.08 ± 0.17, matching typical brewing profiles critical for flavor and microbial stability. Free amino nitrogen (FAN) levels declined from 112.81 ± 11.63 mg/L in the wort to 69.42 ± 10.10 mg/L in the beer due to yeast assimilation. Although this depletion reflects active metabolism, the residual FAN concentration was slightly below optimal yeast health requirements, potentially affecting fermentation kinetics and organoleptic development.

**Table *5* Physicochemical attributes of the unfermented wort and the resulting malt beverage.**

| Analyze | Wort | | Beer | |
|---|---|---|---|---|
| | Wort from the rice malt extract powder | [1]EBC criteria of Wort [42] | Beer from the rice malt extract powder | [2]EBC criteria of Beer (Bamforth,2008; Moll et al.,2013) |
| Pale Malt Color (°EBC) | 5.33±0.27 | 4–12 | 7.84±0.25 | ≤8 (pale), 8–25 (amber), >25 (dark) |
| Turbidity (EBC Helm) | 3.20±0.28 | ≤5.0 NTU (bright wort) | 2.10±0.25 | ≤1.5 NTU (bright beer) |
| Mass (°Plato) | 9.98±0.27 | 10–15°P | 2.54±0.22 | 2–6°P (light), >12°P (strong) |
| pH | 5.01±0.25 | 5.2–5.6 | 4.75±0.22 | 4.2–4.6 |
| FAN (mg/L) | 131.9±9.9 | 150–250 mg/L | 58.5±5.6 | 120–220 mg/L |
| % Extract | 79.01±3.26 | 75–82 % | - | Varies by beer style |
| Specific gravity | 1.0401±0.001 | 1.040–1.060 | 1.008±0.001 | 1.008–1.016 |
| % Alcohol by Vol. (Before evaporation) | 0.0±0.0 | 0.0 | 4.308±0.10 | 3.5–7.5 % (typical beers) |
| % Alcohol by Vol. (After evaporation) | - | - | 0.00±0.0 | <0.5% |
| Bitterness (BU) | 0.00±0.00 | No standard | 18.00±0.50 | 15–35 BU |

Note: Values represent mean ± standard deviation (n = 3).

## Standardization and Adaptation Guidelines for Phitsanulok 80

The bioprocess established in this work provides a standardized methodology for evaluating other regional rice cultivars. When adapting this template for Phitsanulok 80 (a high-yielding Thai cultivar characterized by 18% amylose content), key operational parameters should be calibrated as follows: (1) Adjust steeping time based on grain water absorption kinetics to achieve 25–26% moisture equilibrium; (2) Monitor germination energy and diastatic power to optimize kilning timing at peak enzyme development (~60 h); (3) Tune the ratio of exogenous α-amylase to β-amylase during the 50 °C and 75 °C rest phases to accommodate cultivar-specific starch gelatinization temperatures; and (4) Verify total sugar yield, GABA accumulation, and gluten-free compliance against the baseline benchmarks set in this study.

**Acknowledgements**

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**References**

AOAC International. Official Methods of Analysis of AOAC International, 22nd ed.; Oxford University Press: Oxford, UK, 2023.

Bamforth, C.W. (2008). Beer: Tap into the Art and Science of Brewing; Oxford University Press: New York, NY, USA.

Brand-Williams, W.; Cuvelier, M.E.; Berset, C. Use of a free radical method to evaluate antioxidant activity. LWT - Food Sci. Technol. 1995, 28, 25–30. https://doi.org/10.1016/S0023-6438(95)80008-5

European Brewery Convention. Analytica-EBC: Methods of the European Brewery Convention, 4th ed.; Verlag Hans Carl Getränke-Fachverlag: Zürich, Switzerland, 1987.

Farooq, M.A.; Yu, J. Starches in rice: Effects of rice variety and processing/cooking methods on their glycemic index. Foods 2025, 14, 2022. https://doi.org/10.3390/foods14122022

Global Market Insights Inc. Gluten-Free Products Market Size - Industry Trends and Forecast 2025–2034; Global Market Insights Inc.: Selbyville, DE, USA, 2025.

Guimaraes, B.P.; Schrickel, F.; Rettberg, N.; Pinson, S.R.M.; McClung, A.M.; Luthra, K.; Atungulu, G.G.; Sha, X.; de Guzman, C.; Lafontaine, S. Investigating the malting suitability and brewing quality of different rice cultivars. Beverages 2024, 10, 16. https://doi.org/10.3390/beverages10010016

Gusain, P. Global Malt Extracts and Ingredients Market – Industry Trends and Forecast to 2029; Data Bridge Market Research: Pune, India, 2022.

Kamjijam, B.; Suwannaporn, P.; Bednarz, H.; Na Jom, K.; Niehaus, K. Elevation of gamma-aminobutyric acid (GABA) and essential amino acids in germinated rice traced by MALDI imaging. Food Chem. 2021, 365, 130399. https://doi.org/10.1016/j.foodchem.2021.130399

Kreimeyer, H.; Sydor, S.; Buchholz, L.; Toskal, C.; Özcürümez, M.; Schnabl, B.; Syn, W.-K.; Sowa, J.-P.; Manka, P.; Canbay, A. Non-alcoholic beer influences glucose and lipid metabolism and changes body composition in healthy, young, male adults. *Nutrients* **2025,** *17,* 1625. https://doi.org/10.3390/nu17101625

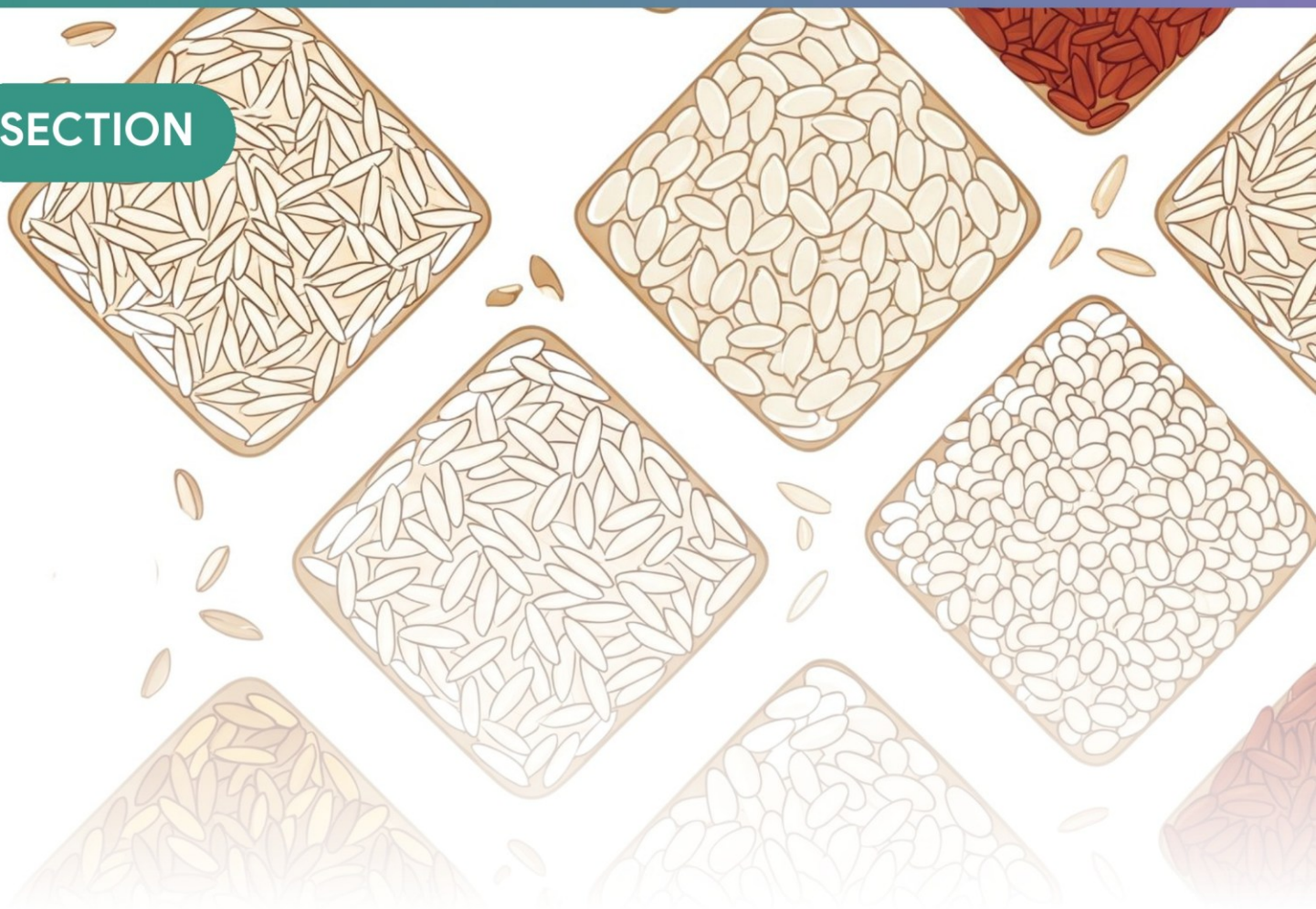
Liu, S.; Zhang, Z.; Liu, Q.; Luo, H.; Zheng, W. Spectrophotometric determination of vitamin B1 in a pharmaceutical formulation using triphenylmethane acid dyes. J. Pharm. Biomed. Anal. 2002, 30, 685–694. https://doi.org/10.1016/S0731-7085(02)00356-4

Moll, M.; Esslinger, H.M. (2013). Handbook of Brewing: Processes, Technology, Markets; Wiley-VCH Verlag GmbH & Co. KGaA: Weinheim, Germany.

Puangwerakul, Y.; Soithongsuk, S.; Wongwailikhit, K. Gluten-free rice malt extract powder: pilot-scale production, characterization, and food applications. Molecules. 30 (21):130.https:doi.org/10.3390/molucules30214279

Singleton, V.L.; Rossi, J.A. Colorimetry of total phenolics with phosphomolybdic–phosphotungstic acid reagents. Am. J. Enol. Vitic. 1965, 16, 144–158.

SECTION



# OS5

## Health, Medical and Pharmaceutical Related Product or Variety

Nutrition, functional foods and health benefits of rice

Oral 2

# Structured Rice Bran Stearin HIPEs as Functional Lipids for Minimizing Invisible Fat Consumption

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## Abstract

With global nutritional guidelines recommending a daily fat intake of only 44–78 grams, the excessive consumption of "invisible fats" embedded in everyday foods has become a growing public health concern. These unseen fats—often solid, saturated, and optimized for palatability—contribute substantially to chronic disease risk despite being largely unnoticed in daily dietary patterns. Although rice bran oil is recognized for its cardioprotective MUFAs, phytosterols, and γ-oryzanol, its liquid nature limits its use in food matrices that require solid-fat functionality. This study introduces a nutritional engineering approach that upcycles Rice Bran Stearin (RBS), a refinery side-stream naturally enriched in waxes and unsaponifiable bioactive lipids such as policosanols, phytosterols, and γ-oryzanol, into structured functional lipids designed to reduce invisible fat exposure in daily diets. Four industrial RBS batches were characterized to establish a functional standardization range, revealing consistent levels of key structural builders despite batch variability. To buffer this variability, RBS was transformed into oleogel-based High Internal Phase Emulsions (HIPEs) using a dual-structuring mechanism that integrates fat crystal networks with self-assembled fibrillar networks (SAFIN). The resulting RBS-HIPEs form a solidified, bioactive-rich lipid fraction with enhanced techno-functionality, including "ball-bearing" plasticity that improves performance in real food matrices subjected to mechanical and thermal stress. By providing a standardized, healthier alternative to conventional solid fats, RBS-HIPEs offer a scalable strategy for minimizing invisible fat consumption and advancing rice-based nutritional solutions within a circular bioeconomy framework.

**Keywords:** *Circular bioeconomy, γ-Oryzanol, Phytosterols, Rice bran stearin, Structured lipids*

# Rice-Derived Biopolymers for Sustainable Pharmaceutical and Biomedical Applications: From Grain and By-products to Health Innovation

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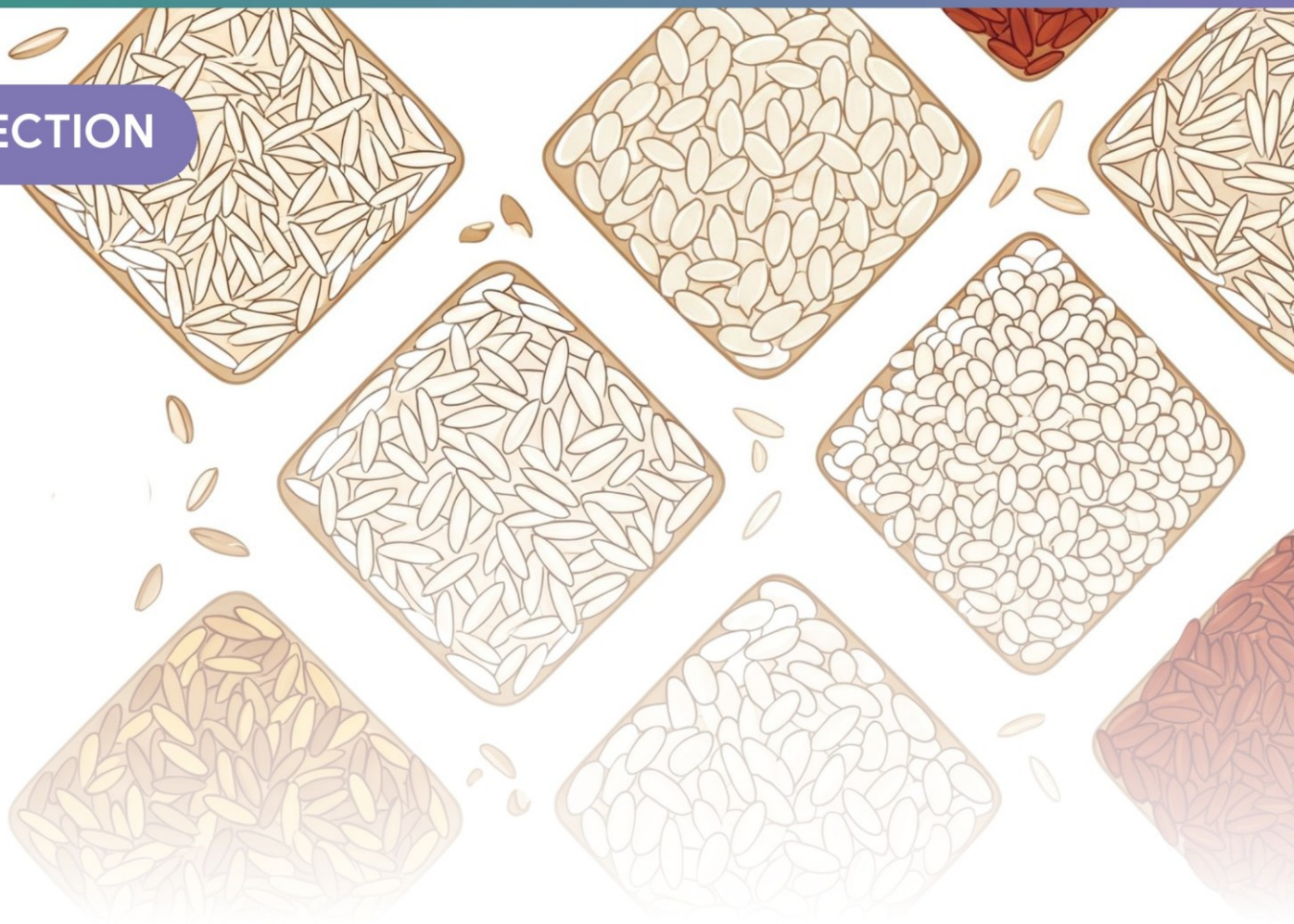
## Abstract

Rice production provides starch-rich grains and cellulose-rich by-products, including bran, husk, and straw, yet these materials remain underutilized as sustainable pharmaceutical resources. This critical review evaluates rice starch and residue-derived cellulose as excipients and delivery platforms, focusing on source–processing–property relationships, pharmaceutical functions, and translational readiness. Peer-reviewed evidence was synthesized according to polymer modification, material performance, biocompatibility, environmental impact, and scalability. Rice polymer shows potential as a binder, disintegrant, film-forming matrix, encapsulating agent, and controlled-release carrier. Modification can improve its functionality; however, moisture sensitivity, retrogradation, limited mechanical strength, and variation in amylose-to-amylopectin ratio remain important limitations. Cellulose recovered from rice residues provide high surface area, reinforcing ability, swelling capacity, and tunable surface chemistry, supporting applications in films, hydrogels, wound-care materials, and drug-delivery systems. Translation is constrained by lignin and silica removal, variable particle characteristics, residual reagent control, energy-intensive processing, and insufficient *in vivo* safety data. Crystallinity, particle size, surface charge, and modification chemistry are key determinants of loading capacity, stability, and release behavior. An emerging opportunity is an "all-rice" delivery platform in which rice-derived polymers encapsulate rice bioactives, including anthocyanins, phenolic compounds, or γ-oryzanol. Such systems could improve bioactive stability, valorize rice-processing residues, and reduce dependence on petroleum-derived materials. Green extraction, standardized quality specifications, safety assessment, and life-cycle evaluation are essential for advancing these polymers into scalable health products. This approach integrates human health, environmental sustainability, and circular rice production within the One Health framework.

**Keywords:** *Rice-derived biopolymers, Rice starch, Drug development, Circular bioeconomy*

SECTION



# OS6

## Agri-tech

Digital agriculture, sensing, automation and data-driven rice farming

Oral 6

# Machine-Learning Prediction of Rice Yield from Satellite-Derived Indices Using PyCaret

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## Abstract

Accurate rice-yield estimation supports agricultural planning, crop monitoring, and food-security management. Satellite remote sensing provides repeated observations over large areas, while machine learning can capture nonlinear relationships between remotely sensed indicators and crop yield. This study applied PyCaret, an open-source automated machine-learning library, to predict average rice yield in Amnat Charoen (ACR) and Surin (SRN), Thailand. The dataset comprised 452 rice-field observations, 39 satellite-derived predictors, and the target variable Avg_Yield_Kg_per_Rai. Candidate regression models were evaluated using a 70:30 train–test split and 10-fold cross-validation. CatBoost achieved the strongest overall cross-validated performance, with an $R^2$ of 0.9762, RMSE of 13.0332 kg $rai^{-1}$, MAE of 4.3345 kg $rai^{-1}$, and MAPE of 3.12%. BI, RI, NDRE2, LAI_CW, and LAI were the most influential predictors. These findings demonstrate the potential of satellite data and automated machine learning for rice-yield estimation, although validation across additional years and provinces is required.

**Keywords:** *Rice yield prediction, Satellite remote sensing, Machine learning, Vegetation indices, Precision agriculture*

# Polymer-R : An Innovative Fertilizer Coating for Mitigating Nitrous Oxide Emissions and Enhancing Nitrogen Use Efficiency in Paddy Fields

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## Abstract

Currently, practical technologies capable of tangibly reducing greenhouse gas emissions in paddy fields remain limited. The agricultural sector still lacks effective approaches to control and mitigate nitrous oxide ($N_2O$) emissions, a gas with a global warming potential nearly 300 times greater than that of carbon dioxide ($CO_2$). Consequently, the necessity to rely on nitrogen fertilizers inevitably equates to the continuous release of greenhouse gases into the atmosphere. This research, therefore, evaluates the efficacy of "Polymer-R," an innovative fertilizer coating (polymer-to-urea ratio of 1:10 by weight) designed to control nitrogen release. Field experiments were conducted across 11 Rice Research Centers, comprising 14 trials over two growing seasons (dry season 2024–2025 and wet season 2025). The study employed a Randomized Complete Block Design (RCBD) with 4 replications and 5 treatments (N-$P_2O_5$-$K_2O$ kg/ha) as follows: 1) 0-37.5-37.5, 2) 37.5-37.5-37.5 (conventional urea), 3) 75-37.5-37.5 (conventional urea), 4) 37.5-37.5-37.5 (coated urea), and 5) 75-37.5-37.5 (coated urea). The results revealed that Treatment 4 (a 50% reduction in nitrogen utilizing coated urea) produced a rice yield not statistically different from Treatment 3 (the full nitrogen rate utilizing conventional urea), despite the reduced urea application. This finding confirms that the Polymer-R coated urea innovation can reduce nitrogen fertilizer usage by up to 50% without compromising crop yield. Hence, implementing this technology effectively lowers nitrous oxide emissions at least 50% as a result of minimized urea usage for 50%. In conclusion, this technology demonstrates high potential in lowering chemical N fertilizer costs while concurrently mitigating $N_2O$ emissions, thereby tangibly supporting environmental sustainability goals.

**Keywords:** *Polymer-R coated urea, Nitrous oxide, Paddy field, Nitrogen use efficiency, Greenhouse gas mitigation*

## Introduction

In rice cultivation, urea (46-0-0) is the primary chemical fertilizer utilized to supply nitrogen. Serving as a main nitrogen source, urea is frequently blended with other straight fertilizers to achieve desired NPK formulations. Due to its chemical properties, urea rapidly hydrolyzes into ammonium, resulting in a high local concentration of ammonium in the soil solution. It is widely recognized that crops absorb no more than 50% of the applied nitrogen, with the remainder being lost through various pathways—most notably via transformation into nitrous oxide (Department of Soil Science Faculty, 1987). Given these inherent characteristics, farmers cannot easily resolve nitrogen loss by applying smaller doses more frequently, as this significantly increases labor costs. Consequently, farmers face two major challenges when using conventional urea:

1. Excessive Vegetative Growth: Rice plants exhibit overly rapid vegetative growth within the first 7–15 days post-application. This surge in lush, succulent leaf tissue is

well documented to increase susceptibility to insect pests and fungal diseases compared to plants with moderate growth.

2. Premature Nutrient Depletion: Because urea dissolves rapidly and is prone to multi-pathway losses, the available nitrogen is largely exhausted within 15 days of application. This rapid depletion causes the rice foliage to yellow well before the next scheduled fertilization interval.

To address these limitations, Polymer-R a novel bio-based fertilizer coating polymer was synthesized by a Thai scientist. Engineered as an innovative controlled-release coating for urea, Polymer-R regulates nitrogen release to align with crop uptake dynamics over time. This approach adheres to established integrated pest management (IPM) principles; continuous over-supply of nitrogen across growth stages induces excessive canopy density and mutual shading, which predisposes rice plants to major diseases and insect infestations (Dobermann and Fairhurst, 2000)**.** The objective of this research was to compare the effects of conventional urea and polymer-R coated urea fertilizers on rice growth and grain yield.

## Materials and Methods

A field experiment was conducted throughout the rice cultivation cycle until harvest. The experiment was carried out in experimental subplots enclosed by 30-centimeter-high earthen bunds, with each subplot measuring 5×7 meters. The experimental design was a Randomized Complete Block Design (RCBD) with four replications and five treatments. Various nitrogen fertilizer formulations were evaluated, in which urea coated with Polymer-R was utilized as a nitrogen source and compared against conventional urea. A control treatment without urea application was also included as follows:

Treatment 1 apply 0 - 37.5 - 37.5 kg/ha (N (urea) - $P_2O_5$ - $K_2O$) (control)

Treatment 2 apply 37.5 – 37.5 – 37.5 kg/ha (conventional urea)

Treatment 3 apply 75 – 37.5 – 37.5 kg/ha (conventional urea)

Treatment 4 apply 37.5 – 37.5 – 37.5 kg/ha (coated urea)

Treatment 5 apply 75 – 37.5 – 37.5 kg/ha (coated urea)

### Crop Establishment and Fertilizer Management

Rice was established using three distinct methods: transplanting, dry-seeded, and wet-seeded. For the transplanted rice, nitrogen (N) fertilizer was applied in two equal splits: the first application at 7–14 days after transplanting (DAT) and the second application at the panicle initiation stage. Phosphorus (P) and potassium (K) fertilizers were applied as a single basal dose at 7–14 DAT. For both dry-seeded and wet-seeded rice, N fertilizer was also applied in two equal splits: the first application at 20–30 days after emergence (DAE) and the second application at the panicle initiation stage. Meanwhile, P and K fertilizers were administered in a single application at 20–30 DAE.

### Rice Cultivars

The rice cultivars used in this study consisted of foundation seed sourced from the Rice Department. Photoperiod-sensitive cultivars evaluated included 'Khao Dawk Mali 105', 'RD6',

and 'Sangyod Phatthalung'. Photoperiod-nonsensitive cultivars included 'RD41' and 'San-pah-tawng 1'.

**Fertilizer**

The chemical fertilizers utilized included urea (46-0-0) and Polymer-R coated urea as nitrogen sources, triple superphosphate (0-46-0) as the P source, and potassium chloride (0-0-60) as the K source. These straight fertilizers were blended to achieve the specific nutrient formulations required for each treatment. The Polymer-R coating agent was procured from Olaf Chemical Co., Ltd.

**Experimental Sites and Duration**

The multi-location field trials were conducted across 11 rice research centers throughout Thailand. The photoperiod-sensitive (in-season) rice cultivars were evaluated at specific locations: 'Khao Dawk Mali 105' in Lop Buri, Roi Et, and Surin; 'RD6' in Udon Thani; and 'Sangyod Phatthalung' in Phatthalung and Nakhon Si Thammarat. The photoperiod-nonsensitive (off-season) cultivars were tested as follows: 'RD41' in Phra Nakhon Si Ayutthaya, Phitsanulok, and Chachoengsao; and 'San-pah-tawng 1' in Chiang Mai and Chiang Rai. The experimental timeline commenced with the off-season crop during the 2024/25 cycle and concluded with the in-season crop in 2025.

**Data Collection and Statistical Analysis**

Data collection was categorized into soil properties, crop growth, and crop yield parameters as follows: Soil samples were collected from the experimental plots both prior to the initiation and after the completion of the experiment. The samples were analyzed for key chemical and physical properties, including pH, electrical conductivity (EC), organic matter (OM), available phosphorus (P), and exchangeable potassium (K). Rice growth parameters were monitored, including plant height, tiller number, leaf color intensity using a leaf color chart (LCC), and leaf area index (LAI). The total number of panicles was determined at the physiological maturity stage. Additionally, the incidence and severity of insect pests and diseases were recorded throughout the growing season. Grain yield was evaluated by manually harvesting a representative area of 2×5 meters within each experimental subplot. All gathered data were subjected to Analysis of Variance (ANOVA) using a Randomized Complete Block Design framework. Mean comparisons among the treatments were performed using Tukey's Honestly Significant Difference (HSD) test at a significance level of $p \leq 0.05$.

## Results and discussions

**Trials with Photoperiod-Sensitive Rice Cultivars**

Field experiments evaluated the comparative performance of conventional urea and Polymer-R coated urea as nitrogen (N) sources in three photoperiod-sensitive cultivars: 'Khao Dawk Mali 105', 'RD6', and 'Sangyod Phatthalung'. These cultivars are characterized as tall, lowland rice varieties with relatively low yield potential. The results indicated that N fertilizer application did not significantly increase grain yields compared to the control (no N fertilizer) in the majority of experimental sites. However, N application yielded significantly higher outputs than the control at specific locations. Crucially, across all trials, a 50% reduction in N rate using Polymer-R coated urea achieved grain yields comparable to the full rate of conventional urea. This lack of significant yield response to N fertilization in most trials (Table

1) is likely attributed to the poor responsiveness of tall, photoperiod-sensitive lowland rice varieties to high N inputs (IAEA, 1984). Furthermore, high initial soil fertility at several experimental sites contributed to this trend. Conversely, low yields and an absent N response at certain sites were associated with high soil acidity (pH 5.1). Nonetheless, prominent N responses were observed at sites where the control yield dropped below 1,875 kg/ha, aligning with the aforementioned explanations. Most importantly, all trials demonstrated that Polymer-R coated urea facilitates a 50% reduction in N fertilizer inputs without compromising grain yield, consistent with the findings of Kruawan et al. (2025), who reported that minimizing urea rates via controlled-release formulations does not penalize rice yield.

**Table 1 Rice grain yield (Ton/ha) from photo sensitive variety experiments**

| Treatment/Location | SRN | UDN | PTL | RET | LBR | NSR |
|---|---|---|---|---|---|---|
| 1. 0 N kg/ha | 2.58 | 2.53 | 3.36 | 1.86 b | 3.66 b | 1.96 |
| 2. 37.5 N (con. urea) | 3.21 | 2.41 | 3.14 | 2.56 a | 4.08 ab | 2.24 |
| 3. 75 N (con. urea) | 3.14 | 2.43 | 3.59 | 2.64 a | 4.84 a | 2.54 |
| 4. 37.5 N (coated urea) | 2.97 | 2.64 | 3.45 | 2.41 a | 4.01 ab | 2.30 |
| 5. 75 N (coated urea) | 3.09 | 2.22 | 2.97 | 2.66 a | 4.59 ab | 2.04 |
| Mean | 2.94 | 2.44 | 3.31 | 2.42 | 4.24 | 2.21 |
| Significant (F-test) | ns | ns | ns | ** | * | ns |
| % CV | 14.4 | 18.3 | 18.7 | 9.63 | 16.1 | 34.0 |

**Table 2 Rice grain yield (Ton/ha) from photo nonsensitive variety experiments**

| Treatment/Location | CRI ds | CRI ws | CCS ds | CCS ws | CMI ds | CMI Ws | AYY | PSL |
|---|---|---|---|---|---|---|---|---|
| 1. 0 N kg/ha | 2.63 b | 2.74 | 1.11 | 3.69 | 3.45 | 4.07 | 4.94 b | 3.33 |
| 2. 37.5 N (con. urea) | 4.00 a | 3.14 | 1.24 | 3.88 | 4.00 | 4.44 | 5.16 ab | 3.58 |
| 3. 75 N (con. urea) | 4.58 a | 3.46 | 1.34 | 4.25 | 4.92 | 4.60 | 3.14 b | 3.43 |
| 4. 37.5 N (coated urea) | 3.91 a | 3.41 | 1.59 | 4.00 | 3.89 | 4.64 | 6.69 a | 3.41 |
| 5. 75 N (coated urea) | 4.16 a | 3.71 | 1.69 | 4.44 | 4.72 | 4.43 | 5.84 ab | 3.01 |
| Mean | 3.86 | 3.29 | 1.39 | 4.05 | 4.19 | 4.43 | 5.16 | 3.35 |
| Significant (F-test) | ** | ns | ns | ns | ns | Ns | * | ns |
| % CV | 10.5 | 16.8 | 42.2 | 26.1 | 17.8 | 5.95 | 18.8 | 16.0 |

**** : Average yield in the same column with the same letter are not significantly difference using Tukey's Honestly Significant Difference (HSD) test at a significance level of $p \leq 0.05$.**

**SRN = Surin Rice research center (RRC), LBR = Lopburi RRC, RET = Roi et RRC, UDN = Udonthani RRC, PTL= Phattalaung RRC, NSR = Nakonsrithammarat RRC, CRI = Chiang Rai RRC, CCS = Chacherngsao RRC, CMI = Chaingmai RRC, AYY = Ayuthaya RRC, PSL = Phitsanulok RRC. ds = dry season, ws = wet season**

### Trials with Photoperiod-nonsensitive Rice Cultivars

Parallel evaluations were conducted using two photoperiod-nonsensitive cultivars, 'RD41' and 'San-pah-tawng 1', which represent semi-dwarf, high-yielding lowland rice varieties. Similar to the photoperiod-sensitive trials, N application did not result in a significant yield increase over the control in most locations, though localized positive responses to N fertilization were observed. In one specific trial, the application of conventional urea at 75 kg

N/ha resulted in the lowest grain yield, falling below even the unfertilized control. Across all environments, the application of Polymer-R coated urea at a 50% reduced N rate consistently maintained grain yields equivalent to the full dose of conventional urea (Table 2). The widespread absence of a marked N response was primarily due to high baseline soil fertility across multiple sites. In contrast, at sites with low soil fertility, the unfertilized control produced significantly lower yields, dropping below 3,125 kg/ha compared to the fertilized treatments. A notable phenomenon occurred in one trial where the highest rate of conventional urea led to the lowest grain yield, likely due to vegetative overgrowth or susceptibility induced by excessive N supply. Interestingly, applying the high rate of Polymer-R coated urea still produced the maximum grain yield. This suggests that the Polymer-R coating effectively regulates N release, preventing excessive uptake and subsequent crop damage. Overall, these findings solidify the conclusion that Polymer-R coated urea can successfully reduce N fertilizer requirements by up to 50% while sustaining optimum crop productivity.

**Recommendations**

The primary finding of this research demonstrates that Polymer-R coated urea can successfully reduce nitrogen (N) fertilizer application by up to 50% without compromising grain yield. This confirms that this innovative coating technology provides a viable pathway to halve chemical N inputs while maintaining optimum crop productivity. Crucially, because Polymer-R is a domestically developed and produced Thai innovation, its manufacturing costs remain insulated from volatile international market dynamics and supply chain disruptions. Consequently, implementing this technology possesses the practical potential to lower N fertilization costs by 30%, a figure that could exceed 40% during periods of high global urea prices. In conclusion, this technology serves as a highly effective intervention for agricultural cost reduction while simultaneously mitigating nitrous oxide emissions. It represents a key sustainable practice for low-carbon rice production, thereby enhancing the global competitiveness of Thai rice and providing concrete support for national and global environmental sustainability goals.

## Acknowledgements

I would like to express my sincere gratitude to the Rice Department for their invaluable support throughout this study. Special thanks are extended to the dedicated researchers and staff across multiple rice research centers nationwide whose exceptional cooperation and technical assistance made the extensive field experiments possible. This research was greatly enriched by their expertise and commitment to data collection. The findings of this study contribute significantly to optimizing nitrogen management, offering practical pathways to reduce urea fertilizer costs in rice production while simultaneously mitigating nitrous oxide emissions from paddy fields.

## References

Chanphen, K., Jaksomsak, P., Insan, J., & Konsaeng, S. (2025). Effects of controlled-release urea on growth and yield of rice varieties Pathum Thani 1 and RD41 rice varieties. *Journal of Agricultural Production, 7*(1), 13–21.

Department of Soil Science, Faculty of Agriculture, Kasetsart University. (1987). *Introduction to soil science* (in Thai). Chuan Pim Press. 673 pages.

Dobermann, A. and T.H. Fairhurst 2000. Rice Nutrient Disorders & Nutrient Management. Oxford Graphic Printers Pte Ltd. 191 pp.

The International Atomic energy Agency 1984. IAEA-TECDOC 307. Semi-dwarf cereal mutants and their use in cross-breeding II. 281 pages.

# From Sequence Reads to Cross Decisions: Genomic Decision-Support System for Rice Breeding

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## Abstract

Genomic selection and progeny simulation are established in rice improvement but running them requires bioinformatics specialists. Genotype data therefore wait on scarce expertise while market targets for grain quality, maturity and disease resistance keep shifting, candidate choice and parent choice still rests on experience that is confirmed only after several generations of field selection. We present a decision-support system that takes a breeder from sequence reads to a cross decision without writing code. Reads are genotyped against a chosen reference genome and panel, and each line receives predicted trait values and genotypes at functional genes. Breeders set targets across several traits; the system then scores every parental pair and simulates the progeny of a chosen cross from F1 up to F10.

We used 700,000 SNP positions on IRGSP-1.0, and trait models trained on 406 Rice Diversity Panel accessions. Under five-fold cross-validation, predictive ability across 22 agronomic and grain-quality traits ranged from r = 0.43 to 0.88 (median r = 0.72). Simulated F2 gametes carried 11.6 crossovers, against 11.4 implied by a reliable genetic map. Ten breeders were asked to use the system for candidate advancement and parent choice. Ratings were highest for relevance to breeding decision and lowest for disruption to current practice. The main barrier was the cost of sequencing breeding lines. Most breeders (7/10) saw the system as a complement to field evaluation that narrows which lines and crosses to advance. The system can bring cross decisions forward in the breeding cycle without requiring bioinformatics expertise.

**Keywords:** *Oryza sativa, Genomic selection, Progeny simulation, No-code bioinformatics*

# Drones, Computer Vision, and Machine Learning for Precision Weed and Crop Management in Rice

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## Abstract

Rice production faces rising input costs, labor shortages, and herbicide-resistant weeds, which creates a need for tools that match management to field variability. Multispectral and hyperspectral sensors, combined with machine learning, can deliver this capability at the scale of commercial rice fields. This presentation summarizes our research at Texas A&M University on spectral sensing for three areas of rice management: growth monitoring, weed–crop discrimination, and crop health assessment. First, we track rice growth through the season using multitemporal vegetation indices, canopy cover, and plant height derived from drone-based multispectral imagery. Second, we exploit differences in canopy reflectance, including the narrow-band and red-edge features that hyperspectral sensors resolve, to separate weeds from rice and from one another. Broadleaf and sedge weeds are generally easier to distinguish than grass weeds, whose spectral and structural similarity to rice remains the main obstacle. Hyperspectral data also help pinpoint the most informative wavelengths, which can inform the design of simpler, lower-cost multispectral sensors for routine field use. Third, we relate spectral signatures to nutrient status and other crop stresses to help guide nitrogen and other input decisions. Because shifts in canopy reflectance can precede visible symptoms, these approaches may allow earlier intervention than visual scouting alone. Taken together, this work suggests that spectral sensing can supply timely, field-scale information for rice management, although models that hold up across environments, growth stages, and sensor platforms are still needed. We will discuss lessons from field deployment, data requirements for robust models, and opportunities to adapt these tools for rice production in Asia.

**Keywords:** *Unmanned aerial systems, Multispectral imaging, Hyperspectral imaging, Weed–crop discrimination, Crop health, Rice crop monitoring*

# AI for Rice Phenotyping: Lessons from the Field

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## Abstract

High-throughput plant phenotyping (HTP) has gained increasing attention with recent advances in artificial intelligence (AI). In rice breeding, phenotyping is a key step for selecting desirable traits, yet it remains labor-intensive and difficult to scale. Many HTP systems rely on large or costly sensor platforms, which limits their use in routine field work. This talk presents an approach that uses a lightweight depth camera mounted on a rail-based platform to capture top-view RGB-D images of rice under field conditions. Fine-tuned deep learning segmentation models, including SegFormer and Mask2Former, identify individual plant parts such as rice panicles. By combining these labels with depth data, we assemble a preliminary top-view 3D model of each plant. From these models, we derive architectural traits, including plant height, canopy structure, and the height and spatial distribution of panicles. The labeled 3D models and derived traits are stored in a cloud database linked to yield data, such as panicles per plant and grain number, with the goal of identifying which plant structures are associated with higher yield. In previous field trials, we compared image-derived traits with manual measurements to assess accuracy. We will also share the challenges we encountered, how we addressed them, and practical considerations for deploying such systems in the field.

**Keywords:** *High-throughput phenotyping, Rice breeding, Computer vision*

# Advancing Rice Safety through Automated Analytical Technologies for Pesticide Residue Screening

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## Abstract

Ensuring rice safety is essential for protecting public health, and rapid, reliable, and accessible analytical technologies are needed to monitor pesticide residues. This study explores automated approaches for residue screening, using methyl parathion, a highly toxic organophosphate insecticide, as a representative analyte. An automated sequential injection analysis (SIA) system with spectrophotometric detection was developed for preliminary screening. Methyl parathion undergoes alkaline hydrolysis with sodium hydroxide (NaOH), producing p-nitrophenolate ions monitored at 400 nm. Reaction kinetics were examined at 0.2, 0.6, and 1.0 M NaOH over 40 min. Because absorbance increased without reaching a plateau, a 5 min reaction time was chosen to balance response and analysis time. The SIA system showed good linearity over 0-8 mg/L ($R^2$=0.9985) and 105% recovery for a 5 mg/L standard. Gas chromatography-flame ionization detection (GC-FID) showed linearity over 20-80 mg/L ($R^2$=0.9939), with no detectable peak below 10 mg/L. Jasmine rice extracts prepared in ethanol/water (70:30, v/v) and spiked at 5 mg/L gave an apparent recovery of approximately 120%, indicating matrix effects. These findings highlight the potential of automated SIA-based spectrophotometry as a preliminary screening tool for pesticide residues in rice. Improved matrix-matched calibration, sample preparation, and interference correction are needed to enhance quantitative reliability for future rice safety monitoring.

**Keywords:** *Rice safety, Automated analytical technologies, Sequential injection analysis, Pesticide residues, Spectrophotometry*



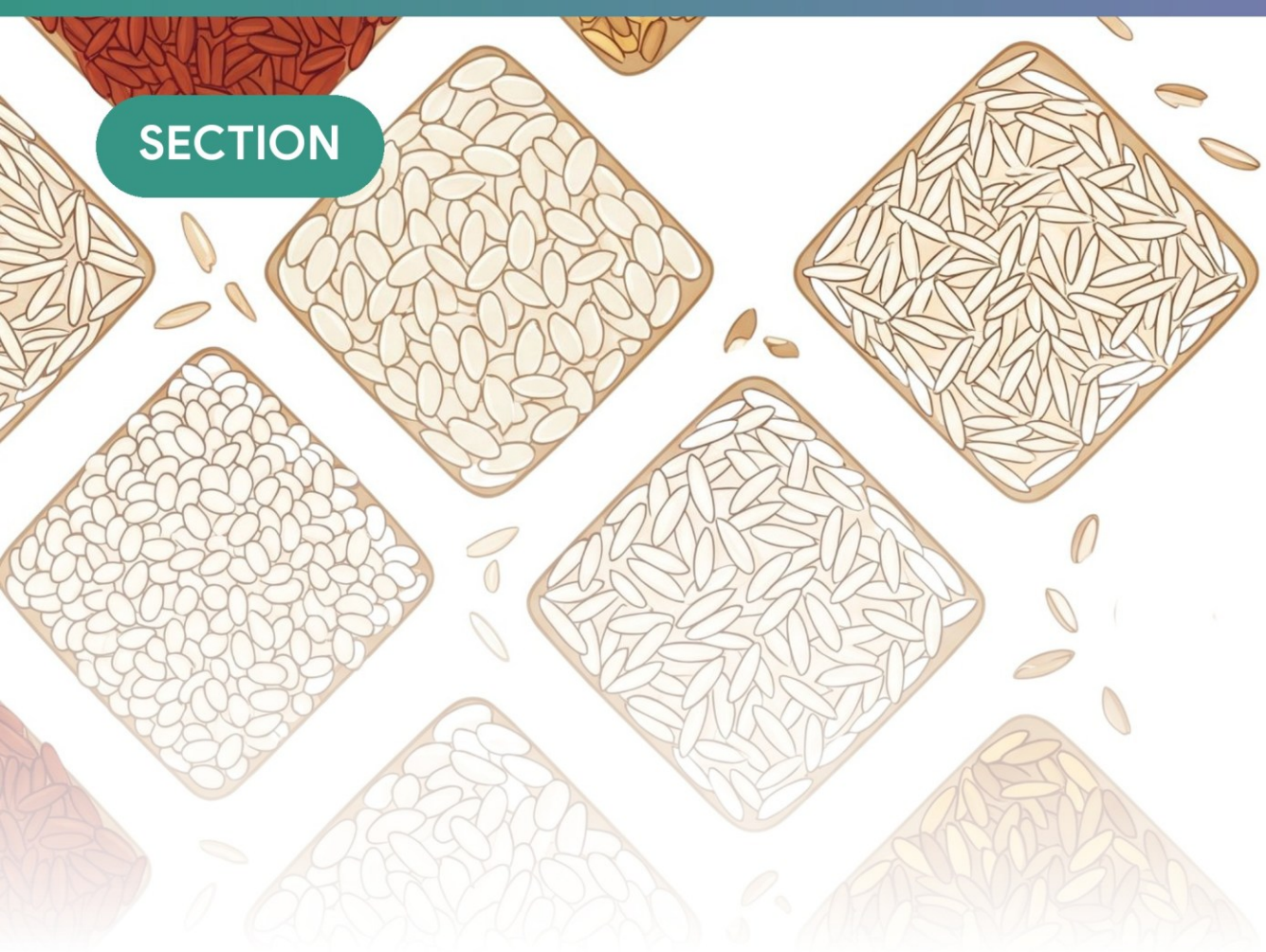
PART

# POSTER

## Poster Presentations

Abstracts of poster presentations, arranged by topic (codes PS1-PS6)

Abstracts 95



SECTION

# PS1

## Rice Genomics / Rice-omics

Genomics, genetics, breeding and multi-omics of rice

Poster 14

# Characterization of Genes and Transcripts Associated with Drought Tolerance in Rice Using RNA-Seq

**Cheila Martins Chicoela [1*], Sebastiao Inacio Famba [2], Amelia Henry [3], Alexis Ndayiragije [4], and Celsa Mondlane Macandza [2]**

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## Abstract

Drought is one of the major environmental constraints limiting rice (*Oryza sativ*a L.) productivity. Understanding the molecular mechanisms underlying drought tolerance is therefore essential for identifying candidate genes and developing rice genotypes better adapted to water-limited environments. This study aims to characterize gene expression patterns and transcripts associated with drought tolerance in contrasting rice genotypes using RNA sequencing (RNA-Seq). Ten rice genotypes previously characterized based on their response to water deficit will be selected, comprising five drought-tolerant and five drought-susceptible genotypes. The experiment will be conducted under controlled greenhouse conditions using a completely randomized design in a factorial arrangement involving genotype and water regime, with three independent biological replicates. The experiment will comprise a total of 60 biological samples, corresponding to 10 genotypes × 2 water conditions × 3 biological replicates. Leaf tissues will be collected from plants subjected to control and water-deficit conditions and subsequently used for RNA extraction and transcriptome sequencing. Sequencing data will undergo quality control, read alignment, transcript quantification, and differential gene expression analysis. Differentially expressed genes (DEGs) will be identified by comparing control and water-deficit conditions within and between contrasting genotypes, followed by Gene Ontology and Kyoto Encyclopedia of Genes and Genomes enrichment analyses. Particular attention will be given to genes and transcripts associated. The study is expected to identify candidate genes and molecular pathways associated with drought tolerance, providing valuable information for understanding the genetic basis of drought adaptation and supporting the development of drought-tolerant rice varieties through molecular breeding.

**Keywords:** *Genes, Rice, Drought*

# Generation of Amphidiploids Between Cultivated Rice and Distantly Related-wild *Oryza* Using *in vitro* Fertilization System

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## Abstract

The genus *Oryza* includes cultivated species with the AA genome and wild species with genome types other than the AA genome (BB to HHJJ genomes). As wild species possess a crucial resource for tolerance and resistance traits, generation of allopolyploid rice across cultivated rice and distantly related-wild rice can be an innovative approach to enlarge genetic diversity toward new rice breeding. However, fertile allopolyploid rice with an AA genome has not evolved in nature, nor has it ever been produced experimentally, because pre- and post-zygotic reproductive barriers exist between cultivated and wild species. Even when hybrids are obtained, they are generally sterile due to meiotic failure resulting from heterologous chromosomes. Therefore, to produce fertile hybrids between cultivated and distantly related wild rice species, it is necessary to overcome the reproductive barriers and between cultivated and wild species and to achieve genome doubling of the hybrids.

In the study, we overcame these reproductive limitations using *in vitro* fertilization system. Allopolyploid hybrid zygotes between cultivated *Oryza sativa* cv. Nipponbare (AA) and distantly related-wild species, *O. officinalis* (CC) and *O. alta* (CCDD), were produced and cultured. These hybrid zygotes developed into plants, and the resulting AACC and AACCDD allopolyploid rice plants were fertile. Notably, their hybrid genomes were stably transmitted across generations. The AACC and AACCDD allopolyploid rice generated in the study will provide a new horizon for allopolyploid rice breeding. (228 words)

**Keywords:** *Cultivated rice, Distantly related-wild rice, Hybridization, Allopolyploidization*

# Multi-omics Approaches to Understanding SUMOylation in Rice (*Oryza sativa* L.)

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## Abstract

SUMOylation is a post-translational protein modification essential for growth and stress responses in eukaryotes. However, understanding of the SUMOylation system remains limited in plants compared to humans and animals. The SUMOylation machinery has been most thoroughly studied in the model plant Arabidopsis thaliana, which contains 32 SUMOylation genes, including eight SUMOs, three E1 activating enzymes, one E2 conjugating enzyme, two ligating enzymes, two polymerising enzymes, eight DeSUMOylating Isopeptidase (DESI), and eight Ubiquitin-Like Protease (ULP). To gain a broader understanding of this system, we identified the SUMOylation machinery across the plant kingdom, with a specific focus on rice — a vital crop in Asian countries that feeds over one-third of the world's population. In addition, we investigated ULP machinery through comprehensive phylogenetic, transcriptomic, and protein structural analyses, focusing on the reference rice genome and a highly annotated 16 rice population reference panel (RPRP), alongside eight wild rice genomes. We found ten major proteins conserved across the plant kingdom. Notably, SUMO proteases are particularly expanded in the domesticated rice genome, with the reference genome and the RPRP panel comprising 32–45 ULPs, compared to 9–36 ULPs in wild rice species. These observations suggest that selective breeding practices may have driven the diversification of this gene family. Furthermore, we present evidence supporting the functionality of ULPs and their potential involvement in conferring tolerance to both biotic and abiotic stresses in domesticated rice, providing critical knowledge for future crop enhancement strategies.

**Keywords:** *SUMOylation, Rice genomics, ULP*

# Optimization of a Diverse Rice Core Collection Using SNP Markers to Enhance Phenotypic Accuracy and Association Studies

**Phasin Sripornthaweesup [1], Wasin Poncheewin [1], Burin Thunnom [1], Meechai Siangliw [1], Jonaliza L. Siangliw [1], Chanakarn Wongsaprom [1], Srisawat Khanthong [1], Watchareewan Jamboonsri [1], Wintai Kamolsukyunyong [1], Samart Wanchana [1], and Vinitchan Ruanjaichon [1]**

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## Abstract

Rice (*Oryza sativa* L.) germplasm collections are a fundamental reservoir of genetic variation for crop improvement. Larger collections capture broader allelic diversity, including rare alleles, and enhance statistical power and mapping resolution in genome-wide association studies (GWAS). However, they also increase genetic redundancy and conservation and evaluation costs. This limits feasible replications and environments, amplifies experimental error, reduces phenotypic accuracy and heritability, and distorts population structure, which raises the risk of spurious associations. Phenotyping has thus become a major bottleneck in population-based genetic studies. A core collection, a reduced yet representative subset capturing the genetic diversity of the whole collection, offers a practical solution that retains adequate power for association mapping. This study aimed to develop a core collection representing approximately [35]% of 625 genetically diverse rice accessions while maximizing retained genetic diversity. Stringent quality filtering of genome-wide single nucleotide polymorphism (SNP) data yielded [103,789] high-quality SNPs, from which pairwise Modified Rogers' distances were estimated. Core subset selection was optimized using Core Hunter 3 to maximize representativeness and minimize redundancy. The resulting core collection comprised 219 accessions (35%). Its mean entry-to-nearest-entry distance (E-NE) was 0.396, 36% higher than random subsets of equal size (0.292 ± 0.006). Its accession-to-nearest-entry distance (A-NE) was lower (0.202 vs. 0.221 ± 0.002). Together, these values indicate reduced redundancy and good representation of the entire collection. This core collection provides an efficient, non-redundant resource that substantially reduces phenotyping costs and serves as a valuable panel for GWAS and targeted rice breeding.

**Keywords:** *Core collection, Genomics, Population, Diversity*

# Analysis of Bacterial Microbiome Diversity and Functional Composition in the Rhizosphere Soil and Root Endosphere of Wild Rice (*Oryza rufipogon*)

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## Abstract

This study investigated the bacterial microbiome diversity, community structure, and functional roles within the root endosphere and rhizosphere soil of wild rice (*Oryza rufipogon*) collected across five locations using high-throughput 16S rRNA gene amplicon sequencing (V3–V4 region) on the Illumina NovaSeq 6000 platform. Bioinformatic analysis of 625,892 bacterial 16S rRNA sequences identified 18,721 OTUs spanning 3,142 species, 1,296 genera, 626 families, 111 classes, and 42 phyla. Alpha and beta diversity analyses (Shannon's index, PCoA, and NMDS with Bray–Curtis distance) demonstrated clear niche differentiation between rhizosphere soil and root endosphere microbiomes (PC1 accounting for 21.15% of variance), with endospheric communities displaying greater compositional consistency across sampling sites. At the class level, the root endosphere was predominantly colonized by Gammaproteobacteria and Alphaproteobacteria, whereas rhizosphere soil harbored higher abundances of Acidobacteriae, Anaerolineae, and Alphaproteobacteria. Key endospheric biomarkers, including Kineosporaceae, Comamonadaceae (*Paucibacter*), Enterobacteriaceae (*Enterobacter*), *Bradyrhizobium*, and *Rhodomicrobium* (*R. vannielii*), coordinately facilitated phytohormone synthesis (auxin/IAA), atmospheric nitrogen fixation, phosphate solubilization, and organic carbon degradation under hypoxic flooded conditions. In contrast, rhizosphere soil was dominated by *Candidatus* Solibacter, *Acidothermus*, and *Pseudolabrys* (*P. taiwanensis*), which offer natural biocontrol potential against soil-borne pathogens. Altogether, wild rice root and soil microbiomes exhibit a specialized functional division of labor, providing essential biomarkers for developing biofertilizers and biocontrol agents to support cultivated rice rewilding.

**Keywords:** *Wild rice (Oryza rufipogon), 16S rRNA amplicon sequencing, Rhizosphere microbiome, Root endosphere, Bacterial diversity, Plant growth-promoting bacteria (PGPB)*

# Characterisation of Transcriptional Regulation in Climate-change-associated Abiotic Stresses using Condition-specific Gene Networks

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## Abstract

Climate change exerts multidimensional pressures that threaten crop productivity and resilience. Engineering climate-resilient rice requires understanding interactions between genetic×environment×management that shape phenotypic plasticity. These phenotypes arise from multilayered regulatory processes, from gene regulation to transcription and metabolism, that can be profiled through multi-omics assays. Here, we inferred context-specific gene co-expression networks (GCNs) using curated publicly available gene expression data related to drought and salinity stress conditions. We also inferred gene regulatory networks (GRNs) by integrating gene expression data with regulatory priors derived from transcription factor (TF) binding motifs, chromatin accessibility, and TF binding evidence. The resulting GRNs comprise the TF-target genes relationship, with the connectivity representing context-specific regulatory strengths. By linking regulation (cause) to expression (consequence), our context-specific GRNs can serve as a hypothesis-generating framework for prioritizing transcriptional regulators as candidate targets for improving climate-resilient rice.

**Keywords:** *Salt, Drought, Prior knowledge, Gene co-expression network, Gene regulatory network, Systems biology*

# Evaluation of the Agronomic and Genotypic Diversity of Thailand Local Rice (*Oryza sativa* L.) Varieties Under Lowland Conditions

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## Abstract

Local Thai varieties of rice contain high levels of genetic diversity. Thus, understanding the genetic structure and relationships among local varieties will be useful for parent selection in rice breeding programs. This study aimed to evaluate the agronomic and genetic variation in a collection of 82 local Thai germplasms from 4 regions of Thailand. The agronomic traits and the Shannon-Weaver index (H′) were used to determine phenotypic diversity. In addition, a set of 82 diverse local varieties were genotyped using 75 SNP markers to assess the structural analysis and phylogenetic tree. The results showed that phenotypic variation among 82 varieties was found in all traits. Most local Thai varieties were photosensitive varieties, the plant height was tall to very tall (> 140 cm), the panicle number was low (10–20 panicles), the panicle length was long (> 25 cm), and the grain shape was slender. A moderate H′ index was found for panicle number, panicle length, and grain weight. The structural analysis was classified into 5 subpopulations. It was clear to separate glutinous rice (group II) and non-glutinous rice (group I, III, IV, and V). In addition, it is sufficient to be able to differentiate by region in some groups, but it cannot be classified according to the ecology (upland and lowland) and grain shape. Moreover, the results of the phylogenetic tree were associated with the analysis of the structure. Therefore, local Thai rice varieties may be beneficial in terms of rice germplasm that can be used in breeding programs.

**Keywords:** *SNP markers, Genetic diversity, Phenotypic diversity, Rice (Oryza sativa L.)*

# Contrasting Gas Exchange Strategies and Their Associations with Drought Injury, Recovery, and Reproductive Performance in Rice under Repeated Drought

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## Abstract

Repeated drought poses a challenge for rice improvement: sustained gas exchange may not ensure a high proportion of filled grains. This study investigated physiological responses, drought injury, recovery, and filled grain weight percentage in eight rice genotypes: IR57514, KDML105, AM13, HS2, S16, EL12, CSSL26, and V6. Plants were evaluated under well-watered and drought conditions in a randomized complete block design with three replications. Two successive drought cycles were imposed by withholding irrigation at 61–66 days after sowing (DAS; DR-I) and 75–82 DAS (DR-II). Gas exchange and leaf rolling were summarized as area under the curve, while leaf drying, recovery, and final filled grain weight percentage per plant were assessed. Pearson correlation and principal component analysis revealed contrasting response patterns across cycles. During DR1, leaf rolling was negatively correlated with photosynthesis and transpiration (both r = -0.88) and stomatal conductance (r = -0.84), whereas transpiration and stomatal conductance showed weak negative associations with final filled grain weight percentage. During DR-II, leaf drying was strongly associated with transpiration (r = 0.96) and stomatal conductance (r = 0.98). V6 aligned with high gas exchange, severe leaf drying, and poor recovery, whereas EL12 combined lower gas exchange with limited injury and a favorable filled grain weight percentage. These findings suggest that balancing carbon acquisition with water conservation is important under repeated drought. EL12 warrants further evaluation, while integrating physiological responses, injury, recovery, and filled grain weight percentage could strengthen drought-resilience screening.

**Keywords:** *Oryza sativa, Repeated drought, Gas exchange, Water conservation, Filled grain weight percentage, Drought resilience*.

# Haplotype-Based Analysis of Photoperiod Sensitivity in Thai Rice

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## Abstract

Flowering time in rice is regulated by complex genetic networks integrating photoperiod signals and developmental pathways. This study investigated photoperiod sensitivity and flowering-time variation in Thailand by combining Hd1 genotyping, flowering phenotypes, and regulatory gene haplotypes. Two *Hd1* marker positions (*GT_9338005* and *GT_9338220_9338221*) were used to classify 201 Thai rice accessions into photoperiod-sensitive (P; n = 139) and non-photoperiod-sensitive (NP; n = 62) groups. The P group exhibited a median difference in days to flowering between long- and short-day conditions (ΔDTF) of 98 days, compared with 18 days in the NP group. Photoperiod-sensitive accessions showed substantial flowering-time variation, with ΔDTF ranging approximately from 39 to 140 days and actual days to flowering ranging from 71 to 136 days. Flowering-time responses were further examined in relation to day length, revealing variation across short, intermediate, and long flowering-time categories. Haplotype analysis was performed using four core flowering-time genes (*Hd1, Ehd1, Hd3a,* and *RFT1*), followed by the individual addition of other regulatory genes. Extended haplotype combinations revealed differences in flowering-time distributions among genetic groups, suggesting potential contributions from upstream and downstream flowering regulators. These findings demonstrate that photoperiod-sensitive rice exhibits considerable flowering-time diversity that may be associated with regulatory genetic variation beyond the four core genes. Integrating flowering phenotypes with regulatory gene haplotypes provides a framework for identifying candidate genetic combinations associated with flowering adaptation and future molecular breeding applications.

**Keywords:** *Rice (Oryza sativa), Days to flowering, Photoperiod sensitivity, Hd1, Regulatory network, Whole-genome resequencing*

# Genome-Wide Association Study (GWAS) for Mesocotyl Length in Rice (*Oryza sativa* L.) under Dark-Chamber Conditions

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## Abstract

Direct seeding is an efficient crop establishment method that helps conserve water and reduce labor requirements. Mesocotyl length is a critical trait influencing the success of direct-seeded rice cultivation. This study aimed to identify genomic regions associated with mesocotyl length in 240 rice varieties and breeding lines evaluated under dark-chamber conditions in 2024. A total of 160,498 single-nucleotide polymorphism (SNP) markers were used to conduct a genome-wide association study (GWAS) using the Bayesian-information and linkage-disequilibrium iteratively nested keyway (BLINK) model. Mesocotyl length ranged from 0 to 40 mm among the evaluated materials. The GWAS identified two quantitative trait loci (QTLs), qML-DS4 and qML-DS11, located on chromosomes 4 and 11, respectively. These QTLs explained 48.69% and 24.18% of the phenotypic variation in mesocotyl length. Haplotype analysis further identified two candidate genes on chromosome 11, *Os11g0638000* and *Os11g0639000*, which were associated with mesocotyl length, seedling elongation under deep-sowing conditions, and plant hormone responses. These findings provide valuable insights into the genetic and physiological mechanisms underlying seedling vigor during germination. The identification of major QTLs and candidate genes associated with mesocotyl elongation under stress conditions can strengthen rice-breeding strategies.

**Keywords:** *Dry direct seeding rice, Mesocotyl length, Genome-Wide Association Study (GWAS), SNP marker*

# Genomic Regions and Candidate Genes Associated with Hull and Pericarp Pigmentation in Rice

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## Abstract

Variation in rice hull and pericarp pigmentation provides an opportunity to investigate the genetic factors underlying grain color diversity. This study examined pigmentation-associated genomic regions in a panel of 306 rice accessions, including both glutinous and non-glutinous types. Hull and pericarp phenotypes were characterized using binary pigmentation scores and ordinal color scales. Genome-wide association analysis was conducted with the FarmCPU model using 1,021,144 high-quality single nucleotide polymorphisms. Genome-wide linkage disequilibrium declined over approximately 200 kb, providing a framework for examining candidate genes near associated markers. The analysis highlighted chromosome 3 regions associated with hull coloration and chromosome 7 regions associated with pericarp coloration. Candidate genes for hull pigmentation included Os03g0421800, encoding an X8 domain-containing protein, and Os03g0425800, encoding a SANT domain-containing protein. Pericarp-associated regions included Os07g0211500 (Rc), which encodes a basic helix-loop-helix transcription factor. Associations near Os03g0421800 were detected for both hull and pericarp color, suggesting a shared genetic contribution to pigmentation in these tissues. Together, these results identify genomic regions and candidate genes for further investigation of rice grain pigmentation. Functional validation and independent evaluation of the associated markers will help establish their potential use in breeding rice varieties with desired hull and pericarp colors.

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

# Reference Genome Choice and Heterozygosity Filtering Shape Genome-wide Association Outcomes in Indica Rice

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## Abstract

Genome-wide association studies (GWAS) in rice predominantly use the Nipponbare Japonica reference genome, despite the predominance of Indica among cultivated varieties and research populations. To assess how reference choice affects association discovery, we compared GWAS results for starch-related traits in 228 Thai Indica accessions mapped to Nipponbare and IR64 reference genomes. Before heterozygosity filtering, Nipponbare mapping identified twice as many QTLs as IR64 mapping (72 vs 36). Reads supporting significant loci were less frequently uniquely mapped than those at control SNPs (50.2% vs 68.5% under Nipponbare and 68.3% vs 82.7% under IR64), suggesting that mis-mapping in duplicated regions absent or structurally divergent in the reference contributed to pseudo-heterozygous calls. Consistent with this, heterozygosity filtering removed 41.8% of Nipponbare SNPs and 30.8% of IR64 SNPs, eliminating most initially detected QTLs (63 of 72 and 27 of 36, respectively). Lead SNPs at these lost loci had median heterozygosity rates of 0.74 and 0.36, respectively. Nine QTLs remained under each reference after filtering, with both analyses identifying the *Waxy* (*Wx*) locus as the primary determinant of apparent amylose content (AAC). Thus, reference choice substantially influenced associations detected before filtering but had a more modest effect on the final results. Heterozygosity filtering was important under both references, while the population-matched IR64 reference reduced, but did not eliminate, mapping artefacts. These findings highlight the importance of heterozygosity filtering and reference genome comparisons for reliable GWAS in Indica rice.

**Keywords:** *Indica rice, Genome-wide association studies (GWAS), Reference genome*

# Uncoupling Panicle Enclosure from Thermosensitive Genic Male Sterility: Evidence of Linkage Between *tms5* and Panicle Exsertion in $F_3$ Rice Populations

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## Abstract

Complete pollen sterility and full panicle exsertion are vital agronomic traits for developing female parents in two-line hybrid rice breeding. Incomplete panicle emergence entraps spikelets inside the flag leaf sheath, substantially impairing outcrossing rates and hybrid seed yield. This study investigated the phenotypic variation and co-segregation of spikelet fertility and panicle exsertion relative to the *tms5* locus on chromosome 2 in 152 selected $F_3$ lines derived from a cross between the improved thermosensitive genic male sterile (TGMS) line FS1 and the soft-textured line RD47-improve. Reproductive traits were scored using the IRRI Standard Evaluation System (SES): spikelet fertility (SpFert) from score 1 (> 90% fertility, highly fertile) to 9 (0% fertility, completely sterile), and panicle exsertion (Exs) from score 1 (well exserted, panicle base > 5 cm above flag leaf collar) to 9 (enclosed). Genotypic analysis using a tightly linked functional DNA marker resolved 24 homozygous *tms5* lines, 73 heterozygotes, and 52 homozygous wild-type lines. Statistical analysis revealed a highly significant association between the *tms5*-linked genotype and poor panicle exsertion ($F$ =16.04, $P = 5.03 \times 10^{-7}$; $\chi^2 = 53.60$, $P = 8.88 \times 10^{-10}$). Among the 24 homozygous *tms5* lines, 62.5% (15 lines) exhibited partly exserted panicles (Exs score of 7), and 11 lines combined complete sterility (SpFert score of 9) with poor exsertion. These results corroborate known panicle exsertion QTLs (*qPE-2*/*qUI-2*) linked to *tms5* on chromosome 2, demonstrating strong linkage drag that must be uncoupled via recombinant selection or *eui1* introgression to eliminate exogenous gibberellin dependency.

**Keywords:** *TGMS, tms5, Panicle exsertion, qPE-2, Linkage drag, Marker-assisted selection (MAS), Two-line hybrid rice.*

# Identification of Genetic Loci Associated with Seed Storage Protein (SSP) in Rice (*Oryza sativa* L.) by Genome-Wide Association Study (GWAS)

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## Abstract

Rice (*Oryza sativa* L.) is a vital source of energy and nutrition, particularly carbohydrates and protein, for human consumption. The impacts of climate change on rice production are multifaceted, influencing various aspects of growth and grain quality. Seed storage protein (SSP) is a key determinant of rice's nutritional, cooking, and eating qualities, and is susceptible to changes in climate. However, understanding the genetic basis of SSP traits in rice remains a significant challenge. In this study, we aimed to identify genes associated with SSP by analyzing seed storage proteins from 210 indica rice varieties from Thai rice germplasm. Seed storage proteins were quantified using Bradford's method, and a Genome-Wide Association Study (GWAS) employing multi-models was conducted to examine genotype-phenotype associations. We identified nine quantitative trait loci (QTLs) associated with SSP across chromosomes 2, 6, 7, 8, 9, 11, and 12. Notably, a QTL on chromosome 7 (*qSSP7*) was consistently detected across all models. Through linkage disequilibrium (LD) analysis, we identified 27 genes within a 400-kb window, eight of which contained functional single nucleotide polymorphisms (SNPs) with moderate effects. Gene expression analysis using the RiceXpro database revealed that five candidate genes were highly expressed specifically in the rice endosperm. Co-expression network analysis using the RiceFREND database identified four candidate genes *Os07g0213600*, *Os07g0213800*, *Os07g0214100*, and *Os07g0214300* that interacted with key regulatory genes such as *GLUD1*, *13 kDa prolamin*, *OsGluC-1*, and *prolamin precursor* genes. These candidate genes show strong potential for involvement in SSP regulation. The findings of this study provide novel insights into the genetic regulatory network controlling protein synthesis and accumulation in rice endosperm. These insights may prove valuable for rice breeding programs aimed at enhancing seed storage protein content.

**Keywords:** *Seed storage Protein (SSPs), Genome-Wide Association Study (GWAS), Endosperm-Specific Gene (OsEns), Rice*



SECTION

# PS2

## Climate Change

Climate-smart rice, low-emission production and resilient systems

Poster 26

# Screening Rice Genotypes for Early-Seedling Drought Resilience under Dry Direct-Seeded Conditions

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## Abstract

Dry direct-seeded rice (DDSR) is highly vulnerable to early water deficit because shallow seedling roots and rapidly declining surface-soil moisture under non-puddled conditions can impair establishment, a risk further intensified by increasing rainfall variability and recurrent intermittent dry periods. However, limited information is available on genotypic variation in early-seedling drought resilience under DDSR conditions. To understand early-seedling drought resilience, ten rice genotypes were evaluated in net-house trials. Drought was initiated on 15 DAS, by allowing soil water to decline to 40% pot water holding capacity by 21 DAS, and stress was maintained until 25 DAS; controls were maintained near 100% pot water holding capacity. Shoot and root growth, root biomass, root relative water content (RRWC), and seedling survival % were assessed at 25 DAS along with drought injury (using the IRRI drought sensitivity scale) based on vegetative-stage leaf rolling and leaf drying. Across genotypes, drought reduced shoot and root length, root fresh and dry weight, and RRWC by 24, 25, 47, 39, and 30%, respectively. Upon exposure to drought RYT12 and Binadhan 18 showed the strongest overall resilience, followed by GAU dhan3 and HRDC 70, maintaining 100% survival with only 4-6% reduction in shoot length and 13-14% reduction in root length with no visible leaf rolling or drying. In contrast, Binadhan 10 and BRRI dhan74 showed 43% survival with severe growth reduction and drought injury. These responses identify promising genotypes for climate-resilient DDSR under intermittent early-season water stress, warranting further field validation.

**Keywords:** *Screening, Dry Direct Seeded Rice, IRRI-SES, Drought Resilience*

# Effects of Top-Dressing Management on Yield and Quality in Ratoon Rice Cultivation in Japan

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## Abstract

Ratoon rice is a sustainable rice cropping system. Our objectives were to clarify (1) the effect of the timing of top-dressing on yield and (2) the quality and eating-quality-related characteristics of rice from the main crop (MC) and ratoon crop (RC). In 2024 and 2025, field experiments on ratoon cultivation were conducted using the japonica varieties 'Koshihikari' and 'Niji no Kirameki' with a stubble height of 25 cm. Fertilization followed conventional practices. For the ratoon crop, two top-dressing treatments were established: nitrogen application at 5 g/m² 25 days after the onset of grain filling (H25) and immediately after harvest (HV0). No significant differences in yield were observed among the top-dressing treatments in the ratoon crop. Quality evaluation focused on MC and RC. The protein and amylose contents of brown rice, as well as the amylose content of milled rice, tended to be higher in RC than in MC. RVA pasting properties consistently differed between MC and RC across both years. In many treatments, MC showed significantly higher peak viscosity and breakdown and significantly lower setback than RC. Our results suggest that top-dressing timing did not affect RC yield. Regarding quality and eating-quality-related characteristics, MC tended to show better eating quality than RC, with differences among cultivars. Previous studies have reported that setback variation is greater between varieties than between years suggesting that varietal characteristics play an important role. Therefore, selecting appropriate varieties and optimizing cultivation may improve RC quality and taste, suggesting its potential as a staple food in Japan.

**Keywords:** *Ratoon rice, Top-dressing, Eating quality, Pasting properties, Yield*

# From Rice Innovation to Farmer Adoption: Strengthening Agricultural Extension Pathways for Climate-Resilient and Sustainable Rice Production in Bangladesh

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## Abstract

Rice is fundamental to Bangladesh's food security, rural livelihoods, and agricultural economy. However, climate change is intensifying production risks through floods, drought, salinity, heat stress, pests, and erratic rainfall. Although climate-resilient rice technologies offer promising solutions, their effectiveness ultimately depends on widespread and sustained farmer adoption. This study examines the role of extension in translating rice innovations into farmer-level adoption in Bangladesh. It focuses on climate-resilient varieties, improved crop management, integrated pest management, water-saving practices, and digital agricultural information. The analysis considers farmers' access to extension services, training, demonstrations, farmer organizations, mass media, and digital platforms, as well as how socioeconomic, institutional, and location-specific factors influence adoption. The study is based on a review of published literature, research findings, and secondary evidence on climate-resilient rice technology adoption and agricultural extension in Bangladesh. Access to information, training, farmer organizations, and extension services can strongly influence the adoption of climate-resilient rice technologies. Smallholder farmers often face limited access to quality extension advice, financial constraints, fragmented landholdings, and location-specific climate risks. These barriers can slow the scaling of promising innovations. A strengthened extension pathway is therefore essential. Demand-driven advisory services, farmer field demonstrations, participatory technology development, digital extension, and stronger linkages among researchers, extension professionals, and farmers can accelerate adoption. The paper proposes an integrated extension framework connecting rice innovation with farmer knowledge, technology adoption, climate resilience, and sustainable production. Strengthening this pathway advances One Health Rice by promoting healthier production systems, resilient farming communities, and sustainable food security across Bangladesh.

**Keywords:** *Agricultural Extension, Climate-Resilient Rice, Farmer Adoption, Rice Innovation, Sustainable Rice Production*

# Spatial and Production-System Variability in Rice Responses to Climate Anomalies in Central Visayas, Philippines

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## Abstract

Rice productivity is considerably influenced by climatic extremes and variations. This study examined the relationships between rice yield and climate anomalies in Bohol, Cebu, and Negros Oriental, all provinces in the Visayas, Philippines, over 30 years (1991-2020). The relationship between the annual rice yield data for rainfed and irrigated systems and rainfall, maximum temperature (Tmax), and minimum temperature (Tmin) anomalies was analyzed using ordinary least squares (OLS) regression, followed by multiple regression models. To improve inference for the annual time-series models, heteroskedasticity and autocorrelation-consistent standard errors were used. Trends of the climate anomalies were assessed using OLS linear trends, the Mann–Kendall test, and Sen's slope estimator. Results showed significant spatial and production-system differences in climate–yield relationships. Temperature anomalies show stronger associations with rice yield than rainfall anomalies. In Bohol, Tmax was negatively associated with yield, whereas Tmin was positively associated with yield in both production systems. In Cebu, both Tmax and Tmin generally exhibited positive yield associations, while rainfall showed a positive partial relationship in the multivariable models. In Negros Oriental, rainfall and Tmax showed positive associations with rainfed rice yield, whereas the relationships with climate were weaker for irrigated rice. Rainfall anomalies showed no significant long-term trend in any province. Significant temperature trends were observed, with increasing Tmin in Bohol and Cebu and increasing Tmax in Cebu and Negros Oriental. The findings show heterogeneous climate–yield relationships across the selected provinces. Also, the results highlight the importance of distinguishing production systems and locations when assessing rice vulnerability to climate variability.

**Keywords:** *Rice, Climate Anomalies, Irrigated, Rainfed*

# Measuring Circularity in Rice Production: A Synthesis and Comparison of Existing Metrics

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## Abstract

Paddy (*Oryza sativa*) production in Asia accounts for a substantial share of global rice and greenhouse gas emissions output. This resulted in increased pressure aligning rice production with sustainability standards. As a resource-intensive commodity, rice requires circular economy strategies that improve resource efficiency and support sustainable production. Many studies have applied Life Cycle Sustainability Assessment (LCSA) to evaluate sustainability dimensions by integrating circularity metrics. However, the integration of circularity into LCSA remains fragmented, resource-intensive, and insufficiently standardized for agricultural systems, particularly rice production. A key methodological gap is the lack of full-phase accounting of material-specific displacement pathways, including how excess materials are redirected and how these pathways influence overall circularity within LCSA. Rigorous analyses of existing metrics were conducted through Scopus, Web of Science, and ScienceDirect databases following the STARR-LCA protocol. A total of 503 studies across 61 countries were identified. The analysis was carried out using the open-source LLM (Mistral-Nemo-Instruct-2407) to conduct a systematic and structured PICOS extraction. The selected studies were analyzed for assumptions regarding the substitution effects of secondary materials and the representation of material recirculation pathways concerning level material flows and full life-cycle impacts in agricultural recirculation. In the keyword analyses, four-thematic-clusters were identified as "Sustainability and Circular Economy," "Biological Cycles," "Weighting Systems," and "Circular Practices". The findings indicate that rice-residue valorization is a core pathway for integrating material recirculation into LCSA, although its sustainability benefits remain context-dependent. The outcome of this study supports selecting circularity indicators for complex biological systems and circular agri-food transitions.

**Keywords:** *Life Cycle Sustainability Assessment (LCSA), Circularity, Rice, Paddy*

# Turning Rice By-Products into Climate Solutions: Life Cycle Assessment of Carbon-Negative Zeolite Production

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## Abstract

Rice husk is a silica-rich agricultural residue that can be converted into zeolites for environmental and industrial applications. However, the energy and chemical inputs required for synthesis may limit its environmental benefits. Here, greenhouse gas (GHG) emissions from the production of nine rice-husk-derived zeolite types were assessed and identified opportunities for emission reduction using life cycle assessment. The functional unit was 10 g of zeolite. Quantified stages included rice husk collection and preparation, ash production, gel preparation, crystallization, washing, chemical loading, drying, calcination, and associated energy use and chemical consumption. Use, transportation and end-of-life stages were excluded from the quantitative assessment because applications and disposal scenarios differed among zeolite types; therefore, the results do not represent complete cradle-to-grave emissions. GHG emissions ranged from 0.33 to 1.64 kg $CO_2$-eq per 10 g of zeolite, with Na-P1 showing the lowest emissions and zeolite T the highest. Raw material preparation, particularly acid washing and rice husk calcination, was a major emission hotspot for eight of the nine zeolite types. These findings identify synthesis processes as key targets for improving environmental performance. Reducing water consumption during acid washing and improving calcination energy efficiency offer opportunities to lower production impacts. This study provides a basis for selecting lower-emission zeolite production pathways and supports the valorization of agricultural residues within a circular economy.

**Keywords:** *Rice husk, Zeolite, Life Cycle Assessment, Carbon-negative materials, Climate change mitigation*

# Biotec 1 + AWD: the Highest Yield with Up to Two-thirds Lower Methane Emissions per kg of Rice

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## Abstract

Flooded rice paddies are a major source of methane ($CH_4$). Alternate wetting and drying (AWD) can reduce these emissions, but perceived yield risk and the need for precise water control hinder its adoption. This study evaluated a low-carbon rice model combining the Biotec 1 variety with AWD and fertilizer management in irrigated paddies (22 rai 3 ngan; 3.64 ha) in Sam Ngam and Wachirabarami Districts, Phichit, Thailand. Continuous flooding (CF) and AWD were compared in the 2025 wet season at both sites and in a four-variety dry-season crop at Sam Ngam. Comparison varieties were RD61 (Sam Ngam) and RD61, RD79 and Homcholasit 2 (Wachirabarami). Under AWD, $CH_4$ emissions of Biotec 1 (as $CO_2e$, $GWP_{100}$ = 28) decreased by 46% at Sam Ngam and 68% at Wachirabarami relative to CF. $CO_2e$ per kg of paddy decreased from 2.06 to 1.14 and from 1.79 to 0.59 kg $CO_2e$, respectively. Water management did not significantly affect grain yield ($p > 0.05$). Biotec 1 yielded 989 (AWD) and 1,009 (CF) kg/rai at Sam Ngam, and 1,154 and 1,195 kg/rai at Wachirabarami (25% moisture). Under AWD, it had the highest mean yield at both sites and, at Wachirabarami, the smallest yield change (−3% versus −8% to −14% in other varieties). The dry-season crop showed a similar emission reduction without yield loss. Biotec 1 with AWD can maintain yield while reducing methane emissions, supporting a "Phichit Model" for low-carbon rice that may be linked to carbon credit schemes.

**Keywords:** *Low-carbon rice, Biotec 1, Alternate wetting and drying, Methane, Carbon credit*

# Reducing Methane Emissions without Yield Penalty through Alternate Wetting and Drying in Rice Production

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## Abstract

Continuous flooding in rice production is an important source of methane ($CH_4$) emissions from the agricultural sector. Alternate Wetting and Drying (AWD) irrigation has been proposed as a water-management strategy to mitigate greenhouse gas emissions while maintaining rice productivity. This study compared AWD with continuous flooding (Control) in terms of field water-level dynamics, greenhouse gas emissions, and grain yield of two rice varieties, BIOTEC 1 and RD61, under field conditions. The experiment was conducted as part of the IAW-CCM Asia project. Under AWD, field water levels were periodically allowed to decline to approximately −15 cm below the soil surface before re-irrigation, whereas Control plots were maintained predominantly under flooded conditions. Methane, carbon dioxide ($CO_2$), and nitrous oxide ($N_2O$) fluxes were monitored on eight occasions between 40 and 89 days after sowing. Mean $CH_4$ flux of RD61 was 0.71 mg $CH_4$ $m^{-2}$ $h^{-1}$ under AWD compared with 4.00 mg $CH_4$ $m^{-2}$ $h^{-1}$ under Control, representing an 82.2% reduction. For BIOTEC 1, AWD reduced mean $CH_4$ flux by 93.7%, from 5.89 to 0.37 mg $CH_4$ $m^{-2}$ $h^{-1}$. Across both varieties, AWD reduced mean $CH_4$ flux by approximately 89.0%. Grain yield under AWD was 787.9 and 508.5 kg $rai^{-1}$ for BIOTEC 1 and RD61, respectively, compared with 553.5 and 378.1 kg $rai^{-1}$ under Control. Overall, preliminary results indicate that AWD substantially reduced $CH_4$ emissions without reducing grain yield, demonstrating its potential as a sustainable water-management strategy for low-emission rice production.

**Keywords:** *Rice, Alternate Wetting and Drying, Water management, Methane, Greenhouse Gas emissions*

# Scaling Up Non-Burning Rice Residue Management for Biomass Pellet Production and Clean Energy in Thailand

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## Abstract

Open burning of rice residues contributes to PM2.5 pollution, greenhouse gas emissions, and biomass resource losses. This project aimed to scale up non-burning residue management, improve rice production efficiency, and create value from agricultural residues. Implemented in 2024 by the Rice Department with support from the Agricultural Research Development Agency (ARDA), the project involved 92 farmers managing 334.56 hectare across Nonthaburi, Pathum Thani and Bangkok, Thailand. Microbial decomposition and mobile biomass pellet production technologies were deployed according to local conditions. Farmer–private sector partnerships supported residue collection, processing, and market linkages.

The project avoided residue burning across 334.56 hectare. Compared with conventional practices, rice yields increased by 19–24%, production costs decreased by 20–32%, and net income increased by 35–49%. Biomass pellet production reached 1,359.15 tones, generating a sales value of 106,377 USD. Processing costs averaged 32.37 USD per ton against an average selling price of 78.26 USD per ton, yielding a margin of 45.89 USD per ton before other costs. Preliminary greenhouse gas emission reductions were estimated at 2,038.73 $tCO_2eq$, assuming an emission reduction factor of 1.5 $tCO_2eq$ per ton of pellets.

These findings highlight the potential of integrated rice residue management to reduce burning, improve farmer livelihoods, and establish biomass energy value chains. Community–private sector collaboration provides a practical mechanism for continued operation and wider adoption.

**Keywords:** *Non-burning management, Rice residues, Biomass pellets, Clean energy, Circular economy*

# Beyond Rice Yields: Integrating Climate-Smart Farming, Circular Bioeconomy and Community Value Creation in Northern Thailand

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## Abstract

Poor resource efficiency, crop residue burning, lack of income diversification in rural areas and greenhouse gas emissions are posing increasing challenges to rice production in northern Thailand. We need integrated innovations that deliver environmental improvements along with tangible economic and social benefits to address these interlinked challenges. This study evaluated the outcome and social value of a community-based agricultural innovation project in Lampang Province, Thailand, which integrated climate-smart rice production, circular bioeconomy, digital agriculture service and agriecotourism. The initiative included 30 pilot rice farmers who cultivated 662 rai (105.9 ha), agricultural machinery service providers, and community tourism stakeholders. Interventions included alternate wetting and drying (AWD), cultivation and use of Azolla, management of rice straw without burning, soil-test-based fertilizer application, safe pesticide practices, digital machinery service coordination and community-based tourism development. Economic, environmental and social outcomes were assessed using field-based project data and Social Return on Investment (SROI) analysis including deadweight, attribution and discounted benefits under conservative and expanded scenarios. The results showed that 85.71% of trained farmers adopted AWD and average rice yields increased from 583 to 630 kg/rai or an 8.06% improvement. The annual net profit of farmers increased by 1.47 million baht. AWD was estimated to reduce greenhouse gas emissions by 450.16 $tCO_2e$ per year and Azolla production could generate an additional THB 225,000 in revenue per year. It was estimated that non-burning straw management could avoid approximately 2.77 tons of PM2.5 emissions per year. Coordination of digital machinery and agriecotourism further added to local economic opportunities. The conservative first year SROI was estimated at 1.38:1 and with sustained outcomes and no further project investment the cumulative SROI is projected to reach 5.01:1 over three years. The results emphasize the potential of integrating low-carbon rice production, circular resource management and community-based economic innovation to create multiple dimensions of value. This integrated approach is a promising model for transforming the traditional rice farming into a more sustainable and economically resilient rural production system.

**Keywords:** *Climate-smart rice, Alternate wetting and drying, Circular bioeconomy, Community value creation, Social Return on Investment*

# Reviving Na Rim Lay: Climate-Resilient Rice and Community Value Chains in a 200-Year-Old Coastal Rice System, Phatthalung, Thailand

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## Abstract

Na Rim Lay is a 200-year-old coastal rice farming system along the brackish shores of Songkhla Lake in Phatthalung, southern Thailand. It is a unique living agricultural heritage built on traditional ecological knowledge that has been accumulated over generations. But its continuity has been threatened by rising soil salinity, salt water intrusion, erratic rainfall and falling agricultural viability. This study explores the potential of combining climate-resilient rice production, traditional knowledge and community-based value chain development to revitalize this heritage system and produce economic, social and cultural benefits. A community based participatory approach that integrated locally adapted, salt tolerant and flood resistant rice varieties with sustainable rice production practices aligned with the Sustainable Rice Platform (SRP). Other complementary interventions were community seed production, rice processing, local product development, community retailing and experiential tourism. Field-based information and Social Return on Investment (SROI) analysis, including deadweight, attribution and discounted future benefits, were used to assess project outcomes. The larger revival project increased the number of participants from 10 to 36 households and sustainable rice assessment involved 32 pilot farmers with 55 rai (8.8 ha). The first year results showed incremental net benefits of THB 530,437 from sustainable rice production and THB 268,800 from community retail profits. The estimated SROI in the first year was 0.53:1 which indicates high initial investment costs. In a conservative three-year scenario, cumulative SROI was projected to be 2.11:1, or THB 2.11 of social value for every THB 1 invested. The results indicate that improved agricultural technologies alone cannot revive traditional coastal rice systems. The integration of climate adaptation with locally managed value chains and the conservation of cultural heritage promises a way to strengthen rural livelihoods, community resilience and the long-term sustainability of vulnerable coastal agricultural landscapes.

**Keywords:** *Na Rim Lay, Coastal agricultural heritage, Community value chains, Sustainable Rice Platform, Social Return on Investment*

# Greenhouse Gas Emissions from Microbial-Assisted Rice Straw and Stubble Incorporation under Alternate Wetting and Drying

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## Abstract

Integrated rice residue and water management may reduce greenhouse gas (GHG) emissions while sustaining rice productivity. This study assessed methane ($CH_4$) and nitrous oxide ($N_2O$) emissions, grain yield, and economic performance of rice cultivar RD41 in an on-farm Technology Verification Experiment (TVE) involving 12 farmers in Nonthaburi Province, Thailand. Demonstration practice (DP) combined straw and stubble incorporation, a microbial consortium comprising *Bacillus subtilis* and *Trichoderma harzianum*, alternate wetting and drying (AWD), and recommended agronomic practices. Farmer practice (FP) involved residue burning and continuous flooding. $CH_4$ and $N_2O$ emissions were monitored at one participating farm using closed chambers with three replicates per treatment and converted to $CO_2$ equivalents using 100-year global warming potential values from IPCC AR5 (28 for $CH_4$ and 265 for $N_2O$). Compared with FP, DP had 69.4% lower $CH_4$ emissions (2.80 versus 9.16 t $CO_2e$ $ha^{-1}$) but 56.6% higher $N_2O$ emissions (0.667 versus 0.426 t $CO_2e$ $ha^{-1}$). Combined field emissions were 63.8% lower (3.47 versus 9.59 t $CO_2e$ $ha^{-1}$), and reported yield-scaled emissions were 69.7% lower. Grain yield was higher under DP (5.38 versus 4.50 t $ha^{-1}$), accompanied by lower production costs and higher net profit. These findings suggest that integrated residue and water management can reduce field GHG emissions while improving rice productivity, highlighting the importance of accounting for $CH_4$-$N_2O$ trade-offs in low-emission rice production.

**Keywords:** *Rice straw incorporation, Alternate wetting and drying, Methane, Nitrous oxide, Greenhouse gas mitigation*

# Agronomic Performance and Greenhouse Gas Emissions of Alternative Nitrogen Fertilizers in Strongly Acidic Paddy Soil

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## Abstract

Identifying alternative nitrogen fertilizers that sustain rice productivity while minimizing environmental impacts is essential for sustainable rice production. This study investigated the effects of nitrogen fertilizer sources on rice growth, grain yield, soil chemical properties, and methane ($CH_4$) and nitrous oxide ($N_2O$) emissions under strongly acidic paddy soil conditions. A greenhouse pot experiment was conducted using rice cultivar Pathum Thani 1 grown in clay soil (pH 4.1) from central Thailand. Four treatments-an unfertilized control, urea, ammonium chloride, and ammonium sulfate-were arranged in a randomized complete block design with four replications. Fertilized treatments received equivalent nitrogen rates based on soil-test recommendations. $CH_4$ and $N_2O$ emissions were monitored using the closed-chamber technique. Grain yield differed significantly among treatments ($p \leq 0.01$), with estimated yields of 38.7, 36.6, 35.0, and 30.9 g $pot^{-1}$ for urea, ammonium sulfate, ammonium chloride, and the control, respectively. Urea and ammonium sulfate produced statistically comparable yields. Cumulative $CH_4$ emissions were 1.664, 1.517, 1.922, and 1.509 t $CO_2e$ $ha^{-1}$ for the control, urea, ammonium chloride, and ammonium sulfate, respectively, while corresponding $N_2O$ emissions were 4.071, 6.419, 5.706, and 7.318 t $CO_2e$ $ha^{-1}$. Combined emissions were lowest under the control (5.735 t $CO_2e$ $ha^{-1}$), followed by ammonium chloride (7.627), urea (7.935), and ammonium sulfate (8.827). These findings underscore the importance of balancing agronomic performance and $CH_4$-$N_2O$ emission trade-offs when evaluating alternative nitrogen fertilizers for sustainable rice production.

**Keywords:** *Alternative nitrogen fertilizers, Rice productivity, Ammonium chloride, Methane, Nitrous oxide*

# Effects of Promoting Rice Production According to the Sustainable Rice Platform (SRP) Standard in Phatthalung Province: A Pre- and Post-Implementation Assessment

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## Abstract

Rice is a staple food crop and an important agricultural commodity in Thailand. Promoting sustainable rice production is important for improving production efficiency, managing resources, and reducing environmental impacts. This study assessed rice production practices against the Sustainable Rice Platform (SRP) Standard among farmers in Phatthalung Province before and after an SRP-based rice production improvement process. The intervention included training farmers on the SRP Standard, providing advice and demonstrations in rice fields, and assessing and monitoring farmers' practices. The assessment involved farmers in the Ban Pak Pra rice-growing group, Lampam Subdistrict, Mueang District, Phatthalung Province. In total, 32 farmers were assessed against 41 practices across eight categories. Before implementation, farmers' assessment scores ranged from 74% to 82%, with an average of 77%; the overall sustainability level was classified as Level C and did not meet the required criteria. After implementation, scores ranged from 96% to 97%, with an average of 97%, and all farmers were classified as Level A. Average scores increased in all eight categories. Categories 3, 4, 5, and 8 each achieved 100%, followed by Category 7 (98%), Category 6 (95%), Category 2 (94%), and Category 1 (89%). These findings indicate that promoting and supporting rice production in accordance with the SRP Standard was associated with improved farmer practices, particularly in water management, nutrient management, rice pest prevention and control, harvesting, and social and labor practices. Overall, the average assessment score increased from 77% before implementation to 97% after implementation.

**Keywords:** *Sustainable rice production, Sustainable Rice Platform, SRP Standard, Pre- and post-implementation assessment, Phatthalung Province*

# Evaluation of Sustainable Rice Production Improvement Based on the Sustainable Rice Platform Standard (SRP Standard) among Farmers in Nong Sano Subdistrict, Sam Ngam District, Phichit Province

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## Abstract

Enhancing sustainable rice production capacity is a key approach to improving yield efficiency, minimizing environmental impacts, and promoting optimal resource management within rice production systems. The Sustainable Rice Platform Standard (SRP Standard) serves as an evaluative and developmental framework to align farming practices with sustainable rice production principles. This study aimed to assess changes in farmers' rice production practices before and after adopting SRP Standard guidelines in Nong Sano Subdistrict, Sam Ngam District, Phichit Province. Individual assessments were conducted with 34 farmers, covering 8 operational categories and 41 compliance indicators, to compare practices pre- and post-implementation. The implementation process included training sessions for participating farmers to enhance their knowledge and understanding of the SRP Standard requirements and to promote the adoption of sustainable rice production practices in their farming activities. The findings revealed that prior to adoption, farmers achieved evaluation scores ranging from 51% to 84%, with an average of 68%. All participants were categorized at Sustainability Level C (Non-compliant), failing to meet the required criteria across key areas, including production planning, pre-production preparation, water management, nutrient management, pest management, harvesting, and farmer health and safety. Following the implementation of SRP Standard practices, evaluation scores increased substantially to between 93% and 97%, with the average score rising to 94%. Consequently, all farmers achieved Sustainability Level A, representing fully sustainable rice production. Category-level analysis further indicated that average scores across all 8 domains increased from 68% to a post-implementation range of 86% to 100%, with an overall average of 94%. All categories demonstrated high-level outcomes. These results highlight a substantial improvement in sustainable rice production capacity, demonstrating that training and the adoption of practices aligned with the SRP Standard can contribute to improving farming practices and meeting sustainability criteria across economic, health, social, and environmental dimensions.

**Keywords:** *Sustainable Rice Production, SRP Standard, Pre- and Post-Assessment, Rice Production, Phichit Province*

# Effects of Synthetic Fertilizer Reduction Combined with Nanofertilizer or Biofertilizer on Plant Growth and Anthocyanin Content of Black Rice (*Oryza sativa* 'Sembada Hitam')

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## Abstract

Black rice (*Oryza sativa* L. 'Sembada Hitam') is a functional food crop valued for its high anthocyanin content. However, the intensive use of synthetic fertilizers may reduce nutrient-use efficiency and negatively affect soil quality. This study evaluated whether the application of nano fertilizer or biofertilizer could maintain the growth and quality of black rice under a 50% reduction in synthetic NPK fertilizer. A completely randomized design was applied with seven treatments namely: control, 100% NPK, 50% NPK, 50% NPK plus nano fertilizer, 50% NPK plus biofertilizer, 100% NPK plus nano fertilizer, and 100% NPK plus biofertilizer. Plant height, tiller number, chlorophyll content, and grain anthocyanin content were determined and analyzed using analysis of variance followed by Duncan's multiple range test at a 5% significance level. The results showed that reducing NPK application by 50% and supplementing it with nano fertilizer or biofertilizer-maintained plant height, tiller number, and chlorophyll content at levels comparable to the control and, in several parameters, to the full-NPK treatment. The 50% NPK plus biofertilizer treatment produced 111.20 cm plant height and 1.20 mg $g^{-1}$ chlorophyll, while the 50% NPK plus nano fertilizer treatment resulted in 112.80 cm plant height, 1.13 mg $g^{-1}$ chlorophyll. Reducing NPK application by 50%—whether alone or in combination with nano-fertilizers or biofertilizers—increased the number of panicles by approximately 25% compared to the control. Although anthocyanin accumulation was highest under 100% NPK plus biofertilizer, both reduced-NPK treatments-maintained anthocyanin levels above the 50% NPK treatment. These findings demonstrate that nano fertilizer and biofertilizer can support a 50% reduction in synthetic fertilizer use without substantially compromising black rice growth and grain quality, thereby offering a more sustainable nutrient-management strategy.

**Keywords:** *Biofertilizer, Nanofertilizer, NPK reduction, Anthocyanin, Sustainable fertilization*

# Effectiveness of Integrated Soil Management Practices for Paddy Rice Production on Salt-Affected Alluvial Soils in the Mekong Delta, Vietnam

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## Abstract

The Mekong Delta is one of the major food-producing regions in Southeast Asia and plays a critical role in ensuring Vietnam's national food security and rice production. In recent years, rice productivity in the region has been increasingly constrained by increased drought and seawater intrusion attributed by climate change. To address these challenges, two experimental sites, each comprising seven demonstration models were established. Rice was cultivated on alluvial soils characterized by shallow acid sulfate conditions and salinity constraints during the dry season. The study aimed to evaluate integrated soil management practices involving the application of organic fertilizers and biochar, improved inorganic fertilizer management, and deep placement of inorganic fertilizers to mitigate saline accumulation, increase fertilizer-use efficiency, and sustain rice productivity. Rice yield was monitored, while selected soil chemical and biological properties were assessed. The results indicated that the application of organic fertilizers and biochar, either individually or in combination, was particularly beneficial for rice production on salt-affected and low-pH soils. The implementation of integrated soil management practices, including the incorporation of organic fertilizers and biochar, maintained or increased rice yields while improving key indicators of soil fertility and biological activity, particularly available phosphorus and soil respiration. Furthermore, these practices enabled a 25% reduction in inorganic fertilizer application relative to the recommended rate without compromising rice productivity. Overall, the findings demonstrate that integrated soil management practices can contribute to improved soil fertility, greater fertilizer-use efficiency, and more sustainable rice production in salt-affected and acid-prone soils of the Mekong Delta.

**Keywords:** *Biochar, Compost, Integrated soil management practices, Paddy rice*

# From Root Anatomy to Methane Emissions: Developing a Multi-Scale Modeling Framework for Rice

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## Abstract

Rice cultivation is a major contributor to global anthropogenic methane ($CH_4$) emissions due to the anaerobic conditions of flooded paddies. However, rice plants can naturally mitigate $CH_4$ production through radial oxygen loss (ROL), which oxygenates the rhizosphere and facilitates aerobic $CH_4$ oxidation. While root anatomical traits are known to govern ROL capacity, quantifying this structural impact at scale remains challenging. To address this, we are developing a multi-scale modeling tool to simulate oxygen release from root cross-sections based on spatial anatomical variations along the root axis. In this study, we established the root anatomical parameters for a baseline rice variety and conducted a comparative analysis of four key anatomical traits between a high-methane and a low-methane emitting cultivar. Our preliminary data provides the necessary localized structural inputs to accurately model ROL at the segment scale. In the future, this cross-sectional model will be scaled up to the whole-plant level and field scale to predict changes in soil redox potential and actual $CH_4$ emissions. By linking physical root anatomy directly to atmospheric methane impact, this modeling framework aims to identify optimal root blueprints, providing geneticists and breeders with precise trait targets to develop climate-resilient, low-methane rice cultivars.

**Keywords:** *Methane emissions, Rice, Root modelling*

# Impact of Diverse Organic Fertilizers and Silicon Supplementation on Soil Properties, Element Uptake, and Yield Performance in Organic Rice Cultivation in the Mekong Delta, Vietnam

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## Abstract

Transitioning from synthetic inputs to organic fertilization is vital for reversing soil degradation in the Mekong Delta. This study, conducted over three consecutive cropping seasons, investigated the impact of diverse organic amendments—specifically fishery by-products—and silicon (+Si) supplementation on the growth, nutrient uptake, and element accumulation of the "Đài Thơm 8" rice variety. Results showed that organic inputs stabilized soil pH, increased electrical conductivity, and improved Bray II available phosphorus. Under flooded anaerobic conditions, nitrogen mineralization maintained a steady ammonium ($NH_4^+$) pool while suppressing nitrate loss. Enhanced growth indices and effective tiller numbers directly supported optimal grain yield. Crucially, silicon (+Si) supplementation suppressed cadmium (Cd) bioaccumulation in plant tissues down to a safe range (0.010–0.015 mg/kg). However, key limitations were noted: total soil organic matter did not increase significantly within three cropping seasons. On the other hand, organic matter decomposition accelerated plant aluminum (Al) concentrations in late seasons. In conclusion, integrated organic-silicon management enhances soil chemical properties and mitigates cadmium toxicity. Future research must focus on multi-seasonal field trials to understand the mechanisms driving aluminum bioaccumulation and assess long-term soil organic carbon sequestration in the organic rice farming system.

**Keywords:** *Organic rice, Fishery by-products, Silicon amendment, Trace element bioaccumulation, Mekong Delta.*

# Aspiration Without Leverage: Sustainability-Oriented Market Expectations and Market Capabilities among Thai Rice Farmers

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## Abstract

Sustainable rice systems will only benefit people, ecosystems and food safety if farmers can sell what they produce on terms that reward better practice. The study examines whether the perceived ability of Thai rice farmers to access and negotiate in markets is consistent with their expectations of sustainability-oriented demand. A cross-sectional survey of 291 rice farmers was carried out in August to October 2025 in eight purposively selected provinces (Lampang, Chiang Rai, Phichit, Bangkok, Surin, Nakhon Phanom, Phatthalung and Pattani) and complemented by ten focus-group discussions. Seventeen five-point indicators were summarized as mean scores and the share of respondents rating 4–5, with 95% Wilson confidence intervals, and compared across provinces using Kruskal–Wallis tests. Most of the farmers expected consumers to be more concerned about health and food safety (69.1%) and environmentally friendly rice (69.1%), and 60.8% thought certification was important. By contrast, only 14.1% gave a high rating to their ability to bargain on price, 14.1% to their access to price information, 21.0% to their access to market information or to their own sales channels and 20.3% to the extent to which public assistance met their needs. Provincial differences were significant for 16 of the 17 indicators ($\varepsilon 2$ up to 0.34). The commercial central and northern sites had the least bargaining power (1.43-1.58 of 5). Specialty rice readiness was the only item that did not differ by province. Farmers reported high level of pride (74.9%) and rice contributed to household food security (71.5%). Thai rice sustainability policy should therefore unite farm-level standards with price transparency, collective marketing, and buyer linkages.

**Keywords:** *Sustainable rice, Market access, Bargaining power, Smallholder well-being*

## Introduction

In Thailand, rice is a commodity, a household food reserve and a carrier of local knowledge and identity. Increasingly, efforts to make rice production more sustainable through water-saving irrigation, reduced agrochemical use, residue management and certification are framed in One Health terms that link farm practices to food safety, environmental quality and producer welfare. However, the diffusion of these practices depends not only on agronomy but also on whether farmers can capture the value that sustainability is expected to generate. Improvements in the field may never be rewarded at the farm gate where farmers sell undifferentiated paddy to a few buyers who have little knowledge of prices or quality premiums.

Information, transaction costs, and bargaining position determine the distribution of benefits from market opportunities [1]. Asymmetric price information allows intermediaries to make large margins [2]. Market information services increase prices received by farmers [3]. Producer organizations can reduce transaction costs and improve market access [4]. Marketing cooperatives in the Thai rice value chain increase the price paid by private intermediaries to

jasmine-rice farmers, including non-members [5]. Value chain governance also affects the degree to which producers can improve through quality, processing or new functions [6, 7].

On the demand side, a national survey of Thai consumers found that 84 % would pay a 5–10 % premium for sustainable rice [8]. The Sustainable Rice Platform (SRP) standard connects farm practices with supply-chain assurance [9]. However, where market power is still unequal, standards do not automatically improve producer outcomes [10]. In addition, Thai rice farmers are also aging quickly [11] and women's needs are frequently ignored in agri-food services [12]. Porter's competitive-advantage framework of factor conditions, demand, strategy and supporting institutions [13, 14] has been adapted to farm level rice competitiveness [15] . Thai development thinking adds a well-being dimension based on self-reliance and the Sufficiency Economy Philosophy [16] expressed locally as Kin Dee, Yu Dee, Mee Suk. This study uses these lenses to investigate whether farmers' expectations of demand for sustainability-oriented products correspond with their perceived capacity to access information, reach buyers, and negotiate prices, and whether this varies with production contexts.

## Materials and Methods

*Study sites and data collection*

A mixed-methods cross-sectional design was used. Eight provinces were selected purposively to represent contrasting rice systems: Lampang (certified seed; n = 31), Chiang Rai (irrigated commercial rice; n = 30), Phichit (cooperatives, irrigated and rainfed; n = 40), Bangkok–Nong Chok (peri-urban commercial; n = 30), Surin (rainfed, household-oriented; n = 30), Nakhon Phanom (organic and processed rice; n = 33), Phatthalung (coastal brackish-water and GI rice; n = 57) and Pattani (local and direct-market rice; n = 40). Farmers were recruited through farmer groups, cooperatives and community enterprises. A structured questionnaire was administered to 291 farmers in August–October 2025, and ten focus-group discussions were held in the same communities.

*Questionnaire and indicators*

The questionnaire had four modules: farmer characteristics; Porter-inspired competitiveness (factor conditions, demand, strategy and supporting institutions); value-chain competitiveness (cost, quality, market linkage and technology); and well-being (*Kin Dee, Yu Dee, Mee Suk*). Items used a five-point scale (1 = lowest, 5 = highest). Seventeen single-response items were selected a priori and grouped as market expectations, market capabilities and support, and well-being (Table 1).

*Statistical analysis*

Responses were compiled as item-level frequency distributions by province. For each item, the mean score and the share rating 4–5 were calculated, with 95% Wilson confidence intervals. Differences among provinces were tested with the Kruskal–Wallis H test (df = 7), with effect size $\varepsilon^2 = H/[(N^2 - 1)/(N + 1)]$. Analyses used Python 3 (SciPy). Focus group notes were synthesized under five themes (market power, enabling organizations, differentiated products, climate and water constraints, and household and community value) to interpret the survey patterns. Participation was voluntary, consent was obtained through a statement in the questionnaire, and only aggregated data are reported.

## Results and Discussion

*Respondent characteristics*

Women made up 62.9% of respondents and men 37.1%. The sample was older: 77.0% were over 50 years and 44.3% over 60, and 59.1% had less than upper-secondary education.

*Strong market expectations, weak market leverage*

The majority of farmers (69.1%) believed that consumers would pay more attention to health and food safety, and to environmentally friendly rice (69.1%). Most farmers (60.8%) considered certification to be important and felt ready to supply specialty rice (57.0%) (Table 1). The self-assessed market capabilities were considerably weaker: only 14.1% gave a high rating to their price-bargaining power (mean 2.27), 14.1% to their access to price information and 21.0% to their access to market information or own sales channels, while only 17.3% were satisfied with current rice markets. The confidence intervals for the two indicator groups did not intersect. As Thai consumers express their willingness to pay a premium for sustainable rice [8], the constraint seems to lie more in the channels through which information and value flow back to producers, rather than in final demand itself, in line with the evidence on information asymmetry and bargaining [2, 3].

**Table 1 Indicator summary: mean score (1–5), share rating 4–5 with 95% Wilson CI, and Kruskal–Wallis test across eight provinces (N = 291)**

| Indicator | Mean | % rating 4–5 [95% CI] | H (df = 7) | $\varepsilon^2$ |
|---|---|---|---|---|
| Expected consumer emphasis: health/food safety | 3.89 | 69.1 [63.5–74.1] | 60.1*** | 0.21 |
| Expected consumer emphasis: environment | 3.91 | 69.1 [63.5–74.1] | 23.6** | 0.08 |
| Importance of rice certification | 3.69 | 60.8 [55.1–66.3] | 70.4*** | 0.24 |
| Readiness to supply specialty rice | 3.60 | 57.0 [51.3–62.6] | 12.1 ns | 0.04 |
| Value of brand/storytelling | 3.32 | 46.4 [40.7–52.1] | 79.2*** | 0.27 |
| Market information and own sales channel | 2.76 | 21.0 [16.7–26.0] | 33.4*** | 0.12 |
| Access to price information | 2.64 | 14.1 [10.6–18.6] | 22.8** | 0.08 |
| Satisfaction with current rice market | 2.52 | 17.3 [13.4–22.2] | 55.8*** | 0.20 |
| Own price-bargaining power | 2.27 | 14.1 [10.6–18.6] | 76.2*** | 0.26 |
| Public assistance matches needs | 2.60 | 20.3 [16.1–25.4] | 81.0*** | 0.28 |
| Capacity to control production costs | 2.90 | 23.4 [18.9–28.6] | 18.1* | 0.06 |
| Digital/modern technology skills | 2.53 | 20.3 [16.1–25.4] | 70.6*** | 0.24 |
| Interest in future public rice projects | 3.57 | 54.0 [48.2–59.6] | 53.0*** | 0.18 |
| Pride in identity as a rice farmer | 4.08 | 74.9 [69.6–79.5] | 52.2*** | 0.18 |
| Rice contributes to food security and household happiness | 3.91 | 71.5 [66.0–76.4] | 99.6*** | 0.34 |
| Rice will remain central to farming life | 3.93 | 71.5 [66.0–76.4] | 42.8*** | 0.15 |
| Sustainability principles applied in production | 3.71 | 57.0 [51.3–62.6] | 54.8*** | 0.19 |

*** p < 0.05; ** p < 0.01; *** p < 0.001; ns, not significant.**

*Differences among production contexts*

For 16 of the 17 indicators, the perceptions differed significantly between the provinces (Table 1). The commercial sites of Chiang Rai (1.43) and Phichit (1.58) and organic-oriented Nakhon Phanom (1.88) had the lowest bargaining power, while Pattani (2.93) and Phatthalung (2.74) had the highest (Figure 1). Chiang Rai and Phichit therefore had some of the highest expectations for environmental demand (4.03 and 4.18) and the weakest bargaining positions. In these sites, focus-group participants described dependence on a few paddy buyers, while Phichit cooperative members reported collective input supply and bargaining. Cooperative marketing could narrow the gap in such systems, with cooperation promoting higher prices for Thai rice intermediaries [5]. Farmers in Pattani and Phatthalung who sold more directly or through place-based products such as GI Sangyod rice and brackish-water heritage rice reported stronger positions, in line with arguments that shorter or differentiated chains give producers more room to upgrade [6, 7].

The only indicator that did not vary across provinces was the readiness to supply specialty rice ($H = 12.1$, $p = 0.097$). There is therefore a widespread willingness to differentiate, but the information and buyer access needed to act on it varies widely. Slow adoption of sustainable or specialty production may be driven by a constraint other than motivation.

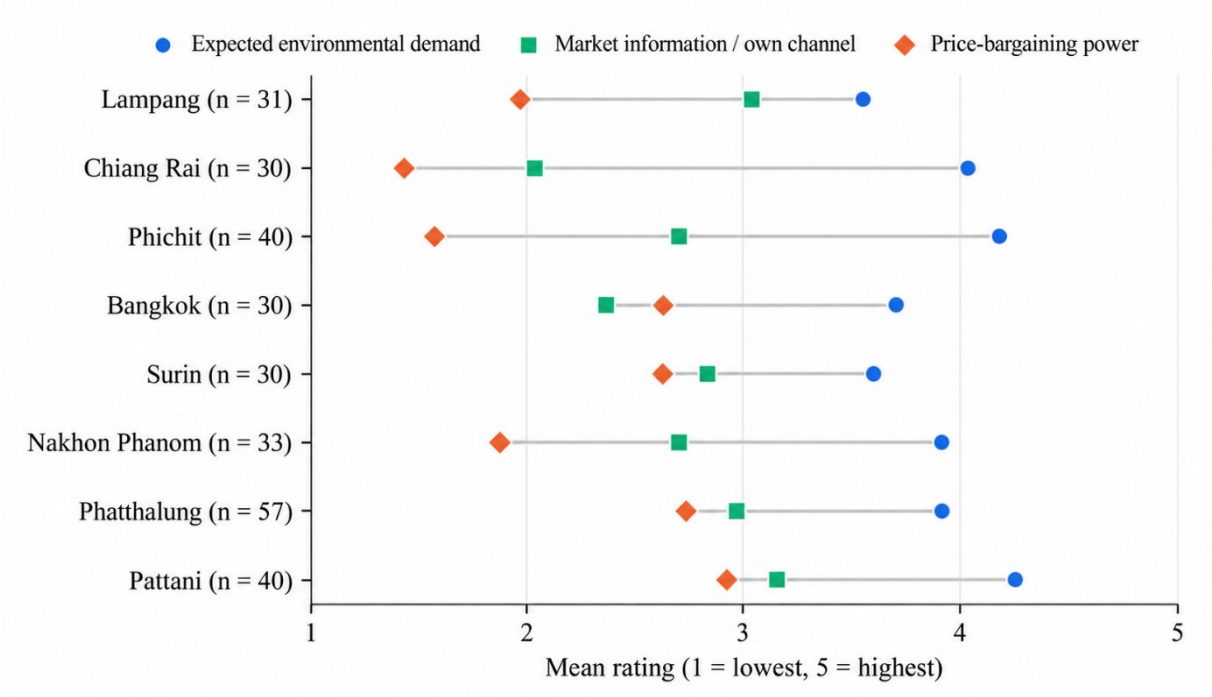


**Figure 1 Province-level mean scores (1–5) for expected environmental demand, access to market information or own sales channel, and price-bargaining power; grey lines show the range in each province**

*Institutional support, technology and well-being*

Only 20.3 percent of farmers considered public assistance appropriate to their needs, but 54.0 percent were interested in future public rice projects, suggesting a demand for better targeted support, not a desire to withdraw. Public support was lowest in Bangkok (1.87) and

Phichit (1.95) and highest in Lampang (3.58). Only 20.3% rated digital and modern technology skills highly, which is important given a sample where 77% were over 50 [11]. Social indicators, in contrast, were very high with 74.9% very proud to be a rice farmer and 71.5% rating highly the contribution of rice to household food security and happiness, the largest difference between provinces for any indicator ($\varepsilon^2 = 0.34$). The peri-urban site in Bangkok scored the lowest for pride (3.33) and food security (2.67), indicating that urban pressure may erode rice's social functions.

*Implications for sustainable rice and One Health*

Farmers valued certification but certification only creates value if buyers recognize and pay for it and compliance costs can fall disproportionately on smallholders [10]. From a One Health perspective, the health and environmental benefits of sustainable rice, safer food, lower agrochemical exposure, and reduced emissions and burning, depend on farmers continuing such practices, which in turn requires viable livelihoods and market signals that reach the farm. Thus, strengthening the position of farmers' market is a precondition, not an alternative, to these goals. Support should be context-specific: transparent grading, price information and collective marketing for commercial paddy systems; market validation, branding and credible verification for specialty producers; climate-adapted seed and water solutions associated with food security for rainfed and coastal communities; and digital services designed for older users and gender-sensitive extension across all sites [12].

Limitations of the study. The sample was purposive, so the results describe the participating groups, not the provinces or Thailand. Indicators are self-reported perceptions and not measured prices or environmental outcomes. Future work should collect household data linked with objective market and environmental indicators.

Overall, farmers in eight contrasting Thai rice-producing contexts widely expected markets to reward healthier and more environmentally friendly rice, but few felt they could access market information, connect with buyers or negotiate prices. The gap between aspiration and capability was the greatest in commercial paddy systems. The willingness to supply specialty rice was similar across the board. A sustainable rice policy should therefore combine farm-level standards with price transparency, collective marketing and buyer linkages, so that the health and environmental benefits of sustainable rice are matched by fair returns to farmers.

**Acknowledgements**

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**References**

1. Barrett C. B. Smallholder market participation: Concepts and evidence from eastern and southern Africa. *Food Policy*. 2008;33(4):299–317. https://doi.org/10.1016/j.foodpol.2007.10.005
2. Mitra S, Mookherjee D, Torero M, & Visaria S. Asymmetric information and middleman margins: An experiment with Indian potato farmers. *Review of Economics and Statistics.* 2018;100(1):1–13. https://doi.org/10.1162/REST_a_00699
3. Courtois P, & Subervie J. Farmer bargaining power and market information services. *American Journal of Agricultural Economics*. 2015;97(3):953–977.

https://doi.org/10.1093/ajae/aau051
4. Markelova H, Meinzen-Dick R, Hellin J, & Dohrn S. Collective action for smallholder market access. *Food Policy*. 2009;34(1):1–7. https://doi.org/10.1016/j.foodpol.2008.10.001
5. Kumse K, Suzuki N, Sato T, & Demont M. The spillover effect of direct competition between marketing cooperatives and private intermediaries: Evidence from the Thai rice value chain. *Food Policy*. 2021;101.
https://doi.org/10.1016/j.foodpol.2021.102051
6. Gereffi G, Humphrey J, & Sturgeon T. The governance of global value chains. *Review of International Political Economy.* 2005;12(1):78–104.
https://doi.org/10.1080/09692290500049805
7. Humphrey J, & Schmitz H. How does insertion in global value chains affect upgrading in industrial clusters? *Regional Student*. 2002;36(9):1017–1027.
https://doi.org/10.1080/0034340022000022198
8. Sustainable Rice Platform. Sustainable rice in Thailand: Insights from consumer behaviors and perceptions. Bangkok: SRP; 2023 Nov 28. Available from: https://sustainablerice.org/sustainable-rice-consumer-survey-thailand/
9. Sustainable Rice Platform. *The SRP Standard for Sustainable Rice Cultivation (Version 2.2)*. Bangkok: Sustainable Rice Platform; 2023.
10. Dayet A, Diepart J-C, Castella J-C, Thon C, & Demenois J. From theory to paddy: Translating the Sustainable Rice Platform in Cambodia. *Agriculture and Human Values*. 2026;43:108.
https://doi.org/10.1007/s10460-026-10920-7
11. Bunyasiri I, Suchato R, & Sirisupluxana P. Adaptation of rice farmers to aging in Thailand. *Open Agriculture*. 2024;9(1):20220364.
https://doi.org/10.1515/opag-2022-0364
12. Food and Agriculture Organization of the United Nations (FAO). *The status of women in agrifood systems*. Rome: FAO; 2023. https://doi.org/10.4060/cc5343en
13. Porter ME. *Competitive advantage: Creating and sustaining superior performance*. New York: Free Press; 1985.
14. Porter ME. The competitive advantage of nations. *Harvard Business Review*. 1990;68(2):73–93.
15. Yaacob A, Abdul Malek S, Yusop Z. The determinants of competitiveness based on Porter's Diamond Model: The case of paddy farming in Kelantan. In: *Proceedings of the Conference on Business Management and Marketing (CBMM 2017)*; 2017; Penang, Malaysia.
16. Mongsawad P. The philosophy of the sufficiency economy: A contribution to the theory of development. *Asia-Pacific Development Journal*. 2010;17(1):123–143.
https://doi.org/10.18356/02bd5fb3-en

# Effects of Slow-Release Urea and Alternate Wetting and Drying on Nitrous Oxide Emissions and Nitrogen Use Efficiency in Rice

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## Abstract

Continuously flooded rice cultivation is a major source of greenhouse gas emissions, particularly methane ($CH_4$). Alternate wetting and drying (AWD) is therefore a promising water management practice for reducing $CH_4$ emissions. However, repeated soil drying and rewetting can alter soil redox conditions, which may increase nitrous oxide ($N_2O$) emissions and reduce nitrogen-use efficiency (NUE). Slow-release nitrogen fertilizers such as urea-triazone (UT) may improve nitrogen availability and NUE under AWD, but information on the combined effects on $N_2O$ emissions, yield, and NUE in rice production systems in Thailand remains limited. This study therefore aims to evaluate the effects of combining urea-triazone with AWD on $N_2O$ emissions, rice growth, yield, and NUE. A two-season field experiment will be conducted using a randomized complete block design (RCBD) with four treatments and four replications: continuous flooding with farmers' practice (CF + FP); AWD with farmers' practice (AWD + FP); and AWD + FP with nitrogen supplied as urea-triazone at 100% (AWD + FP+ UT100) and 75% (AWD + FP + UT75) of the recommended rate, respectively. For each treatment, soil properties, plant growth, yield and yield components, $N_2O$ emissions, and economic returns will be assessed, with $N_2O$ fluxes measured using the closed chamber method and analyzed by gas chromatography. The results are expected to support the development of integrated water and nitrogen management practices that improve NUE while reducing greenhouse gas emissions from rice production in Thailand.

**Keywords:** *Alternate wetting and drying, Urea-triazone, Nitrous oxide, Nitrogen-use efficiency, Rice*

# Long-term Evaluation of Crop Management Practices on Greenhouse Gas Emissions and Rice Productivity under Dry-Season Conditions

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## Abstract

Greenhouse gas emission due to rice cultivation is strongly influenced by water and crop residue management. This study evaluated the effects of different crop management practices on greenhouse gas emissions and rice productivity during the 2026 dry season. The experiment was conducted using Thai rice variety RD61. Alternate wetting and drying (AWD), continuous flooding (CF), phosphogypsum application, and rice straw and stubble management were arranged in a split-plot randomized complete block design with three replications. Greenhouse gas fluxes, including methane ($CH_4$), nitrous oxide ($N_2O$), and carbon dioxide ($CO_2$), were monitored at approximately 10-day intervals from 9 to 83 days after sowing (DAS). Grain yield and plant growth characteristics were also evaluated. The results showed 38% reduction of cumulative $CH_4$ emission under AWD than under CF, with mean values of 2,914.29 and 4,735.93 mg $m^{-2}$, respectively. Among the treatments, AWD combined with phosphogypsum application and 10-cm stubble height resulted in the lowest cumulative $CH_4$ emission (1,487.4 mg $m^{-2}$) whereas CF with 30-cm stubble and retained rice straw produced the highest emission (6,870.0 mg $m^{-2}$). However, comparisons of mean $CH_4$ emissions across sampling collection dates showed no significant difference between AWD and CF ($P > 0.05$). Although plant height and tiller number were the same under two management systems, 10% reduction of grain yield was observed under AWD. These findings indicate that AWD has potential to reduce $CH_4$ emissions under dry-season conditions, although this may compromise with a slight reduction in grain yield. The integration of water management with appropriate straw and stubble management may provide opportunities to improve the balance between greenhouse gas mitigation and rice productivity. Further evaluation across subsequent seasons is required to confirm the long-term effects of these management practices.

**Keywords:** *Alternate wetting and drying (AWD), Continuous flooding, Methane emission, Rice straw management, Rice yield.*

# Yield Potential and Farmer Acceptance of Three New Rice Lines for Climate-resilient Rice Production

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## Abstract

Rice production is increasingly challenged by climate variability and changing production conditions. This study evaluated the yield performance of three new rice lines, Biotec1, Biotec3, and Biotec4, compared with two check cultivars, RD41 and RD61, under wet direct seeding and transplanting systems. Farmer acceptance was also assessed in irrigated areas of Chainat Province, Thailand, during the 2025/2026 dry season. Grain yield was determined using crop-cutting methods, while farmer acceptance was evaluated through field preference voting and questionnaires involving 32 farmers. Under wet direct seeding, Biotec1 produced the highest grain yield (1,220 kg rai$^{-1}$), significantly exceeding Biotec4 (1,050 kg rai$^{-1}$), Biotec3 (960 kg rai$^{-1}$), RD61 (918 kg rai$^{-1}$), and RD41 (748 kg rai$^{-1}$). Under transplanting, Biotec3 (1,168 kg rai$^{-1}$) and Biotec4 (1,144 kg rai$^{-1}$) produced the highest yields. Biotec1 had the highest harvest index (0.621). Mean grain yield did not differ significantly between transplanting and wet direct seeding (1,053 vs. 979 kg rai$^{-1}$; $P > 0.05$). Wet direct seeding produced significantly more panicles m$^{-2}$ and heavier grains, compensating for fewer grains per panicle ($P < 0.01$). Farmer preference differed significantly among genotypes ($\chi^2 = 215.52$, $P < 0.01$). Biotec1 received the most highly preferred votes (28). Higher yield than current cultivars was the most important adoption criterion (4.08/5). Overall, 53.8% of farmers intended to grow Biotec lines in the following season. Biotec1 showed strong potential for wet direct-seeded systems, whereas Biotec3 and Biotec4 were promising for transplanted systems.

**Keywords:** *Climate resilience, Grain yield, Rice production systems, Farmer preference, Varietal adoption, Rice breeding, Genotype evaluation*

# Supporting Reliable Greenhouse Gas Measurements in Rice Cultivation through SI-Traceable Reference Materials

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## Abstract

Rice cultivation is a significant source of agricultural greenhouse gas (GHG) emissions, particularly methane ($CH_4$) and nitrous oxide ($N_2O$). Accurate quantification of these emissions is essential for evaluating mitigation strategies, such as alternate wetting and drying (AWD), and improving national GHG emission inventories. Common measurement techniques, including static chamber sampling followed by gas chromatography (GC) and advanced trace gas analysers, require reliable calibration standards to ensure accurate, comparable results. The National Institute of Metrology (Thailand) (NIMT) has developed SI-traceable certified reference materials (CRMs), designated as Thailand Reference Materials (TRMs), using primary gravimetric preparation methods. NIMT's internationally recognised Calibration and Measurement Capabilities (CMCs), published in the BIPM Key Comparison Database (KCDB), cover gas mixtures in a nitrogen balance for carbon dioxide ($CO_2$) at 1.6 µmol mol$^{-1}$–50 cmol mol$^{-1}$, methane ($CH_4$) at 500 µmol mol$^{-1}$–50 cmol mol$^{-1}$, and nitrous oxide ($N_2O$) at 100 µmol mol$^{-1}$–50 cmol mol$^{-1}$, with relative expanded uncertainties of 0.2%, 0.4% and 0.4%, respectively. NIMT also has the capability to prepare $CO_2$, $CH_4$ and $N_2O$ gas mixtures at atmospheric concentration levels. Building on these capabilities, NIMT can support agricultural GHG measurements by providing reference gas mixtures for instrument calibration and measurement quality assurance. Calibration against gas mixtures with accurately assigned concentrations enables instrument responses to be linked to SI-traceable reference values, helping to minimise measurement bias and improve the comparability of results across laboratories. This metrological support contributes to more reliable GHG emission estimates and assessments of mitigation practices in rice cultivation, supporting evidence-based climate change mitigation and sustainable rice production in Thailand.

**Keywords:** *Certified reference materials, Greenhouse gas emissions, Rice cultivation, Measurement traceability, Methane, Climate change mitigation*

# Management of Coastal Paddy Fields in Phatthalung Province under Flood and Drought Conditions for Sustainable Income Enhancement

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## Abstract

Coastal paddy fields, locally known as Na Rim Le, along Songkhla Lake in Lam Pam Subdistrict, Phatthalung Province, Thailand, are repeatedly affected by flooding, drought and brackish-water intrusion, which result in unstable yields and low farm incomes. Consequently, the cultivated area has declined from about 200 rai to 63 rai (1 rai = 0.16 ha). This study aimed to improve water management in Na Rim Le rice production and to add value through rice-based products and agritourism. Participatory action research using mixed methods was conducted with a community enterprise, local farmers and partner agencies. Activities included household and plot surveys; water-risk zoning; matching rice varieties to risk zones (RD43 and RD79 for drought-prone plots; Hom Na Le 1 and Hom Na Le 2 for flood- and brackish-prone plots; and KDML105 and Hom Jasmine where suitable); adjusting cropping calendars; alternate wetting and drying (AWD); community seed production; crop-cut yield assessment; and farmer–researcher training. The farmer network expanded from 36 pilot households to 138 households (138% of the target), covering 116 rai: 96 rai of flood-prone land, 14 rai of drought-prone land and 6 rai of rehabilitated abandoned fields. In 2025, the 63-rai pilot area produced about 32,000 kg of rice, an average yield of 508 kg/rai (about 3.2 t/ha). Selling milled rice through the community enterprise increased the average net rice income of pilot households from THB 16,283 to THB 60,507 per household per year, while producing their own seed saved THB 379 per household per year. The social return on investment (SROI) was 1.62 over five years and is projected to reach 2.85 over ten years. Combining risk-based variety selection, water management, value addition and agritourism provides a practical model for strengthening coastal rice communities under climate variability.

**Keywords:** *Coastal rice, Flood and drought, Climate variability, Social return on investment*

# Two Microplastic Sinks Found in Nature-based Lagoon Treatment Chain System

**Sweety Jane Ocoy [1,2], Onanong Phewnil [1*], Watcharapong Wararam [1], Parkin Maskulrath [1], Thanit Pattamapitoon [1], Noppawan Semvimol [1], Manlika Srichomphu [1,3], Chalisa Tudsanaton [1,3], Onnicha Sungkpoh [1], and Kasem Chunkao[1]**

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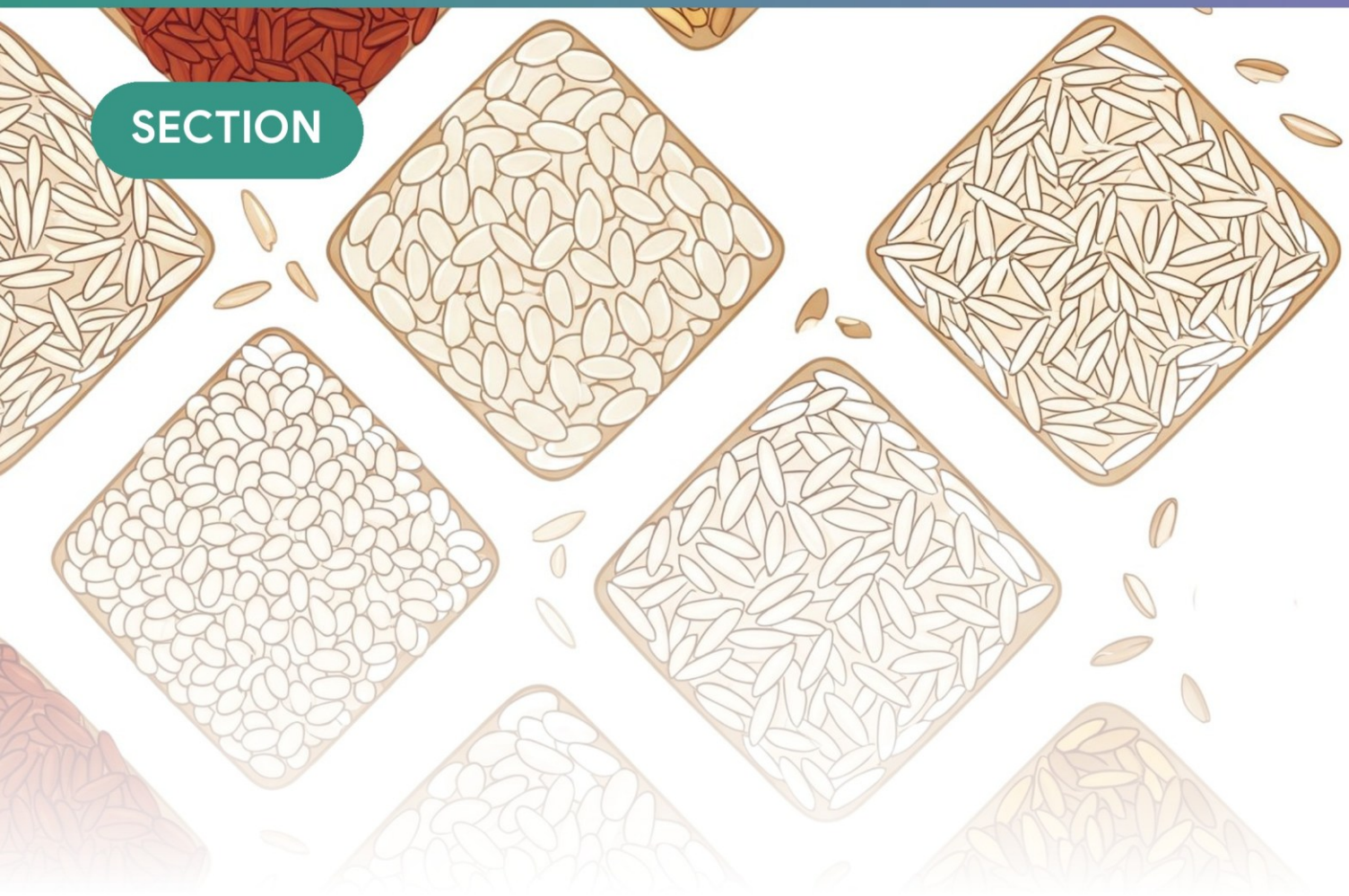
## Abstract

Modernized wastewater treatment plants (WWTPs) in developed countries achieve 90–100% microplastic removal, yet adoption of these technologies in the Global South remains limited due to high costs and operational complexities. To evaluate viable alternatives on par with advanced WWTPs, a lagoon treatment chain system built on nature-based principles was studied. Wastewater and sludge were collected and analyzed for microplastics from Phetchaburi City sewer to the Royally Initiated Laem Phak Bia Environmental Research and Development Project (H.M. LERD) treatment facility in Thailand. The second order influent (3,328 ± 3,675 MP $L^{-1}$) at the city was a major entry pathway for microplastics into the treatment chain. Wastewater had elevated fibers (41.9%), while fragments dominated sludge (72.7%). The H.M. LERD achieved an overall microplastic removal of 92.74% and further revealed two microplastic sinks in sludge: blow-off points (MRE, -79.68%) and Pond III (MRE, -22.58%). Fourier-transform infrared spectroscopy with attenuated total reflectance (FTIR-ATR) showed a dominance of acrylonitrile butadiene styrene (ABS) at the second order (57.45%, wastewater) and sludge (51.16% blow-off; 22.58% Pond III), followed by high impact polystyrene (HIPS) and styrene acrylonitrile (SAN), classified as a severe hazard polymer (V), a threat if sludge is treated and reused in agriculture as biosolids through land application. These findings elucidate a shift in focus from wastewater effluent to the fate of retained sludge and source interventions aimed at domestic and urban plastic inputs.

***Keywords:*** *Plastic, Wastewater, Sludge, Fate, Southeast Asia*



SECTION

# PS3

## Abiotic and Biotic Stresses

Tolerance and resistance to environmental stress, pests and diseases

Poster 28

# Potential of Rhizospheric Fungi to Reduce Copper and Lead Toxicity in *Triticum aestivum* L.

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## Abstract

Plants have adapted to various heavy metals and environmental situations during anthropogenic evolution. The most common heavy metal contaminants are lead (Pb) and copper (Cu), which can be found in both natural and industrial settings. Microorganisms play a crucial role in the biotransformation of heavy metal-contaminated environments. To successfully remediate heavy metals, a combination of microbial strains should be used instead of a single strain culture. In this study, four rhizospheric fungus strains were extracted from *Parthenium hysterophorus* and tested for their tolerance to lead and copper. These strains were selected for their ability to promote plant growth under heavy metal stress. When inoculated to *Triticum aestivum* L. under heavy metal stress, the fungal isolates NMG, Ng, N6, and NB showed promising results in the form of increased secondary metabolites. Different concentrations of specific heavy metals (Pb25, Pb75, Cu100, Cu200, Pb25+Cu100, and Pb75+Cu200g/mL) were applied to wheat plants. The plants exposed to metal stress without microbial inoculation displayed a reduction in growth. However, when rhizospheric fungal inoculation was introduced, it not only restored plant growth and development but also enhanced the symbiotic relationship between the fungus and the host plant roots under heavy metal stress conditions. The fungal isolates were able to survive concentrations as high as Pb75+Cu200 g/mL of the selected heavy metals. The isolates have the ability to transform HMs, making them unavailable for plant uptake and accumulation, which prevents harm to plants. Apart from their bioremediation properties, some isolates can create secondary metabolites like IAA, GA, ABA, H2O2, Electrolytic leakage, SA, lipid, DPPH, flavonoids, phenols, and proteins, which can stimulate plant growth and make them suitable for use as bio-fertilizers and bio-remediating agents in areas with high levels of heavy metal contamination.

**Keywords:** *Bioreduction, Bioremediation, Heavy metals uptake (lead, copper), Heavy metal tolerance, Rhizospheric fungi, Triticum aestivum L.*

# Responses in Growth Dynamics and Yield Formation of Diverse Rice Varieties Following Vegetative-Stage Leaf Pruning

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## Abstract

Variations in tillering ability among rice cultivars cause differences in resource uptake and assimilate distribution, potentially influencing responses to leaf pruning. However, how vegetative-stage leaf pruning affects growth and yield across rice varieties remains unclear. This study evaluated the effects of leaf pruning on growth and yield formation in five rice varieties using a 5 × 2 factorial experiment in a randomized block design with three replications. Leaves were pruned once, 21 days after planting, by cutting them 25 cm above the soil. Traits were analyzed using two-way ANOVA followed by Duncan's Multiple Range Test (DMRT), and relationships using Pearson's correlation analysis. Pruning increased total tillers (from 20.60 to 25.21) and productive tillers (from 17.25 to 20.55), and delayed flowering and harvest by one day ($P < 0.001$). Variety affected 13 out of 15 traits ($P \leq 0.05$), indicating genetic background in phenotypic variation. Significant pruning × variety interactions occurred for weight per clump, flag leaf length, and flag leaf width, indicating genotype-specific compensatory responses. After pruning, IPB13S retained the largest flag leaves, while Cakrabuana achieved the highest weight per clump. Total and productive tillers were positively correlated, whereas tiller production was negatively correlated with panicle length and flag leaf size, suggesting different resource-allocation strategies during yield formation. Vegetative-stage leaf pruning promoted compensatory growth and altered reproductive development, depending on varietal traits.

**Keywords:** *Agronomic traits, Canopy architecture, Growth dynamics, Leaf pruning, Rice varieties, Vegetative stage.*

# Screening for Submergence Tolerance at the Germination Stage in Rice (*Oryza sativa* L.) Germplasm

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## Abstract

Rice production currently faces environmental challenges and climate change, particularly flash flooding during the main cropping season. This directly impacts seed germination and seedling establishment in direct-seeded rice systems. Germinating rice seeds are sensitive to oxygen deficiency (hypoxia or anoxia), which is necessary for respiration and the growth of the coleoptile and radicle. Oxygen deprivation during this stage can lead to germination failure and significantly reduce crop yield. Therefore, this study aimed to screen 526 rice germplasm accessions, comprising 70 landrace varieties, 120 commercial varieties, 37 exotic varieties, and 299 fast neutron mutant lines for anaerobic germination (AG) capability under hypoxia conditions. Screening was conducted across three submergence simulation systems*: in vitro,* greenhouse, and experimental field, to identify accessions with high anaerobic germination tolerance. For *in vitro* screening, seeds were tested in test tubes filled with deoxygenated boiled water (<1 mg/L dissolved oxygen) arranged in a Completely Randomized Design (CRD, 4 replications, 10 seeds/replication). Germination percentages were recorded on days 4, 7, 10, and 14, and coleoptile lengths were measured on days 7 and 14. Promising accessions (≤30 lines) were advanced to greenhouse screening in soil trays submerged under 10 cm of stagnant water for 14 days. Subsequently, the top 5 accessions were evaluated in field trials (RCBD, 3 replications, 1×1 m subplots, 50 seeds/subplot) under immediate 10 cm submergence post-sowing. *In vitro* and greenhouse evaluations revealed that the cultivars 'Jateh', 'Thanya6401', and 'MU2-2232' exhibited the highest hypoxia tolerance, achieving germination rates >80%, coleoptile lengths >25 mm, and post-drainage survival rates >70%. In field trials, 'MU2-2232' and 'Jateh' demonstrated rapid seedling emergence above the water surface and rapid establishment, achieving >85% survival and a 15–20% increase in grain yield compared to control varieties. Consequently, 'Jateh', 'Thanya6401', and 'MU2-2232' serve as valuable genetic donor resources for breeding programs aimed at improving AG tolerance to support sustainable direct-seeded rice production in flood-prone areas.

**Keywords:** *Anaerobic germination, Rice germplasm, Submergence tolerance, Direct-seeded rice*

# A SRL10-AHP2 Signaling Module Coordinates ROS Homeostasis and Ion Balance for Salt Stress Adaptation in Rice

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## Abstract

Soil salinity severely limits crop growth and yield. Deciphering the molecular basis of salt tolerance is thus critical for enhancing food security. We previously identified the SRL10-CATB module in leaf development and thermotolerance. Here, we reveal an additional, essential role for *OsSRL10* in salt stress adaptation. *OsSRL10* overexpression confers enhanced seedling-stage salt tolerance by promoting ROS scavenging and suppressing $Na^+$ accumulation. Mechanistically, SRL10 physically interacts with the histidine phosphotransfer protein AHP2, a known positive regulator of salt tolerance. Genetic analyses show that the *ahp2/srl10* double mutant exhibits salt sensitivity indistinguishable from the *srl10* single mutant, and *AHP2* overexpression in the *srl10* background only partially rescues the phenotype. Together, these results support a model where SRL10 and AHP2 function cooperatively as a functional complex in salt stress adaption. Our study establishes the SRL10-AHP2 module as a key regulatory node in rice salt stress tolerance, serving as a key resource for both understanding stress adaptation and directly improving salt tolerance in rice through breeding.

**Keywords:** *Rice, Salt stress, SRL10-AHP2 module, ROS scavenging, Ion homeostasis.*

# Effects of Biofang Microbial Consortium on Germination-Ready Rice Seeds: Implications for Weedy Rice Management

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## Abstract

Weedy rice is difficult to manage selectively because of its close biological relationship with cultivated rice and persistence in the soil seed bank. This study investigated the effects of Biofang, a microbial consortium used to accelerate rice straw decomposition, on germination-ready cultivated rice seeds as an experimental model for potential application in weedy rice management. Three experiments were conducted from 2022 to 2024 using a Randomized Complete Block Design with four replications. High-germination seeds of RD41 and RD85 were used, with 100 intact seeds per experimental unit. Seeds were exposed to different Biofang concentrations for 7 or 14 days and subsequently evaluated for their ability to develop into normal seedlings. Data were analyzed by ANOVA and Duncan's Multiple Range Test at $P < 0.05$. Biofang significantly reduced subsequent normal seedling development. In RD41 after 14 days, Biofang treatments produced 28 and 19 normal seedlings per 100 seeds, compared with 50 in the water-soaked control and 75 in the unsoaked control. In RD85, normal seedlings decreased from 77 in the water-soaked control to 61, 51, and 32 with increasing Biofang concentrations. Germination reduction reached approximately 70% after 14 days. These findings suggest that germination-ready rice seeds undergoing water imbibition may become susceptible to microbial degradation. Although seed decomposition was not directly quantified, the results support further evaluation of Biofang using weedy rice seeds under field conditions, particularly during post-harvest flooding and residue decomposition.

**Keywords:** *Weedy rice, Biofang, Microbial consortium, Seed germination, Seed bank*

## Introduction

Weedy rice comprises unwanted *Oryza* populations occurring in rice production systems and is especially problematic in direct-seeded rice. Its close morphological, physiological, and genetic relationship with cultivated rice restricts selective control options within the crop, so effective management generally requires integration of preventive, cultural, mechanical, and chemical tactics (Ferrero, 2003; Nadir et al., 2017; Dilipkumar et al., 2021). Seed shattering and variable dormancy allow weedy rice to replenish and persist in the soil seed bank, making management before crop establishment particularly important.

Seed dormancy in weedy rice varies among populations. Recent work has shown that some weedy rice ecotypes may lack primary dormancy and that post-harvest irrigation can stimulate germination, creating opportunities to reduce the seed bank before the next crop (Zhang et al., 2023). This suggests that the germination-ready fraction of the seed bank may represent a biologically vulnerable stage for non-chemical management.

In Thailand, integrated weedy rice management has emphasized combining preventive, cultural, mechanical, and chemical measures rather than relying on a single control tactic (Promnart et al., 2018). Post-harvest land preparation may include incorporation of rice straw and stubble with water management to promote residue decomposition. Soil microorganisms are central to organic-matter transformation and decomposition processes in agricultural soils (Department of Soil Science, 1987). Biofang is a microbial consortium used to accelerate

decomposition of rice straw and stubble. The original research underlying this paper proposed that microbial activity during residue decomposition may also affect rice seeds that have begun imbibition. Because the experiments did not use weedy rice seeds directly, cultivated rice seeds with high initial germination were used as a reproducible experimental model. The objective was to determine whether exposure to Biofang reduces the subsequent ability of germination-ready rice seeds to develop into normal seedlings and to assess the implications for future weedy rice management research.

## Materials and Methods

Three experiments were conducted during 2022–2024. Seeds were obtained from the Phra Nakhon Si Ayutthaya Rice Research Center, Thailand, as reported in the source study. RD41 was used in Experiments 1 and 2, and RD85 in Experiment 3. Seed lots were less than four months old and had high initial germination. Intact seeds were selected, and each experimental unit contained 100 seeds. All experiments were arranged in a Randomized Complete Block Design (RCBD) with four replications.

Experiment 1 evaluated RD41 after 7 days of exposure. Four treatments were used: unsoaked seed, water-soaked seed, Biofang at 2 g per 4 L water, and Biofang at 4 g per 4 L water. The Biofang solutions in this experiment were prepared 12 h before use to activate the microbial consortium. After 7 days of exposure, seeds were transferred for a further 7-day germination assessment.

Experiment 2 evaluated RD41 after 14 days of exposure using four treatments: unsoaked seed, water-soaked seed, Biofang at 0.5 g per 4 L water, and Biofang at 1.0 g per 4 L water. After exposure, seeds were assessed for germination for 7 days. Experiment 3 used RD85 and five treatments: unsoaked seed, water-soaked seed, and Biofang at 0.75, 1.25, and 2.50 g $L^{-1}$. Seeds were exposed for 14 days and then assessed for germination for 5 days.

Germination response was determined from the number of seeds producing normal seedlings. Seeds that failed to germinate or produced abnormal seedlings were classified as non-germinated for the purpose of the study. Treatment means were analyzed by analysis of variance (ANOVA), and mean separation was performed using Duncan's Multiple Range Test (DMRT) at $P < 0.05$. The experiments quantified subsequent germination performance; seed decomposition itself was not directly measured.

## Results and Discussion

Biofang exposure consistently reduced the number of normal seedlings relative to the corresponding controls. In Experiment 1, unsoaked and water-soaked RD41 produced means of 84 and 83 normal seedlings per 100 seeds, respectively, whereas Biofang treatments produced 48 and 52. The two Biofang treatments were statistically lower than both controls (Table 1). This result indicates that the effect observed after 7 days was associated with Biofang exposure rather than soaking in water alone.

**Table 1. Normal seedlings from RD41 after 7-day exposure and 7-day germination assessment.**

| Treatment | Mean normal seedlings / 100 | DMRT group |
|---|---|---|
| Unsoaked control | 84 | a |
| Water-soaked control | 83 | a |
| Biofang 2 g/4 L | 48 | b |
| Biofang 4 g/4 L | 52 | b |

*CV = 15.9%. Means followed by different letters differ at $P < 0.05$ according to DMRT.*

Extending exposure to 14 days produced a stronger response in RD41 (Experiment 2). The unsoaked control produced 75 normal seedlings and the water-soaked control 50, showing that prolonged water exposure alone affected subsequent germination. Nevertheless, Biofang

further reduced normal seedling development to 28 and 19 seedlings at 0.5 and 1.0 g per 4 L, respectively. All four means were assigned to different statistical groups (Table 2). Relative to the unsoaked control, Biofang at 1.0 g per 4 L reduced normal seedling development by approximately 75%. This is consistent with the approximately 70% maximum reduction reported in the source study.

**Table 2. Normal seedlings from RD41 after 14-day exposure and 7-day germination assessment.**

| Treatment | Mean normal seedlings / 100 | DMRT group |
|---|---|---|
| Unsoaked control | 75 | a |
| Water-soaked control | 50 | b |
| Biofang 0.5 g/4 L | 28 | c |
| Biofang 1.0 g/4 L | 19 | d |

*CV = 14.6%. Means followed by different letters differ at P < 0.05 according to DMRT.*

Experiment 3 tested whether the response was also evident in a second cultivated rice variety. RD85 showed higher baseline germination than RD41, with 88 normal seedlings in the unsoaked control and 77 after water soaking. Biofang produced a clear concentration-related decline to 61, 51, and 32 normal seedlings as concentration increased from 0.75 to 2.50 g $L^{-1}$ (Table 3). Each treatment mean was statistically distinct. The response in RD85 supports the reproducibility of the Biofang effect across the two cultivated rice varieties tested.

**Table 3. Normal seedlings from RD85 after 14-day exposure and 5-day germination assessment.**

| Treatment | Mean normal seedlings / 100 | DMRT group |
|---|---|---|
| Unsoaked control | 88 | a |
| Water-soaked control | 77 | b |
| Biofang 0.75 g/L | 61 | c |
| Biofang 1.25 g/L | 51 | d |
| Biofang 2.50 g/L | 32 | e |

*CV = 9.76%. Means followed by different letters differ at P < 0.05 according to DMRT.*

Taken together, the experiments demonstrate a significant reduction in subsequent normal seedling development following Biofang exposure, with stronger effects after longer exposure and, in RD85, with increasing Biofang concentration. These findings are relevant to seed-bank management because a portion of weedy rice populations can be non-dormant or become germination-ready under favorable moisture conditions (Zhang et al., 2023). Integrated weedy rice management in Thailand similarly emphasizes combining management practices across the production cycle (Promnart et al., 2018). Internationally, practices such as stale seedbeds, flooding, and induced germination have also been used to reduce seed-bank recruitment (Ferrero, 2003; Dilipkumar et al., 2021). Biofang may represent an additional biological component worth evaluating within this pre-planting window.

The mechanism, however, should be interpreted cautiously. The present experiments measured the capacity of treated seeds to produce normal seedlings; they did not directly quantify microbial penetration, tissue degradation, seed viability by biochemical assay, or specific metabolites. The observed pattern is consistent with the hypothesis that germination-ready seeds undergoing imbibition and early germination may become more susceptible to microbial degradation, but alternative mechanisms, including changes in the aqueous environment generated by microbial activity, cannot be excluded. Direct imaging of seed deterioration, viability testing, microbial profiling, and measurements of oxygen, pH, and relevant metabolites would be needed to establish the mechanism.

A second limitation is that cultivated rice, not weedy rice, was used as the experimental material. This choice improved repeatability because certified varietal seed lots were more uniform than field-collected weedy rice populations, but it limits direct inference to weedy rice.

Weedy rice is biologically close to cultivated rice yet exhibits substantial diversity in dormancy and other adaptive traits (Nadir et al., 2017; Zhang et al., 2023). Consequently, the next step should test multiple weedy rice populations with known dormancy status under controlled and field conditions, including treatments with rice straw and stubble to better represent practical land preparation.

In conclusion, Biofang significantly reduced the subsequent formation of normal seedlings from germination-ready RD41 and RD85 seeds. The effect was reproducible across experiments and reached approximately 70% reduction after 14 days in the source study. The results provide proof-of-concept for investigating microbial treatment during post-harvest flooding as a potential approach to target the germination-ready fraction of the weedy rice seed bank. Confirmation of direct seed decomposition and field efficacy using weedy rice seeds is required before agronomic recommendations can be made.

## Acknowledgements

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## References

1. Department of Soil Science. (1987). Introduction to Soil Science. Faculty of Agriculture, Kasetsart University, Bangkok, Thailand. 673 pp. [In Thai].
2. Dilipkumar, M., Kumar, V., Song, B.K., Olsen, K.M., Chuah, T.S., Ahmed, S., & Qiang, S. (2021). Weedy rice (Oryza spp.). In B.S. Chauhan (Ed.), Biology and Management of Problematic Crop Weed Species (pp. 285–309). Academic Press. https://doi.org/10.1016/B978-0-12-822917-0.00007-0
3. Ferrero, A. (2003). Weedy rice, biological features and control. In R. Labrada (Ed.), Weed Management for Developing Countries: Addendum 1. FAO Plant Production and Protection Paper 120 Add. 1. Food and Agriculture Organization of the United Nations, Rome.
4. Nadir, S., Xiong, H. B., Zhu, Q., Zhang, X. L., Xu, H. Y., Li, J., Dongchen, W., Henry, D., Guo, X. Q., Khan, S., Suh, H. S., Lee, D. S., & Chen, L. J. (2017). Weedy rice in sustainable rice production: A review. Agronomy for Sustainable Development, 37, 46. https://doi.org/10.1007/s13593-017-0456-4
5. Promnart, P., Kukham-oo, A., Inthalaeng, S., Ruensuk, N., Mongkolbanjong, P., Inthalaeng, W., Ruechaikham, C., Inman, A., Changsri, R., Boonyanupong, O., Paothong, K., Wongsupthai, S., Chankham, S., & Khoksungnoen, O. (2018). Integrated Weedy Rice Management (6th ed.). New Thammada Printing (Thailand) Co., Ltd., Thailand. 31 pp. [In Thai].
6. Zhang, Y., Gao, H., Xu, J., Liu, Q., & Dong, L. (2023). Weedy rice (Oryza sativa L.) seed dormancy features and potential usage for management. Crop Protection, 169, 106240. https://doi.org/10.1016/j.cropro.2023.106240

# Development of a Rapid Test Kit for the Detection of Bacterial Panicle Blight in Rice

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## Abstract

Bacterial panicle blight (BPB) in rice significantly impacts grain yield and quality by causing floret and panicle discoloration, shriveled or unfilled grains, and reduced seed germination. The pathogen can be transmitted via infected seeds. Conventional methods for diagnosing the pathogen are time-consuming and require specialized equipment. Therefore, this research aimed to develop a rapid test kit using an immunochromatographic assay for screening the pathogen in rice seeds, tailored for field-level applications. Preliminary evaluations showed that the developed test kit had a limit of detection of $10^4$ cells/mL for the causal bacterial pathogen and could detect seed-borne infection in rice seed samples diluted at 1:4,000 (w/v) in extraction buffer. Testing on 25 rice seed samples collected from fields in Suphan Buri and Nan provinces revealed that 4 samples of the RD113 variety tested negative, whereas 15 samples of the RD119 variety and 6 samples of upland rice tested positive. These diagnostic results were consistent with standard detection methods, including ELISA and PCR. The findings indicate that the developed rapid test kit provides accurate and reliable detection of bacterial panicle blight in rice seeds, yielding results within 15 minutes. Consequently, it holds high potential for on-site field screening and effective disease management.

**Keywords:** *Bacterial panicle blight, Immunochromatographic assay, Rice seeds, Screening*

# Effect of Water Stress on Allelopathic Activity and Growth of Rice in Southern Thailand

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## Abstract

Global warming brings temperature rise including drought and flooding in some areas. This research studied the effect of water stress on allelopathic activity of six rice cultivars, i.e. Khao Dawk Mali 105, Phathum Thani 1, Chai Nat 1, Sang Yod Muang Phattalung, Leb Nok Pattani and Dawk Kha. Five soil relative water content (RWC) levels were used, i.e. 25%, 50%, 75%, 100% (water at soil surface) and 1 cm water above soil level. Rice plants were grown for three weeks and allelopathic activity was tested using water extraction method on lettuce seeds. Results showed that rice plants had lowest growth at 25% soil RWC but highest growth at 100% soil RWC and 1 cm water above soil surface. Moreover, rice plants had highest root/shoot length ratio at 25% soil RWC followed by 50%, 75%, 100% and 1 cm water above soil surface, respectively. Lettuce seedings had different allelopathic responses upon receiving water extracts from different rice cultivars. Lettuce seedings receiving extract from Dawk Kha cultivar were short and thick while those receiving extract from Lab Nok Pattani cultivar were long and thin with low dry weight. Rice plants receiving 1 cm water above soil surface had lowest lettuce seedling inhibition percentages of germination, shoot length, root length and average inhibition percentage, while 25-100% soil RWC results were not significantly different. This research can be further applied for using allelopathic rice cultivars to control weeds.

**Keywords:** *Rice, Southern Thailand, Allelopathy, Water stress, Soil relative water content*

# Development and Characterization of Polyclonal Antiserum for Serological Detection of *Burkholderia glumae*, the Causal Agent of Bacterial Panicle Blight of Rice

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## Abstract

*Burkholderia glumae*, the causal agent of bacterial panicle blight (BPB) of rice, is an important seed-borne pathogen that can adversely affect seed quality and rice yield. Rapid and accurate detection of *B. glumae* is essential for effective disease management and the prevention of pathogen dissemination through infected seeds. In this study, polyclonal antiserum against *B. glumae* was produced and evaluated for its sensitivity and specificity using an enzyme-linked immunosorbent assay (ELISA). The antiserum exhibited antibody titers ranging from 16,000 to 2,048,000. For detection of pure bacterial cultures, the antiserum at a dilution of 1:5,000 detected *B. glumae* at a minimum concentration of $10^5$ cells/mL, demonstrating its suitability for sensitive serological detection. Specificity testing was performed against five bacterial taxa, including *Enterobacter* sp., *Pectobacterium carotovorum, Xanthomonas citri* pv. *glycines, Xanthomonas oryzae* pv. *oryzae*, and *Agrobacterium* sp. No cross-reactivity was observed with any of the tested non-target bacteria, indicating high specificity of the antiserum toward *B. glumae*. These preliminary results demonstrate that the developed polyclonal antiserum possesses suitable sensitivity and specificity for the serological detection of *B. glumae*. The antiserum therefore has strong potential for further development into a rapid and cost-effective diagnostic kit for bacterial panicle blight of rice, which could facilitate early detection and support disease management and seed health monitoring.

**Keywords:** *Burkholderia glumae, Bacterial panicle blight, Rice, Polyclonal antiserum, ELISA, Serological detection, Diagnostic kit*

# Rice–Barnyard Grass (*Echinochloa crus-galli* (L.) P.Beauv.) Coculture Reduces Plant Growth and Enhances the Allelopathic Activity of Root Exudates

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## Abstract

Barnyard grass (*Echinochloa crus-galli* (L.) P.Beauv.) is one of the most competitive weeds of rice (*Oryza sativa* L.), and part of its interference with rice may be mediated by allelopathy. This study aimed to evaluate the effects of rice–barnyard grass interaction on plant growth and to assess the allelopathic potential of their root exudates. Rice cultivar Dawk Kha and barnyard grass were grown hydroponically for three weeks in monoculture and coculture (20 plants per container; four replicates per treatment). Shoot and root lengths of both species were then measured, and the culture solutions were tested on lettuce (*Lactuca sativa* L.) seeds, with fresh nutrient solution as the control. Lettuce germination, shoot length, root length and dry weight were recorded after five days. Coculture significantly reduced the shoot and root lengths of rice (22.01% and 25.94% reduction, respectively) and barnyard grass (29.35% and 35.00% reduction, respectively) compared with monoculture ($p < 0.05$). The coculture solution caused the strongest inhibition of lettuce germination (57.75%), shoot length (43.82%), root length (55.33%), and dry weight (66.03%) followed by solutions from barnyard grass monoculture (42.25%, 30.65%, 42.50% and 62.21%, respectively) and rice monoculture (19.01%, 11.40%, 15.97% and 50.18%, respectively). These preliminary findings indicate that rice–barnyard grass interaction suppresses the growth of both species and increases the phytotoxicity of the root-zone solution, possibly through enhanced release of allelochemicals. Chemical characterization of exudates and gene expression analysis will clarify the underlying mechanisms.

**Keywords:** *Echinochloa crus-galli, Oryza sativa, Allelopathy, Root Exudates, Plant–Plant Interaction*

# Bacteria Associated with the Cause of Rice Seed Rot

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## Abstract

Rice seeds infected with bacterial pathogens are important sources of primary inoculum and a means of dissemination to new areas. The spread of seed borne pathogens has a negative effect on rice yield. *Burkholderia glumae* (bacterial grain rot), *Xanthomonas oryzae* pv. *oryzae* (bacterial leaf blight), and *Acidovorax avenae* subsp. *avenae* (bacterial brown stripe) are major seedborne bacterial pathogens of rice. In 2024, rice seeds of the cultivars RD85 and RD111 with low germination rates were randomly collected from Suphan Buri and Chai Nat provinces, Thailand, to investigate the causes of poor germination. Bacteria associated with rice seed rot were isolated and characterized. The bacterial isolates were Gram-negative, grew on media containing 3% NaCl, hydrolyzed gelatin, and were positive for the oxidase test, but were unable to hydrolyze starch. Pathogenicity tests based on Koch's postulates using rice seedlings produced symptoms characteristic of bacterial panicle blight caused by *Burkholderia glumae*. PCR amplification using the GL-13f/14r primers produced positive results. Furthermore, analysis of the 16S rRNA gene using the 27F/1492R primers showed that the nucleotide sequences shared 100% identity and 100% query coverage with *B. glumae* strain PA22.1 (EF193638.1), isolated from rice in the Philippines, and strain GR20007 (PV760244.1), isolated from rice in China, with an E-value of 0.0. Based on the morphological, biochemical, pathogenicity, and molecular characteristics, the results indicate that *Burkholderia glumae* is associated with rice seed rot and may contribute to reduced seed germination.

**Keywords:** *Rice, Bacterial Panicle Blight, Burkholderia glumae*

# First Record of *Oomyzus scaposus* (Hymenoptera: Eulophidae), a Parasitoid of Coccinellids in Rice and Vegetable Fields in Padang, Indonesia

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## Abstract

Coccinellids (Coleoptera: Coccinellidae) are important predators in rice and vegetable agroecosystems, yet information on their associated parasitoids in Indonesia remains limited. This study investigated the occurrence of coccinellid parasitoids in agricultural areas of Padang City, Indonesia. All developmental stages of coccinellids were collected from rice, eggplant, chili, and long bean fields using hand picking technique. Sampling followed a diagonal pattern within fields measuring 10 × 20 m. Collected specimens were reared at the Insect Bioecology Laboratory, Faculty of Agriculture, Universitas Andalas, Padang, Indonesia, to monitor parasitoid emergence. Emerging parasitoids were observed using a Zeiss primostar 3 trinocular microscope at magnifications of 40×, 100×, and 400×, and individuals emerging from each host were counted. The study found *Oomyzus scaposus* (Hymenoptera: Eulophidae) emerged from field-collected coccinellid pupa, with a mean of 17.64 individuals per parasitized pupa. This finding represents the first record of *O. scaposus* parasitizing coccinellids in Indonesia, expanding its known geographical distribution and documenting its host associations. Further research is needed to assess its effects on coccinellid survival, population dynamics, and biological control potential.

**Keyword:** *Exploration, Lady beetle, Natural enemies, Parasitism rate, Pupa*

# Adoption of Bioproducts for Rice Disease Management through Technology Transfer and Community-Based Production

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## Abstract

Bacteria genus *Bacillus* are widely used as biological control agents for plant diseases because of their potential to suppress plant pathogens and their applicability in plant disease management. Rice Department (RD) has developed a rice disease management technology based on the antagonistic bacteria *Bacillus amyloliquefaciens*. However, the production of bioproduct to meet farmers' needs remains a major constraint. This project aimed to disseminate the RD's antagonistic bacterial technology to farmers within community rice center networks and to develop a simplified production method to facilitate technology transfer and promote its adoption at the community level. Demonstration plots were established to compare the RD's technology with farmers' conventional practices during the dry-season 2024/2025 in three provinces: Sakon Nakhon, Chiang Rai, and Chiang Mai. Technology Verification Experiments (TVE) were conducted using 12 plots per province. Disease incidence and severity were assessed at different rice growth stages, and dirty panicle symptoms were evaluated before harvest. Grain yields were standardized to 14% moisture content. In addition, a questionnaire survey involving 150 farmers, including project participants and other farmers in the surrounding areas, was conducted to assess awareness of and acceptance of the technology. The results indicated that brown spot was a major rice disease observed in the study areas during the dry season. Disease incidence and severity tended to be lower in plots using the RD's technology than in those managed according to farmers' conventional practices. However, the differences were not statistically significant. Comparison of yield differences between the two treatments showed that plots using the Rice Department's technology produced average yield increases of 153, 23, and 94 kg/rai in Sakon Nakhon, Chiang Rai, and Chiang Mai, respectively. The corresponding increases in farm income were 584, 755, and 144 baht/rai, respectively. Furthermore, 90% of farmers reported increased profit per rai. The assessment of technology awareness and acceptance indicated that farmers had become more aware of the benefits of biological agents for rice disease management and had accepted the RD's antagonistic bacterial technology. Eighty percent of farmers reported an increased likelihood of using biological agents, while 75% reported that they were able to produce biological agents for their own use after the project ended. These findings suggest that demonstration-based technology transfer, combined with simplified production methods, has the potential to promote the adoption of biological control technologies within community rice center networks. Nevertheless, further evaluations across multiple growing seasons and locations are needed to confirm the technology's effectiveness in disease management, its effects on rice yield, and its economic benefits.

**Keywords:** *Bacillus amyloliquefaciens, Biological control agents, Brown spot disease, Rice disease management, Technology transfer*

# Stomatal Haplotype Diversity and Longitudinal Phenomics Reveal Soil-Specific Drought Resilience Strategies in Rice

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## Abstract

Water scarcity threatens global rice production, necessitating climate-resilient cultivars. This study evaluates eight rice varieties across contrasting soil textures (silty clay versus sandy loam) and water regimes (well-watered control versus a managed drought of -25 kPa) to understand their adaptive strategies. Whole-genome sequencing identified haplotypes across 19 stomatal regulatory genes, grouping the varieties into three main clusters based on their genetic fingerprints. Morphological analysis showed that clay soil maximized growth, with variety HCS achieving peak biomass. Conversely, sandy soil suppressed growth, where EL06 and EL14 performed poorly, while PTT1 and HNL maintained stable tiller production and leaf width. Under severe sandy drought, EL06 and EL14 suffered severe photo-inhibition and premature senescence. In contrast, PTT1 and HNL successfully maintained high photochemical integrity and stay-green traits. Gas exchange evaluations revealed that HCS and EL14 acted as highly productive "water-spenders" in clay but suffered sharp photosynthetic declines in sand. Meanwhile, PTT1 and HNL employed proactive stomatal control to preserve internal moisture and achieve highly stable water-use efficiency (WUE). Multivariate analysis separated these diverging strategies by metabolic vigor traits under optimal conditions versus photochemical health traits under severe stress. Ultimately, biomass stability relies on distinct pathways: metabolic momentum (driven by high transpiration and photosynthesis) is advantageous in heavy clay soils, whereas photochemical resilience and stomatal plasticity (characterized by stable QYmax and high WUE) are essential in light, sandy soils.

**Keywords:** *Rice, Soil texture, Drought, Morphology, Physiology and Phenomics*

# Identification of Mating Types of *Pyricularia oryzae* Isolated from Rice Fields in Phrae Province, Thailand

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## Abstract

Rice blast, caused by *Pyricularia oryzae*, is one of the most destructive diseases affecting rice production in Thailand. Sexual reproduction is a key mechanism driving genetic diversity and the emergence of new virulent strains in fungal pathogens. However, the teleomorphic stage of *P. oryzae* has not been reported under natural conditions in Thailand. Therefore, understanding the mating type composition of local pathogen populations is important for assessing their potential for sexual recombination. This study investigated the mating types of 40 *P. oryzae* isolates collected from rice blast screening fields at the Phrae Rice Research Center, Thailand, between 2020 and 2024. Mating types were determined using PCR-based markers specific to the *MAT1-1* and *MAT1-2* loci and verified through in vitro four-point culture assays. Paired cultures were examined for hyphal interactions and the production of sexual reproductive structures, including perithecia, asci, and ascospores. PCR analysis revealed that all isolates carried the *MAT1-2* mating type. Consistent with these results, no compatible mating reactions or sexual structures were observed in the culture assays. The combined molecular and physiological evidence indicates that the studied *P. oryzae* population consists exclusively of a single mating type. The absence of mating type diversity among the sampled isolates suggests that sexual recombination is currently unlikely within this local population. This study provides baseline information for monitoring population dynamics of *P. oryzae* and supports the development of sustainable rice breeding strategies for durable blast resistance.

**Keywords:** *Rice blast disease, Pyricularia oryzae, Mating type*

# Evaluation of Blast Resistance in NSTDA Newly Released Rice Varieties against Six *Magnaporthe oryzae* Isolates

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## Abstract

Rice blast, caused by *Magnaporthe oryzae*, is a major constraint to rice production, especially in rainfed ecosystem which takes up more than 80% of rice growing area in Thailand. Blast resistance should be included in any modern breeding program. This study evaluated blast resistance in six NSTDA newly released rice varieties against six geographically diverse *M. oryzae* isolates. Four genotypes were selected by two SNP markers associated with resistance position on chromosomes 1 and 11, while two genotypes lack targeted alleles. Four check varieties were included. Twenty-one-day-old seedlings were spray-inoculated with fungal conidia, and disease severity was assessed at 14 days after inoculation using a 0–6 lesion scoring scale. Blast responses varied among genotypes and isolates. All four marker-selected genotypes exhibited resistant to moderately resistant responses across the six inoculates. Hom Chonlasit 2 showed the most consistent resistance, with mean lesion scores ≤ 1.0. Despite lacking the targeted alleles, Suvarnabhumi 1 showed resistant to moderately resistant responses. Biotec 1 was susceptible with a mean score of 6.0 against isolate PYO61008 collected from Phayao province, indicating that there might be risk of infection if grown in the Northern region of Thailand. The results suggest that these promising new varieties should perform well in most growing areas in Thailand, however actual field responses will determine farmers' adoption in the future. This also highlights the importance of combining marker-assisted selection with multi-isolate phenotypic screening.

**Keywords:** *Rice, breeding, Blast, Resistance, SNP marker*

# Effects of Simulated Martian Gravity and Regolith on the Physiology and Stress Responses of Rice (*Oryza sativa* L.)

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## Abstract

As human space exploration advances toward long-term missions to Mars, developing sustainable food production systems beyond Earth has become increasingly important. However, extraterrestrial environments present challenges to plant growth, particularly altered gravity and unfamiliar growing substrates. This study investigates the early growth and physiological responses of rice (*Oryza sativa* L. cv. Pathum Thani 1) cultivated in Martian regolith simulant under normal gravity and simulated microgravity conditions using a three-dimensional clinostat. Plant growth, oxidative stress responses, and the expression of antioxidant-related genes were evaluated to assess the effects of these conditions. Shoot height was significantly reduced by 28.1% under simulated microgravity compared with the control. Root length and germination percentage were marginally reduced by 38.2% and 10.8%, respectively. DAB staining showed no consistent increase in $H_2O_2$ accumulation under simulated microgravity. However APX gene expression increased by approximately 95% under simulated microgravity compared with the control. These findings provide insights into how rice responds to simulated extraterrestrial conditions and highlight the importance of integrating physiological and molecular approaches to understand plant adaptation. Further investigations will contribute to developing strategies for sustainable crop production in future space exploration missions.

**Keywords:** *3D clinostat, Simulated microgravity, Oxidative stress, Mars regolith simulant, Rice*

# Fine-tuning *OsGTL1* Expression via Multiplex CRISPR/Cas9 Promoter Editing Modulates Stomatal Density and Water-use Efficiency in rice

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## Abstract

*GT2-LIKE1* (*GTL1*) is predicted to regulate stomatal development and drought response in rice (*Oryza sativa* L.), yet its regulatory relationships with putative targets like S*tomatal Density and Distribution 1 (SDD1)* is not fully understood. We employed a promoter-targeted strategy to fine-tune gene expression, addressing the inability to produce fertile seeds in complete knockout lines. We designed a multiplex tRNA-based CRISPR/Cas9 system utilizing seven single-guide RNAs (sgRNAs) targeting ~1,500 bp upstream of the *OsGTL1* transcription start site. Despite high genetic chimerism (35%) in the $T_0$ generation, stable, transgene-free lines with various promoter modifications, including large and small deletions, single-base insertions and deletions, and inversions, were successfully recovered in following generations. Two recessive promoter-edited lines with the large deletions showed downregulated *OsGTL1* expression in developing leaves. This downregulation led to arrested mother cells from completing symmetrical division, significantly reducing stomatal density. Lower stomatal density maintained net photosynthetic rates while improving water-use efficiency (WUE) during tillering and under drought during the reproductive stage. However, this revealed an agronomic trade-off in which edited lines had lower yield components than wild-type plants under normal conditions, while yield reductions under reproductive drought were less severe in the edited lines. These results demonstrate that modifying *OsGTL1* expression optimizes stomatal patterning and water-use efficiency, while highlighting a critical trade-off between water conservation and yield penalties depending on water availability.

**Keywords:** *CRISPR/Cas9, Drought, Rice, Stomata, Food security*

# Assessment of Genetic Diversity of *Pyricularia oryzae* from Thailand Using Genomic Sequences of Avirulence Genes (*AVR-Pi9, AVR-Pik, AVR-Pita*)

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## Abstract

Rice blast fungus (*Pyricularia oryzae*), widely distributes and damages rice-growing areas around the world, it is one of the most dangerous threats to the world's food security. The genetic diversity of the rice blast population in Thailand was investigated based on the genomic sequences of three avirulence genes, *AVR-Pi9*, *AVR-Pik*, and *AVR-Pita1*. Sixty rice blast isolates were collected from rice-growing areas around Thailand. Gene-specific primers were used to amplify and sequence these avirulence genes. The results showed that *AVR-Pi9*, *AVR-Pik*, and *AVR-Pita1* were detected in all, 57 and 23 isolates, respectively. Different avirulence genes have different levels of genetic variation: *AVR-Pi9* and *AVR-Pik* genes have relatively low genetic diversity. In contrast, the *AVR-Pita1* gene has high genetic diversity. In two rice blast isolates, *AVR-Pi9* sequences showed evidence indicating a potential movement of this isolate from Japan to Thailand. Three *AVR-Pik* alleles were found, including *AVR-PikA* (3.51%), *AVR-PikD* (71.93%), and isolates with two copies of *AVR-PikD* and *AVR-PikF* (24.56%). *AVR-PikA* and *AVR-PikF* are virulent to Thai rice variety Jao Hom Nin. Six haplotypes of *AVR-Pita1* were identified with one deletion and 12 amino acid substitutions. These genome adaptations will lead the pathogen to overcome host resistance. The finding provided useful information to predict the possible future adaptation of Thai rice blast isolates and lead to the development of a rice-blast-resistant breeding program.

**Keywords:** *Avirulence gene, Genetic variation, Resistance gene, Rice blast disease*

# Identification and Functional Characterization of Bacterial Leaf Blight Resistance Candidate Gene Using CRISPR/Cas9 Technique

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## Abstract

Rice is an important crop for human consumption around the world. Its production can be reduced by bacterial leaf blight, caused by *Xanthomonas oryzae* pv. oryzae (*Xoo*). One of the most important 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 CRISPR/Cas9. sgRNAs were designed to target the first exon of a resistant gene, *LOC_Os11g40840*, which is predicted to encode a receptor-like protein kinase 2 precursor. The constructs were introduced into Nipponbare rice variety. One editing line (Nipponbare 71/1) showed 1 bp deletion, and a pathogenicity assay will be performed in the future.

**Keywords:** *Bacterial Leaf Blight, CRISPR/Cas9, Gene Editing, Disease Resistance, Rice (Oryza sativa)*

# Development of a CRISPR-Cas12a-Based Detection Method for Identification of *AVR-Pik* Alleles in Rice Blast Fungus

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## Abstract

The rice blast pathogen, *Magnaporthe oryzae*, possesses avirulence (AVR) genes that play an important role in determining fungal pathogenicity and interactions with rice resistance genes. Identification of these AVR genes is essential for the development and improvement of rice varieties with disease resistance. Among them, *AVR-Pik* is highly polymorphic and comprises six known allelic variants: *AVR-PikA*, *AVR-PikB*, *AVR-PikC*, *AVR-PikD*, *AVR-PikE*, and *AVR-PikF*. Conventional approaches for identifying AVR genes and their alleles include pathogenicity assays using rice near-isogenic lines (NILs), followed by PCR amplification and DNA sequencing. However, these approaches are relatively labor-intensive and time-consuming. Therefore, this study aimed to establish a simple fluorescence-based detection approach for differentiating *AVR-Pik* alleles using the CRISPR-Cas12a system. Allele-specific CRISPR RNAs (crRNAs) were designed to recognize the corresponding *AVR-Pik* variants. The detection reaction consisted of crRNA, Cas12a nuclease, a fluorophore-quencher (FQ)-labeled reporter, and target DNA. The reactions were incubated at 37 °C for 5 minutes. Fluorescence signals were subsequently observed using an LED transilluminator and quantified with a real-time PCR instrument. The results demonstrated that different *AVR-Pik* alleles could be distinguished through specific combinations of crRNAs. The detection sensitivity reached 3 ng/μL of target DNA. Further development is underway to improve the assay for field applications, including simplified DNA extraction, recombinase polymerase amplification (RPA)-assisted target amplification, and optimization of the CRISPR-Cas12a detection system.

**Keywords:** *Rice blast fungus, AVR-Pik alleles, CRISPR-Cas12a, Fluorescence detection, Molecular diagnostics.*

# Effect of *Chlamydomonas reinhardtii* as a Biostimulant Inducing Plant Growth and Plant Defense Against *Magnaporthe oryzae* in Rice

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## Abstract

Rice blast disease, caused by *Magnaporthe oryzae*, poses a significant threat to global rice production, leading to annual yield losses of 10%–30% and, under favorable conditions, potentially resulting in total crop failure. The necrotic lesions induced by the disease reduce photosynthetic efficiency, thereby compromising food security worldwide. As concerns over the environmental and health impacts of chemical fungicides continue to grow, farmers are increasingly seeking sustainable alternatives. Among these, algae-based biostimulants have emerged as promising, environmentally friendly options. These biostimulants are rich in bioactive compounds, including polysaccharides, phytohormones, polyunsaturated fatty acids (PUFAs), and amino acids, which not only promote plant growth and yield but also enhance plant defense mechanisms. One of their key modes of action involves the induction of damage-associated molecular patterns (DAMPs), which can trigger systemic acquired resistance (SAR) in plants. In this study, we investigated the potential of *Chlamydomonas reinhardtii* strain cc-4414 a well-established model organism for photosynthesis as a biostimulant. This strain is particularly promising due to its high content of polysaccharides and phytohormones, which are known to act as elicitors of DAMPs and phytohormone to induced plant growth. *C. reinhardtii* was cultured in Tris-Acetate-Phosphate (TAP) medium for seven days. Rice leaves were then treated with the algal extract, incubated for one hour, and subsequently inoculated with M. oryzae spores ($1 \times 10^5$) using the punch inoculation method. The inoculated leaves were maintained under dark, humid conditions, and disease symptoms were monitored over a five-day period. Lesion length, width, and area were measured across four treatment groups. Preliminary results revealed significant differences in lesion parameters among treatments, suggesting that *C. reinhardtii* extract may be effective in mitigating the symptoms of rice blast disease. This research aligns with Sustainable Development Goal (SDG) 2: Zero Hunger, particularly Target 2.1, by exploring innovative, sustainable, and non-toxic strategies to protect rice crops. The findings underscore the potential of algae-based solutions to enhance agricultural resilience and support global food security.

**Keywords:** *Algae-biostimulant, Chlamydomonas reinhardtii, Oryza sativa, Magnaporthe oryzae, Plant defenses responses*

# Silicon-Induced Resistance in Thai Rice (*Oryza sativa* L. cv. Niaw Dam Chor Mai Pai 49): An Eco-Innovative Strategy for Sustainable Aphid Management

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## Abstract

The rusty plum aphid (*Hysteroneura setariae*) is an important sap-sucking insect that threatens rice production. Silicon (Si) supplementation has emerged as a promising strategy for enhancing plant resistance to insect pests while reducing reliance on chemical pesticides. This study evaluated the effects of calcium silicate ($Ca_2SiO_4$) supplementation on silicon accumulation, aphid infestation, and defense-related enzyme activities in Thai rice (*Oryza sativa* L. cv. Niaw Dam Chor Mai Pai 49). Rice plants were amended with 0%, 2%, and 4% $Ca_2SiO_4$ (w/w), followed by infestation with 20 adult aphids per plant. Silicon accumulation in leaf tissues was examined using scanning electron microscopy coupled with energy-dispersive X-ray spectroscopy (SEM–EDS), while peroxidase (POD), polyphenol oxidase (PPO), and phenylalanine ammonia-lyase (PAL) activities were evaluated at 0, 24, and 72 h after infestation. Silicon supplementation significantly reduced aphid infestation from 65% in untreated plants to 18% and 10% in plants treated with 2% and 4% $Ca_2SiO_4$, respectively. SEM–EDS analysis revealed increased silica deposition in leaf tissues, with 4% $Ca_2SiO_4$ producing more than twice the silicon content of the control. Furthermore, Si-treated plants exhibited enhanced POD, PPO, and PAL activities, suggesting activation of biochemical defense responses. These findings indicate that silicon supplementation enhances rice resistance to *H. setariae* through both physical reinforcement by silica deposition and activation of plant defense mechanisms. Calcium silicate application therefore represents a promising eco-innovative approach for sustainable aphid management and environmentally friendly rice production.

**Keywords:** *Silicon supplementation, Calcium silicate, Rice resistance, Hysteroneura setariae, Sustainable pest management*

# Wall-Associated Kinase as a Key Regulator Controlling Bacterial Leaf Streak Resistance in Rice

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## Abstract

Bacterial leaf streak, caused by *Xanthomonas oryzae* pv. *oryzicola* (*Xoc*), is one of the devastating bacterial diseases that impose significant annual threats to global rice production. Although the deployment of host plant resistance is the most sustainable management strategy, the characterized resistance and defense-related genes against BLS remains limited. In this study, a combination of whole-genome resequencing and QTL-seq approach were employed in a $F_2$ mapping population derived from a cross between two Thai rice varieties, Homcholasit (susceptible), and Niaw Dam Chaw Mai Pai 49 (resistant). Phenotypic screening was conducted using the virulent Thai *Xoc* isolate, 1NY2-2. The QTL-seq approach identified a major quantitative trait loci (QTL) region on chromosome 2, encompassing 16,689 single nucleotide polymorphisms (SNPs) and 1,883 annotated genes. Expression analysis by RNA-seq was performed on SNPs within the 200 kb spanning region of the peak SNP and a member of wall-associated kinase family, *OsWAK16* has most significant and highest expression fold change between two parental lines. Marker trait association analysis also showed that *OsWAK16* is responsible for BLS resistance in this population. To validate the function of this candidate, CRISPR/Cas-9 mediated knockout was developed. Two independent *oswak16* mutant lines exhibited significantly enhanced susceptibility and more severe disease symptoms upon *Xoc* inoculation compared to wild type. Collectively, this study demonstrates that *OsWAK16* is a novel resistance gene providing a valuable genetic resource for molecular breeding programs aimed at improving rice resilience against BLS.

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

# From QTL to Function: Insights into Rice Root Penetration

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## Abstract

Soil compaction restricts root growth and limits crop productivity, highlighting the need to understand the genetic and molecular mechanisms underlying root penetration ability (RPA). This study integrated quantitative trait locus sequencing (QTL-seq), CRISPR/Cas9-mediated gene editing, and transcriptome analysis to investigate rice root responses to compacted conditions. QTL-seq analysis of an $F_2$ population derived from Dharia (high RPA) and PTT1 **(**low RPA) identified a significant SNP with a maximum ΔSNP-index of approximately 0.7 on chromosome 3 containing one candidate gene, *OsPYL6*, encoding an abscisic acid (ABA) receptor. Functional characterization revealed that two independent *ospyl6* knockout lines exhibited significantly higher RPA than the wild type under compacted gel and soil conditions ($P < 0.05$), with *ospyl6-2* reaching approximately 80% RPA in compacted gel. Furthermore, *ospyl6* mutants displayed reduced sensitivity to exogenous ABA, supporting the involvement of ABA signaling in regulating root growth under mechanical impedance. RNA sequencing of root tips from Dharia and PTT**1** under control and compacted conditions revealed genotype-dependent transcriptional responses. Functional analyses highlighted contrasting regulation of translation, microtubule-based processes, cell-cycle functions, and reactive oxygen species metabolism between the genotypes. Growth-associated programs were comparatively less suppressed in Dharia, while several jasmonate-related genes showed stronger induction in PTT1; ethylene-response gene expression also differed between genotypes. Together, these findings identify ABA signaling and cell growth-related pathways as important components of rice root responses to compaction and provide potential targets for improving root adaptation to mechanically constrained soils.

**Keywords:** *Rice, Soil compaction, Root penetration ability, OsPYL6, Transcriptome analysis*

# The Unconventional Resistance Protein PTR Recognizes the *Magnaporthe oryzae* Effector AVR-Pita in an Allele-Specific Manner to Confer Blast Resistance in Rice

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## Abstract

Blast disease, caused by the fungus *Magnaporthe oryzae*, is a major threat to global rice production. Resistance genes are crucial tools for sustainable disease control. For decades, *Pi-ta* resistance was attributed to the NLR protein NLR Pi-ta through direct binding to the fungal effector AVR-Pita. However, this long-standing paradigm was challenged by the discovery of *Ptr*, an unconventional resistance gene encoding a membrane protein with an intracellular Armadillo (ARM) repeat domain. Here, using CRISPR/Cas9 knockout and RNAi knockdown lines in rice, we demonstrate that AVR-Pita recognition and both *Pi-ta* and *Pi-ta2* resistances rely solely on Ptr, whereas NLR Pi-ta is entirely dispensable and has no role in AVR-Pita detection. Furthermore, we show that different *Ptr* alleles exhibit distinct recognition specificities. The *PtrA* allele confers broad-spectrum *Pi-ta2* resistance by recognizing all natural variants of AVR-Pita. In contrast, the *PtrB* allele confers *Pi-ta resistance* with a narrower spectrum. By analyzing natural *M. oryzae* isolates and functional mutant strains, we identified a single non-synonymous polymorphism at position 191/192 (tyrosine to cysteine, Y191C) in AVR-Pita that enables fungal evasion specifically from PtrB-, but not PtrA-mediated resistance. Our findings establish Ptr as the true *Pi-ta* and *Pi-ta2* resistance gene and clarify the mechanisms of allele-specific pathogen recognition by an unconventional plant immune receptor. This work provides critical insights and molecular tools for precision breeding and CRISPR-based engineering of durable blast resistance in rice.

**Keywords:** *Resistance gene, AVR Effector, Allele-specific recognition, Rice blast disease, Plant immunity*

# Phenotypic Screening of Rice Genotypes for Brown Planthopper Resistance: A Foundation for Novel QTL Identification

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## Abstract

The brown planthopper (*Nilaparvata lugens* Stål; BPH) constraints rice production through phloem feeding and virus transmission. Novel sources of BPH resistance are therefore essential for molecular breeding and novel QTL identification, yet remain limited. In this study, five diverse rice genotypes were evaluated for BPH resistance at the early seedling stage using the Standard Seedbox Screening Test. Damage was scored according to the Standard Evaluation System for Rice (SES; 0-9 scale) through five assessments at 48-hour intervals, beginning when the susceptible check, Taichung Native 1 (TN1), exhibited complete damage (SES score 9), producing a five-point longitudinal damage record. The popular cultivar IR64 showed a moderately resistant response (mean score: 4.13). In contrast, Rathu Heenati, Biotec1 (A1), and HomMali-803-2 exhibited resistant responses, with mean scores ranging from 1.53 to 2.07 and no significant differences among them. Under continued BPH infestation, the genotypes showed differential damage progression. Rathu Heenati showed the lowest relative damage progression (5.04 ± 0.96). However, the temporal damage progression scores of two Thai rice genotypes, Biotec1 (A1) and HomMali-803-2, developed by the Rice Science Center, Kasetsart University, Kamphaeng Saen, were statistically non-significant compared with Rathu Heenati, a widely used donor in BPH resistance breeding and QTL-seq studies. Therefore, further molecular characterization of Biotec1 (A1) and HomMali-803-2 may identify novel BPH resistance sources. These genotypes could serve as potential parents for QTL identification and the development of improved BPH-resistant rice lines, contributing to global food security under increasing biotic stress.

**Keywords:** *Nilaparvata lugens, Thai rice, Standard Seedbox Screening Test, BPH resistance, Novel QTL*

# Phenotypic Evaluation of Blast Resistance in Multi-stress Tolerant $F_5$ Rice Breeding Lines for Rainfed Lowland Production

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## Abstract

Rice blast, caused by *Pyricularia oryzae*, is a major constraint to rice production in northeastern Thailand, particularly in rainfed lowland systems. The genetic diversity of pathogen populations poses a significant challenge to the development of rice cultivars with effective blast resistance. This study evaluated blast resistance in 45 advanced $F_5$ rice breeding lines derived from the cross UBN14012-451-1-1-2 × RGD13215-MS13-MS37-MS68 comparing with parental lines and resistance check varieties. The lines were developed through marker-assisted selection (MAS) to incorporate two blast resistance genes, *Pish-J* on chromosome 1 and *Pi7-J* on chromosome 11. Seedlings were artificially inoculated under controlled greenhouse conditions using a composite inoculum comprising 39 *P. oryzae* isolates representing seven genetic lineages from Thailand. Disease severity was assessed at 7 days post-inoculation. All 42 lines carrying both resistance genes exhibited resistant reactions, with disease severity scores ranging from 0.0 to 2.0, comparable to those of the resistant maternal parent and Jao Hom Nin, the resistant check cultivar. Notably, lines carrying either *Pish-J* or *Pi7-J* alone, as well as non-target resistance gene introgression lines, also exhibited resistant reactions, suggesting the contribution of additional resistance factors in their genetic backgrounds. By contrast, KDML105 was susceptible to six isolate groups but resistant to the M4 group, whereas Sariceltik was susceptible to all groups, whereas Sariceltik was susceptible to all tested isolate groups. These findings confirm blast resistance in $F_5$ breeding rice lines carrying *Pish-J* and *Pi7-J*, highlighting the potential of MAS for developing blast-resistant rice cultivars for rainfed lowland production in northeastern Thailand.

**Keywords:** *Blast resistance, Marker-assisted selection, Pyricularia oryzae, Rainfed lowland rice*

# Bacterial Diversity and Community Composition in Lagoon-Connected Rice-Growing Soils of Southern Thailand

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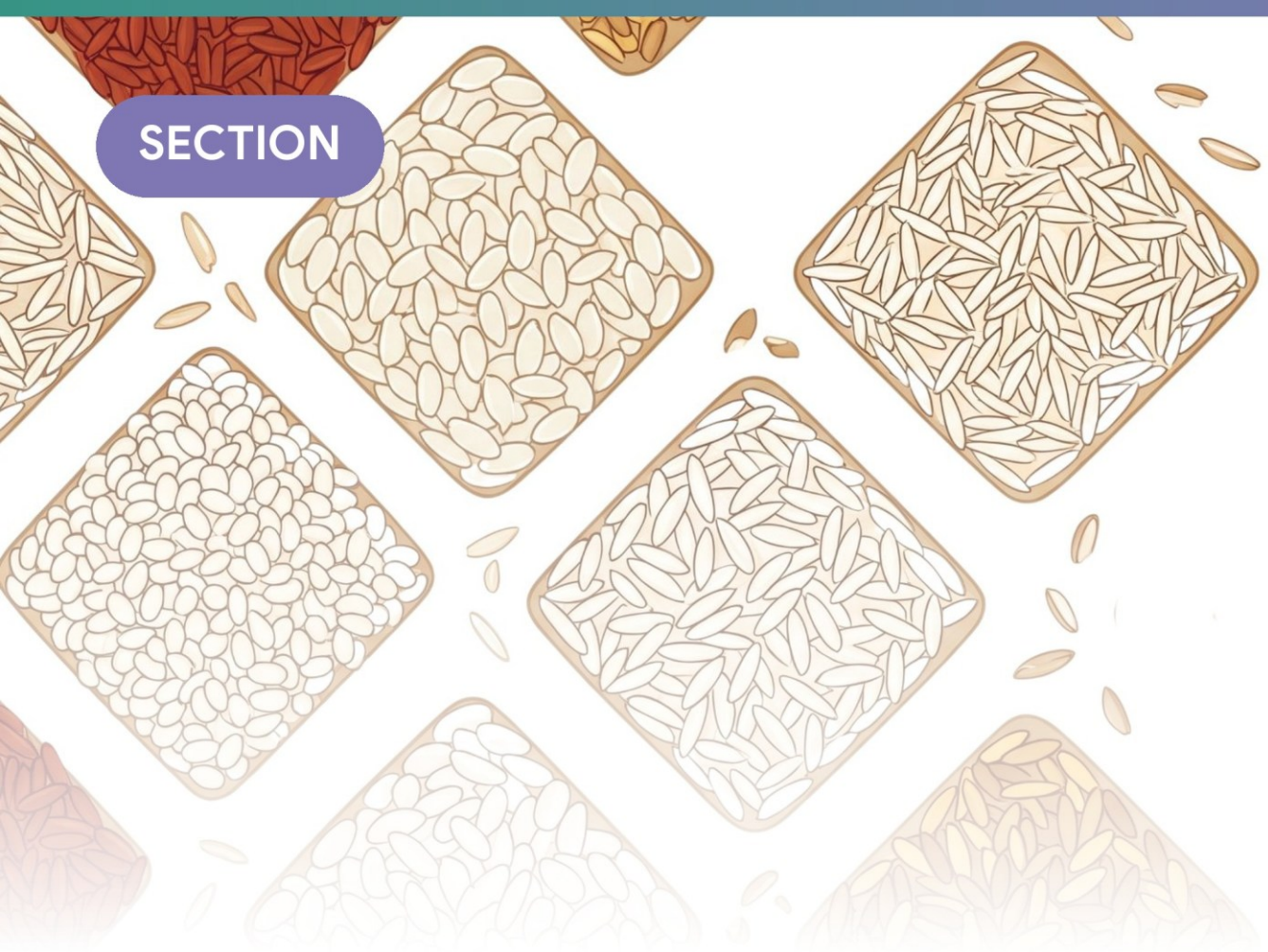
## Abstract

Hydrological connectivity can create distinctive environmental conditions in rice-growing soils, potentially shaping soil bacterial communities and their ecological functions. This study characterized bacterial diversity, community composition, and predicted functional potential in lagoon-connected rice-growing soils (Na Rim Le; NRL) in Phatthalung Province, southern Thailand. Three composite soil samples were collected from NRL rice fields and analyzed using Oxford Nanopore full-length 16S rRNA gene sequencing. Soil physicochemical properties, bacterial taxonomic composition, and predicted functional profiles were examined. The NRL soils exhibited slightly acidic to near-neutral conditions (pH 6.05–6.77) and non-saline conditions, with electrical conductivity ranging from 87.13 to 264.77 µS/cm. Proteobacteria was the predominant bacterial phylum (57.5%), followed by Acidobacteria (10.8%) and Firmicutes (5.8%). At the species level, *Candidatus Koribacter versatilis*, *Burkholderiales bacterium* GJ-E10, *Gaiella occulta*, and *Vicinamibacter silvestris* were among the most abundant taxa. Predicted functional profiles indicated a broad range of potential respiratory pathways, including nitrate, iron, manganese, sulfur, sulfate, and thiosulfate respiration, suggesting diverse potential redox-related metabolic processes. Additional predicted functions included nitrogen transformation processes, particularly nitrification and ammonification; degradation of complex organic compounds, such as aromatic hydrocarbons and cellulose; and C1 metabolism, including methylotrophy and methanotrophy. These findings provide a baseline characterization of bacterial diversity and predicted metabolic potential in lagoon-connected rice-growing soils. The predicted functional profiles suggest the potential importance of microbial-mediated biogeochemical processes in rice soils within hydrologically connected landscapes, although direct measurements are needed to establish their activities and relationships with water-regime dynamics.

**Keywords:** *Soil bacterial diversity, Hydrological connectivity, 16S rRNA gene sequencing, Bacterial functional potential*



SECTION

# PS4

## Novel Rice Processing and Product Innovation

From grain to food: processing technology, quality and new products

Poster 11

# Physicochemical Properties and Carbohydrate Digestion Characteristics of Riceberry-Mung bean Porridge

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## Abstract

Rice-based instant foods are important carbohydrate sources, and their starch digestibility is a key determinant of their potential glycemic response. This study aimed to investigate the effects of different mung bean proportions in Riceberry porridge on the physicochemical properties and reducing sugar release during digestion. Riceberry rice porridge and mung bean were separately processed and drum-dried at 125 °C. The resulting Riceberry and mung bean powders were blended at ratios of 100:0, 75:25, 50:50, 25:75, and 0:100. All porridge formulations had moisture contents below 7%, complying with the Thai Industrial Standard for instant porridge products (TIS 315-2548), and water activity values ranging from 0.31 to 0.36. Increasing the mung bean proportion increased lightness (L*) and yellowness (b*), while redness (a*) decreased, leading to increased overall color difference (ΔE). Viscosity and water absorption index tended to decrease as mung bean proportion increased. *In vitro* digestion was conducted using the standardized INFOGEST static gastrointestinal digestion model. Reducing sugar release, expressed as glucose equivalents, decreased with increasing mung bean proportion. The corresponding area under the curve (AUC) values over 120 min of intestinal digestion were 8745.2, 8067.5, 6944.9, 6212.0, and 5530.2 mg glucose equivalents·min/g sample for the 100:0, 75:25, 50:50, 25:75, and 0:100 Riceberry:mung bean formulations, respectively. These findings demonstrate that mung bean incorporation modified the physicochemical properties and lowered reducing sugar release during *in vitro* digestion of drum-dried Riceberry porridge, suggesting that formulation with mung bean may be a useful approach for modulating carbohydrate digestion characteristics in rice-based instant foods.

**Keywords:** *Riceberry rice, Mung bean, Instant porridge, in vitro digestion, Reducing sugar*

# Development of Thai Sweet fermented Rice (Khao-Mak) using Konjac Blended with Hom Mali

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## Abstract

This study examined the sensory acceptability of glutinous rice and konjac rice Khao Mak. Khao-Mak was produced from five treatments. There are the ratio of glutinous rice and konjac rice treatment 1 (control): 100:0, treatment 2: 75:25, treatment 3: 50:50, treatment 4: 25:75, and treatment 5: 0:100, respectively. It aimed to determine the sensory acceptability of each treatment in terms of texture, color, odor, and flavor. This study used a completely randomized design composed of thirty (30) untrained panelists. The mean and analysis of variance were used to analyze the data. The results indicated that the treatment 1 and 2 received acceptable ratings for texture, color, odor, and flavor. The average mean of treatment 2 was not significantly different from the treatment 1. This means that the panelists liked the treatment 2 product as much as they liked the control product. The physico-chemical characteristic of treatment 2 product was found that the TSS, alcohol, pH and total dietary fiber (TDF) value were 30.25 ±0.03◦brix, 3.26 ±0.09 % v/v, 3.88 ±0.05 and 4.29 ±0.09 %dry weight, respectively. TDF content was higher than control (2.70 ±0.33 %dry weight). The color of treatment 2 final product was found that the L, a and b value were 79.28 ±0.12, -5.43 ±0.02 and 12.14 ±0.00, respectively.

**Keywords:** *Dietary fiber, Functional food, Glucomannan, Khao-Mak, Konjac rice*

## Introduction

Khao-Mak is a traditional Thai sweet fermented rice product prepared by fermenting cooked glutinous rice with Look-Pang, a traditional starter culture containing molds, yeasts, and lactic acid bacteria. During fermentation, starch in the cooked rice is hydrolyzed into fermentable sugars by microbial enzymes, while yeasts convert part of the sugars into ethanol and other volatile compounds. Lactic acid bacteria contribute to organic acid formation and consequently influence the acidity and characteristic flavor of the product. These biochemical transformations result in the characteristic sweet taste, soft and succulent texture, mild alcoholic aroma, and slightly acidic flavor.

Glutinous rice (*Oryza sativa* L. var. glutinosa) is the main ingredient, which is also high in carbohydrates, low glycemic index (GI) and low dietary fiber. Konjac rice, also known as shirataki or miracle rice, is high fiber, low caloric and carbohydrate content, this food matrix is primarily composed of water and glucomannan. Furthermore, the soluble glucomannan fiber promotes satiety and supports gastrointestinal health. Being naturally gluten-free and vegan, it serves as a suitable dietary option for blood glucose management. Therefore, the present study aimed to develop Khao-Mak containing different levels of konjac rice and evaluate its physicochemical properties and sensory characteristics.

## Materials and Methods

### Materials

Glutinous rice was obtained from a local market in Bangkok. Commercial konjac rice containing glucomannan and Thai jasmine rice was used as the functional ingredient. Look-Pang was purchased from a local market in Suphanburi province.

**Preparation of Khao-Mak**

Glutinous rice was soaking in warm water for 2 hours then steaming over simmering water to cooked. Konjac rice was cooked by boil in water for 10 minutes. Then, cooked glutinous rice were mixed with konjac rice as the various ratio such as 100:0, 75: 25, 50:50, 25:75 and 0:100, respectively. The batter was mixed with Look-Pang 0.2 % w/w of sample, and fermented in the plastic cup at room temperature (30-35 ºC) for 3 days and keep in refrigerator at 5-8◦C for analyzed.

**Physico-chemical analysis of Khao-Mak**

The pH values and alcohol content of Khao-Mak samples from all treatments were examined by a pH meter and a vinometer, respectively. Khao-Mak samples were ground, and the TSS of the resulting liquid was evaluated by a refractometer.

The total dietary fiber (TDF) content by means of enzymatic-gravimetric method based on the procedure of AOAC (1997). For each samples (0.3-0.5 mm mesh) were gelatinized with heat stable α-amylase and then digested with protease and amyloglucosidase to remove the protein and starch present in the samples. Ethanol was added to precipitate soluble dietary fiber. After filtration the residue was washed with ethanol and acetone, followed by drying and weighing. Half of the samples were analyzed for protein by Kjeldahl nitrogen analysis and the other halves were ashed (525◦c, 5 h). TDF value was the weight of the residue less the weight of the protein and ash.

**Color Measurement**

Color parameters were measured using a Hunter Lab Colorimeter (Chroma Meter CR-400, Konica Minolta, Tokyo, Japan) and recorded as L*, a*, and b* values, where L* represents lightness (0–100 scale), a* represents green (−) to red (+) chromaticity, and b* represents blue (−) to yellow (+) chromaticity

**Sensory acceptability test**

The sensory acceptance was performed using hedonic scale of 1 to 5 where 1 = dislike extremely and 5 = like extremely. Evaluation was based on texture, color, odor, and flavor. Sensory quality evaluation of samples was performed by 30 untrained panelists. (Daneshi et al., 2013)

**Statistical analysis**

All experiments were done in triplicate, and are presented with mean ± standard deviation (SD). Data analysis was performed with the SPSS program using ANOVA, followed by Duncan multiple comparison tests. Statistical significance was defined as $p < 0.05$. Analysis of Variance (ANOVA) was used to analyze significant differences among the experimental treatments in terms of texture, color, odor, and flavor.

**Results and Discussion**

Khao-Mak was produced from five treatments. There are the ratio of glutinous rice and konjac rice 100:0, 75:25, 50:50, 25:75, and 0:100, respectively. The fermentation period was

3 days. The results of physico-chemical properties consisting of TSS, pH, alcohol and total dietary fiber (TDF) are shown in table 1.

**Table 1 Physico-chemical characteristics of the Khao-Mak produced from glutinous rice and konjac rice**

| Treatment | glutinous rice: konjac rice | Total soluble solid (◦brix) | Alcohol (% v/v) | pH | Total dietary fiber (TDF) (% dry weight) |
|---|---|---|---|---|---|
| 1 | 100:0 | 33.42 ±0.03 | 3.60 ±0.03 | 3.85 ±0.01 | 2.70 ±0.33 |
| 2 | 75:25 | 30.25 ±0.03 | 3.26 ±0.09 | 3.88 ±0.05 | 4.29 ±0.09 |
| 3 | 50:50 | 26.00 ±0.00 | 2.14 ±0.05 | 4.00 ±0.00 | 5.74 ±0.05 |
| 4 | 25:75 | 22.50 ±0.00 | 1.62 ±0.03 | 4.30 ±0.03 | 7.41 ±0.23 |
| 5 | 0:100 | 12.14 ±0.05 | 1.03 ±0.01 | 4.65 ±0.00 | 8.82 ±0.18 |

The total soluble solid of Khao-Mak was produced by mold in Look-Pang. Mold could hydrolyzed starch to sugar. Therefore, the sugar could be increased. In the fermentation using only glutinous rice, the total soluble solids value was 33.42 ± 0.03◦brix. The results showed that increasing the proportion of konjac rice leaded to decrease of total soluble solid. Because the glucomannan in konjac rice is a natural polymer with a very high molecular weight (Ueno et al. 2023) that cannot be digested by the mold. The konjac rice alone was found total soluble solids, as it also includes Jasmine rice 44% (w/w) as an ingredient.

Yeast could play an important role for fermentation system which ferments monosaccharide (sugar) to ethyl alcohol. The fermentation of glutinous rice exhibited high alcohol content 3.60 ±0.03% (v/v). The ethyl alcohol could be decreased due to the increasing of konjac rice.

The fermentation process started when the pH of Khao-Mak was declined sharply to approximately 4.00 at day 3 of fermentation. Because, yeast and mold could play an important role for fermentation system which ferments monosaccharide (sugar) to ethyl alcohol and acids (Mongkontanawat and Lertnimitmongkol, 2015). In the experiment, increasing the amount of konjac rice resulted in a higher pH.

Glucomannan can slow down the absorption of sugar released from food and consequently reduces the increase in blood sugar level. Therefore, overall diabetes control can be improved in patients with diabetes by giving them a glucomannan-rich diet

Total dietary fiber (TDF) is the edible portion of plants or analogous carbohydrates that are resistant to digestion and adsorption in the human small intestine with complete or partial fermentation in the large intestine. Dietary fibers promote laxation, and blood cholesterol and glucose attenuation (Daou& Zhang, 2014). Glutinous rice contains total dietary fiber (TDF) 2.70 ±0.33% dry weight. Konjac rice is also rich in dietary fiber. Konjac rice blended with Hom Mali (Thai Jasmine) rice provides a high amount of soluble dietary fiber known as glucomannan, typically containing between 3-6 grams of fiber per 100 grams. Therefore, increasing the amount of konjac rice increases the TDF value.

**Table 2 Color characteristics of the Khao-Mak produced from glutinous rice and konjac rice**

| Treatment | glutinous rice: konjac rice | Color | | |
|---|---|---|---|---|
| | | L | a | b |
| 1 | 100:0 | 78.66 ±0.03 [a] | -5.44 ±0.05 [a] | 12.21 ±0.03 [a] |
| 2 | 75:25 | 79.28 ±0.12 [a] | -5.43 ±0.02 [a] | 12.14 ±0.00 [a] |
| 3 | 50:50 | 79.85 ±0.02 [a] | -5.36 ±0.12 [a] | 12.06 ±0.33 [a] |

| | | | | |
|---|---|---|---|---|
| 4 | 25:75 | 80.57 ±0.00 [a] | -5.28 ±0.33[b] | 11.87 ±0.25 [b] |
| 5 | 0:100 | 81.35 ±0.33 [a] | -5.25 ±0.00 [b] | 11.63 ±0.33 [b] |

**Note:** Values are means ± standard deviations of attribute values. Mean values along the same column with different superscript letters are significantly different ($p < 0.05$).

According to the findings presented in table 2, it is evident that the quantity of konjac rice in khao mak doesn't play a crucial role in determining its color characteristics. Due to konjac rice also looks white similar to glutinous rice.

**Table 3 Sensory scores of Khao-Mak produced from glutinous rice and konjac rice**

| Sensory quality evaluation | glutinous rice: konjac rice | | | | |
|---|---|---|---|---|---|
| | Treatment 1 (control) | Treatment 2 | Treatment 3 | Treatment 4 | Treatment 5 |
| | 100:0 | 75:25 | 50:50 | 25:75 | 0:100 |
| texture | 4.28 ±0.71[a] | 4.33 ±0.67 [a] | 4.30 ±0.33 [a] | 4.29 ±0.95 [a] | 4.28 ±0.50 [a] |
| color | 4.35 ±0.95 [a] | 4.37 ±1.09 [a] | 4.34 ±1.12 [a] | 4.29 ±1.20 [b] | 4.30 ±0.75 [b] |
| odor | 4.16 ±1.12 [a] | 4.18 ±0.58 [a] | 3.31 ±0.89 [b] | 3.20 ±0.33 [b] | 2.72 ±0.45 [c] |
| flavor | 4.38 ±0.97[a] | 4.41 ±0.56 [a] | 3.34 ±0.77 [b] | 3.28 ±0.67 [b] | 2.82 ±1.12 [c] |
| Mean | 4.29 | 4.32 | 3.82 | 3.76 | 3.53 |
| Interpretation | Acceptable | Acceptable | Acceptable | Acceptable | Acceptable |

**Note:** Values are means ± standard deviations of attribute values. Mean values along the same row with different superscript letters are significantly different ($p < 0.05$).

Interpretation 4.5 – 5.0 = Highly Acceptable; 3.5 – 4.49 = Acceptable; 2.5 – 3.49 = Moderately Acceptable; 1.5 – 2.49 Fairly Acceptable; 1.0 – 1.49 = Not Acceptable

Sensory acceptance tests of glutinous rice and konjac rice Khao-Mak are shown in table 3. Five point hedonic scales were used to evaluate the acceptance of participants. The 30 attendants were recruited with 30% being male and 70% being female. Treatment 2 (glutinous rice: konjac rice; 75:25) was most generally accepted among the samples and significantly different ($p \leq 0.05$) from other treatments. This could be because this treatment was accurated the needs of consumers.

The obtained results showed that the optimum ratio of glutinous rice: konjac rice for Khao-Mak production were 75:25. This treatment was the high acceptable from the sensory evaluation. Physico-chemical properties could be served as a source of total dietary fiber (TDF) 4.29 ±0.09% dry weight. The color of final product tended to be white, the L*, a* and b* value were 79.28 ±0.12, -5.43 ±0.02 and 12.14 ±0.00, respectively.

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**References**

*1.* Aneshi, M., Ehsani, M. R., Razavi, S. H., Labbafi, M. (2013). Effect of refrigerated storage on the probiotic survival and sensory properties of milk/carrot juice mix drink. *Electronic Journal of Biotechnology*. 16(5): 1-12. DOI: 10.2225/vol16-issue5-fulltext-2

*2.* Busaba, T., Busakorn, T., Puttinan, P., Khon-Sue, W., & Siriporn, L. (2023). Quinoa as functional ingredient in Thai indigenous sweet fermented rice (Khao-Mak). *Proceedings of the International Conference on Food, Nutrition, Health and Lifestyle, 2*(1), 1–7. https://doi.org/10.17501/26827026.2023.2101

*3.* Daou, C., & Zhang, H. (2014). Functional and physiological properties of total, soluble, and

insoluble dietary fibres derived from defatted rice bran. *Journal of food science and technology*, *51*(12), 3878–3885. https://doi.org/10.1007/s13197-013-0925-y

*4.* Mongkontanawat, N., & Lertnimitmongkol, W. (2015). Product development of sweet fermented rice (Khao-Mak) from germinated native black glutinous rice. *International Journal of Agricultural Technology, 11*(2), 501–515.

*5.* Wilianto, Y. R., Tjahjono, Y., Foe, K., Wijaya, S., Ervina, M., Setiadi, D. A., Wihadmadyatami, H., Dewi, B. D. N., & Wijaya, H. (2024). A novel konjac rice formula with glucomannan and tapioca starch improve postprandial glycemic response—A randomized single-blind clinical trial. *Nutrition & Food Science, 54*(8), 1437–1450. https://doi.org/10.1108/NFS-12-2023-0290

*6.* Ueno, H., Haraguchi, N., Azuma, M., Shiiya, T., Noda, T., Ebihara, E., Nakazato, M. (2023). Active Consumption of Konjac and Konjac Products Improves Blood Glucose Control in Patients with Type 2 Diabetes Mellitus. *Journal of the American Nutrition Association*, *42*(2), 123–129. https://doi.org/10.1080/07315724.2021.2002739

# From Traditional Rice to Future Food: Transforming Rice into Healthy Emergency Food

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The growing demand for alternative food options highlights the need to transform traditional rice into healthy emergency foods requiring minimal preparation. This study aimed to develop whole-grain instant rice from traditional Thai rice germplasms through optimized hydrothermal processing. Building on research on polished Indian soak-and-eat rice (Vogali Bora), characterized by non-pigmented kernels and very low amylose content (AC) associated with a high glycemic response, conventional parboiling was explored to improve water absorption during room temperature soaking. Vogali Bora, with 3.54% AC and low gelatinization temperature (GT), required one hour of soaking for consumption. Genomic analysis identified starch biosynthesis-related genes as major determinants of instant rice quality. These findings guided the development of whole-grain instant rice using Thai pigmented rice. Riceberry (15% AC) underwent four parboiling treatments followed by dehusking. Double parboiling enabled consumption after 30 minutes of room temperature soaking, with desirable softness and a peak compression force of 798 gf. However, applying this treatment to six additional Thai rice lines revealed variable textural properties. Neaw Hom Nuan and Redberry remained relatively hard despite low AC, potentially due to high GT, whereas Pinkaset+4117A08 showed unsuitable instant rice quality despite low GT and high AC. These findings suggest that AC and GT jointly influence whole-grain instant rice quality. Instant Riceberry contained 1.957 g/kg anthocyanins, with cyanidin-3-glucoside identified as a major compound by UPLC. Overall, double parboiling offers potential for transforming traditional pigmented rice into healthier whole-grain emergency food. Further research should investigate grain composition, bioactivity and QTL underlying instant rice quality.

**Keywords:** *Traditional Thai Rice, Hydrothermal Processing, Emergency Food, Starch Biosynthesis, Anthocyanin*

# Enhancing the Functional Potential of Thai RD43 Rice through Mung Bean Protein-Enriched Gels for 3D Food Printing

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## Abstract

Thai RD43 rice offers considerable potential as a health-oriented and value-added food ingredient due to its gluten-free nature, low glycemic index, and favorable gel-forming properties. However, expanding its application into nutritionally enhanced and shape-customized foods requires improved nutritional functionality and structural performance during processing. In this study, mung bean protein isolate (MBPI), a nutrient-rich plant protein derived from an economically important Thai crop, was incorporated into RD43 rice gels for extrusion-based three-dimensional (3D) food printing. The effects of MBPI concentration on rheological behavior, printability, dimensional accuracy, and texture of the printed products were investigated. Four formulations containing 0%, 10%, 15%, and 20% MBPI were prepared and designated RM0, RM10, RM15, and RM20, respectively. All formulations exhibited elastic solid-like behavior ($G' > G''$) and shear-thinning characteristics, indicating their potential for extrusion-based printing. Increasing MBPI concentration enhanced the structural strength of the rice gels, with RM20 exhibiting the highest storage modulus. However, printability varied substantially among formulations. RM10 showed poor post-print structural stability, extensive lateral spreading, and the greatest dimensional deviation (48.54%), resulting in collapse of the printed structure and preventing subsequent texture evaluation. In contrast, RM15 achieved the highest dimensional accuracy, with only 2.24% deviation and 97.76% height retention, while RM20 exhibited comparable dimensional accuracy (2.56% deviation) and the greatest height retention (99.31%). Texture analysis further demonstrated that RM20 produced the firmest and most resilient structures, with the highest hardness, gumminess, adhesiveness, and resilience, whereas RM15 exhibited greater springiness, chewiness, and cohesiveness. Overall, the findings demonstrate that MBPI concentration is a critical factor governing the relationship between rheological behavior, print fidelity, and texture in 3D-printed RD43 rice gels. RM15 provided a favorable balance between dimensional accuracy and moderate textural characteristics, while RM20 offered enhanced firmness and structural stability. This study highlights the potential of combining Thai RD43 rice and mung bean protein to create nutritionally enriched, shape-customized foods through additive manufacturing, providing a promising approach for value-added utilization of locally available Thai crops.

**Keywords:** *Kor Khor 43 rice, Mung bean protein, 3D food printing, Rheology, Texture*

# Identification of Process Limitations in Pilot-Scale Isomalto-Oligosaccharide Production and Characterization of Product Properties

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## Abstract

This study investigated the pilot-scale production of isomalto-oligosaccharides (IMOs) from Riceberry rice flour, and functional properties of the resulting syrup. Polished Riceberry rice was milled and sieved through a 100-mesh screen. Pilot-scale production was conducted in a 50-L jacketed mixing vessel using 8 kg of rice flour and 32 L of reverse osmosis water, followed by sequential enzymatic liquefaction, saccharification, and transglycosylation. The pilot-scale process achieved a starch hydrolysis efficiency of 80.46 ± 0.71%, comparable to that obtained at the laboratory scale. However, the maltose concentration after saccharification was 50.60 ± 17.05 mg/L, approximately 2.76-fold lower than that achieved at the laboratory scale. This reduction was accompanied by a lower IMO concentration of 39.30 ± 12.27 mg/L, corresponding to a 1.47-fold difference between the two production scales. The overall pilot-scale IMO yield was 12.23 ± 3.55% (w/w), based on the initial starch content. The resulting syrup was clarified by filter-press filtration, purified by nanofiltration, and concentrated under vacuum to 70 °Brix. The final syrup contained glucose (12%, w/v), maltose (5%, w/v), and several IMOs, predominantly isomaltose (13%, w/v), isomaltotriose (9%, w/v), and panose (3%, w/v), 3% (w/v) isomaltotetraose, 1% (w/v) isomaltopentaose, 4% (w/v) isomaltoheptaose, and 1% (w/v) isomaltooctaose. The syrup provided 278.33 kcal/100 g and achieved a prebiotic activity score of 0.263. These findings demonstrate the feasibility of pilot-scale IMO production from Riceberry rice while identifying saccharification as a potential process bottleneck. Improving maltose availability may enhance subsequent transglucosylation efficiency and overall IMO yield

**Keywords:** *Riceberry Rice, IMO synthesis, Pilot-scale production*

# Aligning Ubon Ratchathani Jasmine Rice Supply Chains with the Customer Decision Journey: A Qualitative Multi-Stakeholder Study

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## Abstract

Commercial value realization in premium agriculture requires synchronizing upstream agronomy and midstream processing with downstream consumer decision-making. This study explores the operational and informational mechanisms needed to align the Ubon Ratchathani Thai Hom Mali rice supply chain with the contemporary Customer Decision Journey (CDJ). Using an exploratory qualitative design, empirical data were collected from purposive in-depth sessions with upstream farmer leaders (n=4), midstream mill executives (n=2), and an agronomy and genetics researcher. Thematic analysis with triangulation revealed five primary challenges and opportunities: (1) production consistency is hindered by water-regime and input variability; (2) varietal purity and certification details face midstream dilution and physical co-mingling; (3) market preference signals degrade into basic commodity pricing; (4) authentic provenance, sensory quality, and sustainability serve as vital consumer cues; and (5) multi-stakeholder governance with commercial contracting is essential for equitable value distribution. Addressing these findings, the study proposes a three-tier product architecture and a five-stage Supply-Chain-to-CDJ Alignment Framework. This model demonstrates that robust traceability and verifiable chain-of-custody protocols are essential for cultivating brand trust across evaluation, purchase, and advocacy stages, providing a strategic blueprint for specialty rice commercialization.

**Keywords:** Jasmine rice; Customer decision journey; Supply chain alignment.

## Introduction

Thai Hom Mali rice (Oryza sativa L.), particularly varieties KDML105 and RD15 cultivated in Northeastern Thailand, represents one of the world's most renowned aromatic staple foods, characterized by its distinctive floral-pandan aroma (2-acetyl-1-pyrroline, 2-AP), slender grain morphology, and soft, cohesive texture upon cooking (Kongsri et al., 2021; Suwannaporn & Linnemann, 2008). In Ubon Ratchathani province, favorable agro-ecological attributes—including sandy loam soils, long daylight exposure, and terminal water stress during ripening—create optimal physiological conditions for aromatic synthesis (Srisukwatanachai et al., 2025). However, despite possessing exceptional intrinsic agronomic and sensory properties, Thai Hom Mali rice continues to face severe commercial vulnerability in domestic and global markets. Upstream farmers frequently experience volatile farm-gate prices and escalating production costs, while midstream millers grapple with grain contamination, varietal mingling, and fierce price competition from regional competitors such as Vietnamese ST24/ST25 and Cambodian Malys Angkor (Thai Department of Foreign Trade, 2020).

A central root cause of this persistent economic paradox is systemic information asymmetry and operational misalignment across the agricultural value chain. In traditional grain logistics, supply chains are organized as linear, production-driven push systems: upstream farming communities produce undifferentiated paddy, local middlemen and millers

aggregate and homogenize bulk volumes, and downstream retailers sell the final product primarily on price and generic branding. Market signals transmitted upstream are almost exclusively reduced to transactional, short-term price fluctuations, while rich consumer intelligence—regarding health preferences, environmental concerns, culinary performance expectations, and provenance authenticity—is lost along the chain (Furquim et al., 2023).

To resolve this structural disconnect, contemporary marketing theory proposes the Customer Decision Journey (CDJ) framework (Court et al., 2009). Departing from traditional linear sales funnels, the CDJ conceptualizes consumer purchasing as a dynamic, circular process spanning four interactive phases: initial consideration, active evaluation, moment of purchase, and post-purchase experience/loyalty loop. In modern omnichannel retailing, consumer progression through these touchpoints is heavily dictated by brand transparency, digital verification, product differentiation, and experiential consistency (Furquim et al., 2023; Lee et al., 2020). Nevertheless, existing literature has predominantly examined the CDJ as an external, downstream retail marketing construct, rarely investigating how upstream agricultural production and midstream processing must be operationally coordinated to substantiate consumer touchpoints.

This study addresses this significant research gap. Grounded in primary multi-stakeholder empirical evidence collected across the Ubon Ratchathani jasmine rice supply chain, this research aims to: (1) identify empirical operational bottlenecks and latent value opportunities across upstream farming, midstream milling, and agro-ecological science; (2) systematically map empirical stakeholder realities onto the four stages of the CDJ; and (3) propose an actionable, grounded Supply-Chain-to-CDJ Alignment Framework alongside a tiered product architecture. By linking physical supply-chain chain-of-custody practices with consumer cognitive touchpoints, this paper demonstrates that supply chain integrity is the foundational prerequisite for sustainable consumer brand equity and economic resilience in specialty agri-food systems.

## Materials and Methods

### Research Design and Empirical Scope

This study utilized an exploratory qualitative multi-stakeholder research design. Because specialty agricultural chains involve complex socio-technical interactions among agronomy, industrial logistics, and commercial governance, an in-depth qualitative inquiry was selected to capture nuanced behavioral, operational, and institutional mechanisms that quantitative surveys cannot adequately reflect (Lincoln & Guba, 1985).

### Participant Sampling and Characteristics

To ensure comprehensive data coverage across the entire supply chain continuum, purposive sampling was implemented across three distinct stakeholder nodes in Ubon Ratchathani and central academic institutions (Table 1):

- **1.** Upstream Farmer Node: Represented by a focus-group interview with four key farming leaders from a Large-Scale Paddy Field Community Enterprise in Bua Ngam Sub-district, Det Udom District, Ubon Ratchathani. Participants operated household farms ranging from 40 to 70 rai, cultivating KDML105 and RD15 under rainfed conditions, with over 20 years of hands-on farming experience.

- **2.** Midstream Processing & Logistics Node: Represented by in-depth managerial interviews with two senior executive stakeholders from major commercial rice mills in Ubon Ratchathani: the Owner/Executive of Det Udom Sirichoke Rice Mill (former President of the Ubon Ratchathani Rice Millers Association, with over 30 years in export-grade milling) and the General Manager of Ying Phiboon 2007 Rice Mill Co., Ltd. (Samrong District, Ubon Ratchathani). Both facilities process export-standard jasmine rice, operating advanced color-sorting, optical testing, silo aeration, and international certifications (ISO, GMP/HACCP, Halal, SRP).
- **3.** Research & Agro-Ecological Node: Represented by an expert interview with an academic researcher specializing in rice genetics, molecular breeding, and agro-ecosystems from the Rice Science Center, Kasetsart University, possessing extensive experience in varietal purity, low-carbon cultivation, and functional grain innovations.

**Table 1. Overview of qualitative interview participants across the supply chain**

| Stakeholder Node | Target Group / Organization | Key Informants | Operational Scope | Data Source |
|---|---|---|---|---|
| Upstream Producers | Large-Scale Farming Enterprise, Bua Ngam, Det Udom, Ubon Ratchathani | Community enterprise president & committee members (n=4) | Rainfed KDML105/RD15 cultivation, seed retention, farm-gate paddy sales | Audio Record 1 (Field Interview) |
| Midstream Millers | Det Udom Sirichoke Rice Mill & Ying Phiboon 2007 Rice Mill Co., Ltd. | Former Association President & Mill Managing Director (n=2) | Commercial procurement, lab testing, drying, milling, packaging, export supply | Audio Record 2 (Executive Interview) |
| Academic & Expert | Rice Science Center, Kasetsart University / Scientific Research Partner | Principal rice geneticist & agro-ecology researcher (n=1) | Breeding, low-carbon rice protocols, 2-AP aroma volatility, nutritional biochemistry | Audio Record 3 (Expert Dialogue) |

## Interview Protocol and Core Inquiries

Data collection was guided by semi-structured interview protocols structured across four operational and behavioral dimensions for each stakeholder tier (summarized in Table 2). These questions maintained rigorous thematic continuity while allowing deep empirical exploration:

**Table 2. Semi-structured interview protocols structured across supply chain and CDJ dimensions**

| Inquiry Dimension | Upstream Farmer Protocol (Sample Core Inquiries) | Midstream Miller & Expert Protocol (Sample Core Inquiries) |
|---|---|---|
| Dimension 1: Production Quality & Control (Upstream / Intake) | • What unique agro-ecological conditions in Ubon Ratchathani distinguish your Hom Mali from other regions?<br>• How are foundation seeds selected and field contamination (red rice, weeds) controlled? | • What precise quality thresholds (moisture <=14%, DNA purity >92%) govern paddy procurement?<br>• What intake challenges arise during harvest peaks (wet grain, varietal mixing)? |

| | | |
|---|---|---|
| | • What harvesting/drying techniques prevent fissuring and aroma loss? | • How do silo aeration and cold storage preserve 2-AP aroma longevity? |
| Dimension 2: Supply Chain Logistics & Processing (Midstream) | • How is harvested paddy handled (immediate sale at field gate vs. barn storage)?<br>• What factors determine farm-gate bargaining power and price dockage?<br>• What logistical bottlenecks emerge in transport from fields to buying stations? | • How do advanced optical color sorters upgrade paddy into premium export grades?<br>• How are certifications (GMP/HACCP, Halal, GI, Sustainable Rice Platform - SRP) operationalized?<br>• What processing energy, labor, and transport costs constrain price stability? |
| Dimension 3: Consumer Awareness & Decision Journey (Link to CDJ) | • What drives urban consumer choice for Hom Mali (aroma, texture, price, organic certification)?<br>• How does health-conscious consumer demand impact your cultivation methods?<br>• Are farmer groups technically ready to provide field-level traceability data to consumers? | • What retail and omnichannel trends are observed from modern trade, online, and export buyers?<br>• What quality cues do buyers evaluate during Active Evaluation (cleanliness, consistency)?<br>• Can QR-code origin traceability to specific farming districts build verified brand loyalty? |
| Dimension 4: Synergy, Governance & Future Sustainability | • What structural obstacles threaten production (labor aging, input inflation, water stress)?<br>• How does Large-Scale Farming enhance collective bargaining and market access?<br>• What institutional support is needed to build sustainable synergy with downstream buyers? | • What contractual models (OEM, proprietary branding, contract farming) best align incentives?<br>• What information bottlenecks hinder transmission of market demand down to farm level?<br>• How do Low-Carbon Rice protocols and environmental criteria shape future competitiveness? |

**Data Analysis and Trustworthiness**

All three recorded audio sessions (totaling over 180 minutes of rich technical and commercial dialogue) were transcribed verbatim into Thai text. A rigorous two-cycle thematic analysis was conducted following Braun and Clarke (2006). First-cycle coding extracted 78 discrete open codes capturing concrete operational occurrences (e.g., harvesting equipment contamination, moisture penalties, fertilizer cost inflation, aroma dissipation, chemical mingling). Second-cycle coding synthesized these into conceptual categories, which were systematically clustered into five overarching themes.

To ensure analytical trustworthiness and methodological rigor (Lincoln & Guba, 1985), source triangulation was established by cross-verifying findings across the three independent stakeholder groups. Investigator triangulation and peer debriefing were conducted with academic colleagues to resolve interpretive divergences. An audit trail of coding decisions and representative bilingual quote excerpts were maintained to ensure confirmability and transferability.

**Results and Discussion**

Cross-stakeholder thematic synthesis revealed five interdependent themes governing the Ubon Ratchathani jasmine rice value chain. Table 3 details each empirical theme, supported by authentic stakeholder quotations, and delineates its operational translation into consumer-facing CDJ touchpoints.

**Table 3. Empirical interview themes, representative participant quotations, and CDJ touchpoint implications**

| Identified Theme | Empirical Stakeholder Reality & Evidence | Representative Participant Quotations | CDJ Touchpoint Implication |
|---|---|---|---|
| Theme 1: Production Consistency vs. Environmental & Cost Volatility | Paddy yield and sensory attributes are highly vulnerable to climate shifts, drought-rain cycles, labor scarcity, and soaring diesel/fertilizer costs (exceeding 20,000 THB/season for plowing alone). While rotational wet-dry water regimes and high sunlight enhance 2-AP aroma, erratic monsoon conditions cause premature harvesting and high moisture. | Farmer: 'During early harvest, farmers rush to cut paddy before it fully matures because they fear rain... combine harvesters bring weed and red-rice seeds from other fields.'<br>Expert: 'Low-carbon, precision water management (AWD) reduces methane and strengthens grain aroma, but farmers require mechanized precision.' | Initial Consideration & Experience: Eliminates grain brittleness and variable cooking softness, ensuring the regional aroma promise is physically fulfilled in every pot. |
| Theme 2: Quality Information Dilution & Aggregation Asymmetry | Quality dilution occurs during bulk aggregation. Farmers face strict dockage penalties for moisture (>15%) and red-rice/impurity mixtures, yet bulk handling at local buying stations blends premium pure paddy with inferior lots. DNA testing (requiring >92% purity for Hom Mali certification) is rarely accessible at farm-gate. | Miller 1: 'Rice intake requires strict DNA testing (>92% purity) and moisture inspection. If an unverified variety gets mixed, the entire export lot fails certification.'<br>Miller 2: 'Traceability to specific farmer plots is fully achievable via computerized weighbridges, but depends on farmer seed discipline.' | Active Evaluation: QR-enabled lot tracking and DNA purity certificates convert invisible milling quality into verifiable evidence during buyer search. |
| Theme 3: Disconnected Feedback & Transactional Price Traps | Market preferences regarding health, low glycemic index, and packaging sustainability are completely lost in traditional commodity pricing. Upstream producers operate blind to consumer cooking dissatisfaction or retailer brand metrics, responding only to spot paddy prices. | Farmer: 'We have no idea who eats our rice in Bangkok or abroad. We only look at the mill gate price board each morning.'<br>Expert: 'Market intelligence must travel backwards as exact agronomic specifications—grain length, amylose content, organic certification.' | Active Evaluation & Purchase: Transmits shelf data (cooking trends, pack size preferences) into pre-season cultivation contracts. |
| Theme 4: Latent Value Signals: Origin, Safety & Functional Wellness | Authentic Ubon Ratchathani origin, chemical-free/organic practice, low-carbon footprints, and GI certifications possess substantial market appeal. However, uncertified niche grains (e.g., Riceberry, unverified local breeds) face severe market saturation and lack off-take scale. | Miller 1: 'Foreign and high-end Bangkok buyers demand certified Ubon Hom Mali without blending. Ubon rice carries a premium reputation.'<br>Expert: 'Future competitiveness lies in low-carbon rice (SRP standard) and protein-dense rice bran extracts, not just bulk white starch.' | Moment of Purchase: Differentiates shelf offerings through tamper-evident single-origin seals, functional nutritional claims, and eco-labels. |
| Theme 5: Collective Governance, Shared Risk & Reward Mechanisms | Individual smallholders cannot bear the costs of certified organic transition, computerized tracking, or bulk marketing independently. Long-term supply stability | Farmer: 'When the government gave us a single tractor, three households competed for it during harvest. We need collective machinery governance.' | Post-Purchase & Loyalty Loop: Ensures consistent batch supply across seasons, preventing stockouts and |

| | | | |
|---|---|---|---|
| | and quality compliance require formal enterprise contracting, shared drying facilities, and guaranteed price incentives. | Miller 2: 'We are eager to contract with community enterprises if they maintain varietal purity and clean harvest standards.' | protecting consumer brand loyalty. |

**Empirical Supply-Chain to CDJ Integration**

The empirical findings demonstrate that consumer cognitive progression across the CDJ is directly tethered to upstream and midstream operational capabilities. Below is the stage-by-stage grounded integration:

1. Initial Consideration Phase: Consumers enter the purchase journey influenced by regional reputation, cultural prestige, and top-of-mind brand associations. The empirical evidence confirms that 'Ubon Ratchathani Hom Mali' commands an innate price premium (+1 to 2 THB/kg at wholesale) due to historical perceptions of rich pandan aroma and soft texture. However, as revealed in Theme 1 and Theme 4, this brand awareness is easily destroyed if environmental volatility causes grain cracking or varietal contamination. Upstream agro-ecological management (maintaining certified KDML105 foundation seed, preventing field contamination by red weedy rice, and optimizing harvest timing) is therefore not merely an agricultural task—it is the foundational operational requirement for initial consideration equity.

2. Active Evaluation Phase: During evaluation, omnichannel consumers actively benchmark competing products using search terms, certifications, origin disclosures, customer reviews, and pricing. Findings from Theme 2 indicate that midstream commercial mills serve as the critical 'truth-verification node.' Modern optical sorters, moisture-controlled aerated silos, and computerized intake testing ensure that physical paddy meets DNA purity thresholds (>92%) and chemical safety standards (GMP/HACCP, Halal, SRP). When translated into verifiable on-pack QR codes and transparent quality metrics, these internal milling controls directly alleviate consumer perceived risk during brand evaluation.

3. Moment of Purchase Phase: Final conversion at physical shelves or digital e-commerce carts is governed by packaging format, visual trustworthiness, portion convenience, and perceived price-to-value ratio. Theme 4 and Theme 5 demonstrate that forcing a single premium model fails: bulk commercial buyers require standard 50-kg certified sacks, urban families seek 5-kg vacuum-sealed packs with aroma-barrier foil, and health-conscious single consumers demand 1-kg nitrogen-flushed portions. Retail conversion is secured when the supply chain provides channel-differentiated SKU packaging backed by certified origin seals.

4. Post-Purchase Experience & Loyalty Loop: Customer loyalty and organic advocacy are determined by sensory satisfaction in the kitchen—namely, aroma release upon cooking, grain elongation, fluffiness, and softness retention after cooling. Furthermore, modern consumers demand closed-loop accountability: if quality inconsistency occurs, lot-level traceability enables rapid customer service resolution and corrective feedback to farmer groups. This operational responsiveness transforms transactional first-time buyers into active brand advocates.

**Proposed Grounded Frameworks: Tiered Architecture and 5-Step Alignment**

**Framework 1:** Grounded Three-Tier Product Architecture: Rather than enforcing uniform organic or premium standards across all smallholders, production should be structured

into three scalable tiers: (a) Tier 1: Core Quality Hom Mali (Certified DNA purity >92%, moisture <=14%, mechanized optical sorting, competitive mass retail positioning); (b) Tier 2: Verified Provenance & Single-Origin Hom Mali (Traceable to specific Large-Scale Enterprise clusters in Ubon Ratchathani, QR-code field transparency, vacuum packaging, targeted at quality-sensitive domestic omnichannel consumers); and (c) Tier 3: Certified Sustainable & Eco-Health Hom Mali (Certified Organic/GI/SRP low-carbon protocols, functional low-GI attributes, targeted at high-end export, wellness, and corporate gifting markets).

**Framework 2:** Five-Step Supply-Chain-to-CDJ Alignment Framework: Implementing this architecture requires a continuous, synchronized 5-step operating process: (Step 1) Market-Segment Mapping: Identify target consumer profiles and determine critical CDJ decision drivers (e.g., aroma intensity, carbon footprint, packaging size); (Step 2) Specification Translation: Convert consumer decision drivers into concrete farm-level agronomic criteria (certified seed selection, alternate wetting and drying, harvesting at 28-30 days after flowering) and mill intake metrics (optical grading, DNA checks, temperature-controlled storage); (Step 3) Upstream-Midstream Capability Execution: Mobilize community enterprise machinery sharing and mill lot segregation to ensure complete physical chain-of-custody; (Step 4) Omnichannel Evidence Expression: Communicate verified attributes across retail touchpoints via transparent packaging design, certified seals, and interactive digital traceability; and (Step 5) Closed-Loop Market Feedback: Aggregate customer review data, retail return metrics, and channel margins into pre-season governance reviews, adjusting farmer price incentives and seed allocations for the subsequent season.

**Theoretical and Methodological Novelty**

This research contributes novel theoretical insights to both supply chain management and consumer marketing literature. First, while conventional CDJ scholarship focuses on retail and digital communication touchpoints (Court et al., 2009; Furquim et al., 2023), this study proves that CDJ touchpoint efficacy in agri-food markets is fundamentally bounded by upstream operational compliance. Without certified foundation seed, combine harvester sanitation, and moisture-controlled aeration, promotional brand claims collapse during the post-purchase evaluation. Second, the study shifts agricultural supply chain alignment from internal cost-minimization toward customer-journey responsiveness, establishing traceability not as an administrative burden, but as a primary competitive mechanism for value creation and equitable farmer profit distribution.

**Study Limitations and Future Research Directions**

Several methodological boundaries of this study should be recognized. First, the empirical dataset is derived from three qualitative interview sessions within Ubon Ratchathani province; while rich in multi-stakeholder depth (producers, industrial millers, and scientific researchers), the sample size does not capture the full diversity of agro-climatic zones across the wider Thung Kula Ronghai basin. Second, consumer preferences were analyzed through secondary market literature and stakeholder operational perceptions rather than direct consumer focus groups or point-of-sale scanner data. Third, the proposed three-tier architecture and five-step alignment framework represent conceptual models grounded in exploratory qualitative findings that require longitudinal empirical validation. Future empirical research should conduct quantitative consumer choice experiments to measure willingness-to-pay for QR-verified provenance and evaluate pilot contractual implementations between Large-Scale Farmer Enterprises and export rice mills.

## Conclusion

This study demonstrates that adding sustainable value to Ubon Ratchathani jasmine rice requires fundamentally bridging the operational chasm between agricultural production and consumer decision dynamics. Multi-stakeholder qualitative evidence reveals that environmental volatility, quality dilution during aggregation, and disconnected market feedback severely hinder market value realization. Mapping empirical realities onto the Customer Decision Journey demonstrates that consumer consideration, evaluation, purchase, and loyalty are directly contingent upon varietal purity, lot segregation, digital traceability, and tiered product design. The grounded three-tier product architecture and five-step alignment framework formulated herein provide agricultural policymakers, enterprise leaders, and commercial millers with an actionable roadmap to transform commodity rice logistics into a responsive, evidence-backed specialty food value chain.

## Acknowledgements

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## References

Braun, V., & Clarke, V. (2006). Using thematic analysis in psychology. Qualitative Research in Psychology, 3(2), 77-101. https://doi.org/10.1191/1478088706qp063oa

Court, D., Elzinga, D., Mulder, S., & Vetvik, O. J. (2009). The consumer decision journey. McKinsey Quarterly, 3, 96-107.

Furquim, T. S. G., da Veiga, C. P., Veiga, C. R. P., & Silva, W. V. (2023). The different phases of the omnichannel consumer buying journey: A systematic literature review and future research directions. Journal of Theoretical and Applied Electronic Commerce Research, 18(1), 79-104. https://doi.org/10.3390/jtaer18010005

Kongsri, S., Sricharoen, P., Limchoowong, N., & Kukusamude, C. (2021). Tracing the geographical origin of Thai Hom Mali rice in three contiguous provinces of Thailand using stable isotopic and elemental markers combined with multivariate analysis. Foods, 10(10), 2349. https://doi.org/10.3390/foods10102349

Lee, J. Y., Pavasopon, N., Napasintuwong, O., & Nayga, R. M., Jr. (2020). Consumers' valuation of geographical indication-labeled food: The case of Hom Mali rice in Bangkok. Asian Economic Journal, 34(1), 79-96. https://doi.org/10.1111/asej.12196

Lincoln, Y. S., & Guba, E. G. (1985). Naturalistic Inquiry. Sage Publications.

Srisukwatanachai, T., Wang, Y., & Prom-u-thai, C. (2025). The impact of sensory perceptions and country-of-origin information on consumer preferences for fragrant rice in China and Thailand. Foods, 14(4), 603. https://doi.org/10.3390/foods14040603

Suwannaporn, P., & Linnemann, A. (2008). Consumer preferences and buying criteria in rice: A study to identify market strategy for Thailand jasmine rice export. Journal of Food Products Marketing, 14(4), 33-53. https://doi.org/10.1080/10454440801986349

Thai Department of Foreign Trade. (2020). Thai Hom Mali Rice Certification Mark Regulations and Export Standards. Ministry of Commerce, Thailand

# Formulation and Quality Evaluation of Protein-Fortified Puffed Snacks from Luem Pua Black Glutinous Rice (*Oryza sativa* L.)

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## Abstract

Luem Pua (*Oryza sativa* L.), a pigmented Thai glutinous rice, exhibits high potential for functional snack development. This study aimed to develop a protein-fortified puffed black glutinous rice snack and optimize its flavor profile. Soy protein was incorporated at 0%, 10%, 15%, and 20% (w/w), followed by the evaluation of physicochemical and sensory properties. Results indicated that increasing soy protein level from 0% to 20% significantly increased hardness (from 12.32 to 18.39 N), while significantly reducing crispness (number of fracture peaks, from 40.60 to 20.30) and expansion ratio (from 4.13 to 3.27) ($p<0.05$). The 10% soy protein formulation achieved the highest sensory scores for taste (7.0), crispness (7.8), and overall liking (7.4), and was thus selected for flavor optimization. This optimal base was subsequently flavored with green tea, *Sam Klor* (a traditional Thai seasoning blend of coriander root, garlic, and black pepper), or ginger powder. Among these, the ginger-flavored snack exhibited the lowest hardness (23.00 N) and a bulk density of 0.12 g/cm³. Furthermore, it received significantly higher ($p<0.05$) sensory scores for color (7.4), aroma (7.2), and overall liking (7.4). The final products maintained low moisture contents (4.02–4.07%) and water activity values (0.33–0.37). Conclusively, incorporating 10% soy protein with ginger flavoring yields a highly acceptable, value-added puffed snack from Luem Pua rice.

**Keywords:** *Black glutinous rice, Puffed snack, Protein fortification, Sensory evaluation, Physicochemical properties*

# Physicochemical Properties of Functional Plant-Based Milk Developed from Different Purple Glutinous Rice Cultivars

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## Abstract

This study aimed to optimize the rice-to-water ratio and evaluate the effect of different purple glutinous rice (*Oryza sativa* L.) cultivars on the physicochemical, antioxidant, and sensory properties of a functional plant-based milk. A Completely Randomized Design was employed in two experimental phases. First, three rice-to-water ratios (1:10, 1:15, and 1:20) were evaluated. Subsequently, using the optimal ratio, four purple glutinous rice cultivars (Leum Pua, Rachinee, Na Si Nuan, and Phatthalung) were comparatively assessed for color, viscosity, total soluble solids (TSS), total phenolic content (TPC), total flavonoids, total anthocyanins, DPPH radical scavenging activity, and sensory acceptability. Results indicated that the 1:10 ratio was optimal, yielding significantly highest redness (a*), viscosity (34.90 cP), TSS (6.27%), and overall sensory preference ($p \leq 0.05$). Among the cultivars tested at this ratio, the Phatthalung cultivar exhibited the most superior biochemical profile, containing the highest TPC (119.85 mg GAE/100ml), flavonoids (388.77 mg RE/100 ml), anthocyanins (9.27 mg/ml), and DPPH radical scavenging activity (58.38%). Sensorial analysis revealed that plant-based milk from Phatthalung and Leum Pua cultivars achieved the highest overall acceptability scores with no significant difference. In conclusion, utilizing the Phatthalung cultivar at a 1:10 extraction ratio presents an effective formulation for developing an antioxidant-rich purple rice milk.

**Keywords:** *Purple glutinous rice, Plant-based milk, Anthocyanins, Antioxidant activity, Physicochemical properties*

# Instant Lanna Purple Sticky Rice Powder with Durian: Optimization, Bioactive Retention, and Consumer Acceptability

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## Abstract

This study investigated processing parameters and optimized the formulation of instant purple sticky rice powder with durian, utilizing indigenous Lanna purple sticky rice (*Oryza sativa* L. var. *glutinosa*) as a functional base matrix. Lanna purple sticky rice was washed, soaked for 6 hours, steamed until fully gelatinized, dried at 60°C for 6 hours, ground, and sieved (80-mesh). The experiment included a control (100% Lanna purple sticky rice flour) and three formulations partially substituted with durian powder and coconut milk powder at 5% (Formula A), 10% (Formula B), and 15% (Formula C) of total rice flour weight. Formula C was identified as the optimal formulation, comprising 65.3% purple sticky rice powder, 15% durian powder, 15% coconut milk powder, and 4.7% brown sugar. Physicochemical quality analysis of Formula C (15% substitution) yielded optimal results, with lightness (L*), redness (a*), and yellowness (b*) values of 63.50±0.13, 4.32±0.04, and 6.17±0.07, respectively. Proximate analysis showed a low water activity ($a_w$) of 0.46 ± 0.01 and moisture content of 5.93±0.05%, along with 1.23±0.23% ash, 78.74±0.52% total carbohydrates, 8.15±0.20% crude protein, 5.95±0.06% crude fat, and 1.04±0.00% crude fiber, providing a total caloric value of 401.11 kcal/100 g. Bioactive profiling demonstrated total anthocyanin retention of 0.268 µg/kg and total phenolic content (TPC) of 34.92 mg TE/g, with DPPH and ABTS radical-scavenging capacities of 96.59 and 2.13 mg TE/g, respectively. Sensory evaluation using a 9-point Hedonic scale showed statistically significant differences ($p \leq 0.05$) across all attributes, with Formula C achieving the highest mean liking scores (8.50-8.67) corresponding to "like very much". Consumer testing (n = 100) revealed a 98% overall product acceptance rate and 94% purchase intent at 15 THB per 25 g sachet.

**Keywords:** *Lanna purple sticky rice, Durian powder, Anthocyanin retention, Bioactive properties, Consumer acceptability*

# Development and Characterization of a High-Purity Gamma-Aminobutyric Acid Certified Reference Material for Reliable Food Analysis

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## Abstract

Gamma-aminobutyric acid (GABA) is a naturally occurring non-protein amino acid found in various foods, particularly germinated rice and fermented products, and has gained attention for its potential health benefits. Accurate determination of GABA content is essential for quality control, nutritional labeling, and supporting health-related claims. Certified reference materials (CRMs) play a crucial role in ensuring metrological traceability and reliability of analytical results. This study aimed to develop and characterize a high-purity GABA CRM in accordance with ISO 17034, ISO 33405, and ISO 33407. GABA purity was characterized using two independent approaches: the mass balance method and quantitative nuclear magnetic resonance (qNMR) spectroscopy. The mass balance method involved determining structurally related impurities by high-performance liquid chromatography with charged aerosol detection (HPLC-CAD), water content by Karl Fischer titration, and volatile and non-volatile residues by thermogravimetric analysis. The GABA mass fractions obtained by mass balance and qNMR were 985.06 and 990.83 mg/g, respectively, with no statistically significant difference between methods ($p > 0.05$). Between-unit homogeneity and short-term and long-term stability were evaluated to establish material suitability for certification. The certified GABA mass fraction was assigned as 988 mg/g with an expanded uncertainty of 14 mg/g ($k = 2$), corresponding to approximately 95% confidence. The developed CRM provides a metrologically traceable reference for method validation, instrument calibration, and quality assurance, supporting accurate and comparable GABA measurements in food and functional food products.

**Keywords:** *Gamma-aminobutyric acid (GABA), Certified reference material, Purity assessment, Mass balance, Quantitative Nuclear Magnetic Resonance Spectroscopy (qNMR)*

# Optimization of Wort Production for a Low-Calorie, IMO-Enriched Beer Using Pin Kaset 1 Rice

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## Abstract

This study aimed to produce a prebiotic, low-calorie beer using Thai rice as an adjunct. Pin Kaset 1 rice was selected due to gelatinization temperature lower than optimal temperature of alpha-amylase, a catalytic for starch digestion. Isomaltooligosaccharide (IMO) synthesis during wort production was then optimized by adjusting the rice ratio and transglucosidase concentration. The optimal condition provided 17.50 °Brix with IMO content 143±18.80 g/L including of isomaltose, isomaltotriose, and panose. The wort was diluted to 6 °Brix and then commercial yeast strain *Saccharomyces cerevisiae* var. chevalieri (LA01) was used to ferment the low-calorie beer at 10 °C and 20 °C and compared with *Hunseniaspora opuntiae* G77-2. Sensory quality and consumer acceptance did not differ significantly among the beer samples. However, beer fermented at 10 °C with the commercial yeast showed slightly higher flavor scores. A 250-mL serving of the finished beer contained 0.25 g ethanol, 7 g IMO, and 5 g sugar, and provided 50 kcal. These findings support the feasibility of producing a low-calorie, IMO-enriched beer from Pin Kaset 1 rice.

**Keywords** *Isomaltooligosaccharide (IMO), Pin Kaset 1, Low-calorie beer, Prebiotic beer*



SECTION

# PS5

## Health, Medical and Pharmaceutical Related Product or Variety

Nutrition, functional foods and health benefits of rice

Poster 8

# Breeding for White and Pigmented Extra-Long Grain Rice by Crossing Basmati 1121 and Riceberry

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## Abstract

Purple Rice has gained increasing popularity among urban consumers due to rising health consciousness and nutritional awareness, particularly to meet the specific demands of the Middle Eastern rice market. This research aims to improve white and purple extra-long grain rice varieties to meet the needs of health-conscious and nutritionally aware rice consumers in the Middle East. Basmati 1121 was crossed with Riceberry to obtain $F_1$ seeds. An $F_2$ population of 300 plants was then planted, allowing each plant to self-pollinate, and $F_3$ seeds were collected using the single seed descent method. Evaluation of aleurone layer color segregation in the $F_2$ population revealed a 9:3:4 ratio, indicating that aleurone layer color is controlled by two genes via recessive epistasis. The segregation of brown rice grain length and cooked grain elongation was a normal continuous distribution. In $F_4$, eleven lines with brown rice grain lengths greater than 7.0 mm and cooked grain elongation rates greater than 14.0 mm were selected by pedigree selection until $F_5$. These lines included five white lines and six purple lines, which will be tested in a preliminary yield trial in $F_5$. Evaluation of bioactive compounds among the selected lines showed that the purple line RB2-48 exhibited the highest flavonoid content and antioxidant activity, as measured by DPPH and ABTS radical scavenging assays, while Basmati 1121 exhibited the strongest α-amylase and α-glucosidase inhibitory activity. These findings indicate that the selected lines combine favorable grain quality with health-promoting properties, supporting their potential development into new rice varieties for the health-conscious Middle Eastern market.

**Keywords:** *Purple Rice, White Rice, Extra Long Grain, High Nutrition*

# Development and Characterization of Organic Purple Rice Bran Oil-Loaded Niosomes for Skin-Care Applications

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## Abstract

Organic pigmented rice, particularly black glutinous rice (Oryza sativa L.), is a promising source of bioactive compounds for skin-care applications. However, the instability and limited topical delivery of rice bran oil may restrict its use. This study aimed to prepare and characterize organic purple rice bran oil-loaded niosomes and evaluate their biological activities. Niosomes containing 3% (w/w) rice bran oil were prepared by a modified thin-film hydration method using sorbitan monostearate and cholesterol (3:7 molar ratio), followed by microfluidization and lyophilization. The reconstituted niosomes exhibited a pH of 6.42 ± 0.07, particle size of 195.1 ± 1.34 nm, PDI of 0.275, zeta potential of −16.62 ± 0.27 mV, and entrapment efficiency of 69.74 ± 0.05%. Transmission electron microscopy revealed predominantly small unilamellar vesicles. The formulation exhibited DPPH radical-scavenging, lipid peroxidation-inhibitory, and tyrosinase-inhibitory activities, with $IC_{50}$ values of 7.45 ± 1.22, 7.01 ± 1.17, and 8.77 ± 0.08 mg/mL, respectively. No apparent cytotoxicity toward skin fibroblast cells was observed, while cell proliferation increased by approximately 24.96% at 1 mg/mL. These findings demonstrate that organic purple rice bran oil-loaded niosomes possess favorable physicochemical properties and biological activities, supporting their potential for further development as a topical skin-care delivery system.

**Keywords:** *Organic purple rice bran oil, Oryza sativa L., Niosomes, Topical delivery*

## Introduction

Pigmented rice, particularly black glutinous rice (*Oryza sativa* L.), is an indigenous crop widely cultivated in northern and northeastern Thailand and is a rich source of bioactive compounds, including anthocyanins, γ-oryzanol, vitamin E, and ferulic acid. These constituents exhibit antioxidant and skin-protective activities and have been associated with the modulation of oxidative stress, inflammation, pigmentation, and skin aging, supporting the potential of pigmented rice-derived ingredients for topical skin care. (Ito, V. C., et.al. 2019) However, the application of rice bran oil in conventional formulations may be limited by the instability of its bioactive constituents and their poor aqueous dispersibility and limited delivery across the skin barrier. Niosomes, composed primarily of nonionic surfactants with cholesterol or other membrane-stabilizing components, offer a versatile vesicular platform for protecting, dispersing, and delivering hydrophilic and lipophilic bioactive compounds. (Chen, S., et.al. 2019) Despite growing interest in niosome systems for natural products, available information on niosomes containing organic pigmented rice bran oil from Thai agricultural sources is limited. Therefore, this study aimed to prepare and characterize organic purple rice bran oil-loaded niosomes using a modified thin-film hydration method and to evaluate their physicochemical properties, morphology, entrapment efficiency, antioxidant and lipid peroxidation-inhibitory activities, tyrosinase inhibition, and cytotoxicity toward skin fibroblast cells.

## Materials and Methods

### Materials

Organic purple glutinous rice (Oryza sativa L.) was obtained from Khao Kho District, Phetchabun Province, Thailand. Chloroform was purchased from RCI Labscan Co., Ltd. (Bangkok, Thailand), while sorbitan monostearate and cholesterol were obtained from S.M. Chemical Supplies Co., Ltd. (Bangkok, Thailand). All other chemicals and reagents were of analytical grade.

### Methods

#### Preparation of Organic Black Rice Bran Oil-Loaded Niosomes

Organic purple rice bran oil-loaded niosomes were prepared using a modified thin-film hydration method based on Manosroi et al. (2011). Sorbitan monostearate and cholesterol (3:7 molar ratio; total concentration of 20 mM) were dissolved in chloroform, followed by the incorporation of organic purple rice bran oil. The organic solvent was removed using a rotary evaporator at 40 °C for 30 min to form a thin lipid film, which was further dried in a fume hood for 24 h. The lipid film was subsequently hydrated with deionized water at 40 °C, and the resulting dispersion was subjected to high-pressure microfluidization at 10,000 psi for three cycles. Finally, the niosomal dispersion was freeze-dried to obtain organic black rice bran oil-loaded niosomes in powder form.

#### Physical Characterization of Niosome

The appearance, color, and sedimentation behavior of the niosomal dispersions were evaluated by visual observation. The pH of the formulation was determined using an appropriate calibrated pH meter. Particle size, polydispersity index (PDI), and zeta potential were determined using dynamic light scattering with a NanoPlus HD particle analyzer (Micromeritics Instruments Ltd., USA). All measurements were performed in triplicate, and the results were expressed as mean ± standard deviation.

#### Transmission Electron Microscopy

The morphology of the niosomal vesicles was examined using transmission electron microscopy (TEM). Samples were placed onto carbon-coated copper grids and allowed to air-dry at room temperature. The samples were subsequently examined using a FEI Tecnai G2 transmission electron microscope (Eindhoven, The Netherlands) operated at an accelerating voltage of 80 kV (Obeid, M.A., et.al.,2017)

#### Entrapment Efficiency Determination

The entrapment efficiency (EE) of organic purple rice bran oil in the niosomal formulation was determined by gel filtration chromatography using Sephadex® G-50 and purified water as the eluent, following the method of Manosroi et al. (2010). The concentration of free, non-entrapped oil was determined by UV–visible spectrophotometry at 470 nm. The entrapment efficiency was calculated as:

$$EE\ (\%) = [(C_t - C\boldsymbol{f}) / C_t] \times 100$$

where $C_t$ and $C\boldsymbol{f}$ represent the total and free oil concentrations, respectively.

#### Evaluation of Lipid Peroxidation Inhibition via TBARS Assay

Lipid peroxidation inhibitory activity was evaluated using the thiobarbituric acid reactive substances (TBARS) assay with slight modifications from Zeb and Ullah (2016). Briefly, egg yolk homogenate (10%, v/v) was mixed with the test sample at various concentrations and 10 mM $FeSO_4$ to induce lipid peroxidation. The mixture was incubated at 37 °C for 1 h and

subsequently reacted with thiobarbituric acid (TBA) reagent at 95 °C for 60 min. After cooling and centrifugation, the absorbance of the supernatant was measured at 532 nm. Vitamin E was used as a positive control. The percentage inhibition was calculated as:

$$\text{Inhibition (\%)} = A_{control} - A_{sample}/A_{control} \times 100$$

The $IC_{50}$ value was determined by non-linear regression analysis.

**DPPH Radical Scavenging Activity**

Free radical scavenging activity was determined using the DPPH assay according to Manosroi et al. (2012). Briefly, 50 µL of the sample at various concentrations was mixed with 50 µL of DPPH solution (0.5 mg/mL in ethanol) in a 96-well microplate and incubated at 25 °C for 30 min. Absorbance was measured at 515 nm using a microplate reader, with vitamin C as the positive control. Radical scavenging activity was calculated as:

$$\text{\% Scavenging} = [(A0 - A1)/A0] \times 100$$

where $A_0$ and $A_1$ represent the absorbance of the control and sample, respectively. The $SC_{50}$ value was determined from the concentration–response relationship.

**Tyrosinase Inhibition Activity**

Tyrosinase inhibitory activity was evaluated using a modified dopachrome method with L-tyrosine as the substrate. (Manosroi et al.,2012) Sample solution, L-tyrosine (0.1 mg/mL), mushroom tyrosinase (0.1 mg/mL), and phosphate buffer (0.1 mM) were mixed in a 96-well microplate and incubated at 37 °C for 60 min. Absorbance was measured at 450 nm before and after incubation using a microplate reader. Vitamin C was used as the reference standard. Tyrosinase inhibition was calculated as:

$$\text{\% Inhibition activity} = [(A-B) - (C-D)] / (A-B) \times 100$$

where (A) and (B) represent the absorbance of the blank after and before incubation, respectively, while (C) and (D) represent the absorbance of the sample after and before incubation, respectively. The $IC_{50}$ value was determined from the concentration–response relationship.

**In Vitro Cytotoxicity Assay (Resazurin Reduction Assay)**

The cytotoxicity of the niosomal formulations was evaluated using a resazurin reduction assay based on cellular metabolic activity. Skin fibroblast cells were seeded in 96-well plates and cultured in DMEM supplemented with 10% fetal bovine serum and antibiotics at 37 °C under 5% $CO_2$. After 24 h, the cells were treated with different concentrations of the test formulations for a further 24 h. Cells treated with 0.1% DMSO and doxorubicin served as negative and positive controls, respectively. Resazurin was subsequently added, and the cells were incubated for 2 h. Fluorescence was measured at an excitation wavelength of 560 nm and an emission wavelength of 590 nm, following Ahmed et al. (1994). Cell viability was calculated relative to the negative control as:

$$\text{Cell viability (\%)} = [(\text{Signal of treated cells} - \text{Signal of blank}) / (\text{Signal of control cells} - \text{Signal of blank})] \times 100$$

**Statistical Analysis**

The results are expressed as mean ± standard deviation (n±3), and statistical analysis was performed with SPSS 10.1 for Windows® (SPSS®, Chicago, USA).

## Results and Discussion

### Physicochemical Properties and Morphology of Organic Purple Rice Bran Oil-Loaded Niosomes

Organic purple rice bran oil-loaded niosomes were successfully prepared by a modified thin-film hydration method using sorbitan monostearate and cholesterol at a molar ratio of 3:7, with 3% (w/w) rice bran oil. Microfluidization markedly improved the physicochemical properties of niosomal dispersion. The mean particle size decreased from 541.2 ± 0.21 nm before microfluidization to 195.1 ± 1.34 nm after treatment, while the PDI decreased from 0.471 ± 0.00 to 0.275 ± 0.00, indicating the formation of a smaller and more homogeneous vesicle population.

The zeta potential also increased in magnitude from −8.79 ± 0.12 to −16.62 ± 0.27 mV following microfluidization, suggesting improved electrostatic stabilization of the dispersion. The reconstituted niosomes appeared as a clear, pale-yellow dispersion without visible sedimentation and exhibited a pH of 6.42 ± 0.07, supporting their potential suitability for topical application. The color parameters were L* = 41.49 ± 0.02, a* = −1.77 ± 1.23, and b* = −4.89 ± 2.07 (Table 1; Figure 1).

Transmission electron microscopy confirmed the formation of nanoscale vesicular structures in both blank and oil-loaded formulations, predominantly exhibiting small unilamellar morphology (Figure 2). These observations were consistent with the particle size reduction obtained after microfluidization.

**Table 1.** Physicochemical characteristics of blank niosomes and organic purple rice bran oil-loaded niosomes before and after microfluidization

| Blank niosomes and loaded niosomes (3% organic purple rice bran oil) | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| cycle | Appearance | pH | L* | a* | b* | size (nm) | Polydispersity Index (PDI) | Zeta potential (mV) |
| 0 | Turbid yellow, no sedimentation | 6.30±0.02 | 56.61±0.03 | -0.12±1.02 | -6.54±1.05 | 541.2±0.21 | -8.79 ±0.12 | 0.471±0.0 |
| 3 | Pale yellow, Clear, no sedimentation | 6.42±0.07 | 41.49±0.02 | -1.77±1.23 | -4.89±2.07 | 195.1±1.34 | -16.62±0.27 | 0.275±0.0 |

Data was expressed as mean ± S.D. (n=3)



**Figure 1.** Physical appearance of freeze-dried organic purple rice bran oil-loaded niosomes. rice bran oil- loaded niosomes containing 3% (w/w) oil

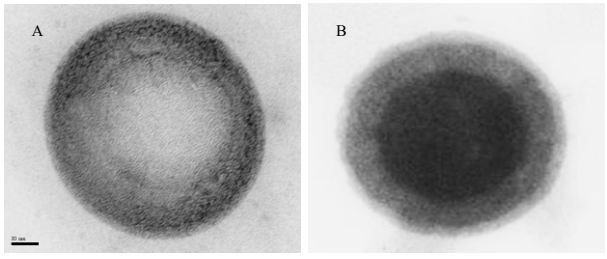


**Figure 2** Transmission electron micrographs of niosomes at 80,000× magnification: (A) blank niosomes and (B) organic purple

**Entrapment Efficiency of Organic Purple Rice Bran Oil**

The entrapment efficiency of organic purple rice bran oil was 69.74 ± 0.05%, indicating successful incorporation of a substantial proportion of the oil into the niosomal system. The lipophilic nature of rice bran oil may facilitate its incorporation within the hydrophobic region of the nonionic surfactant bilayer, contributing to the observed entrapment efficiency.

**Biological Activities and Cytocompatibility**

The biological activities of the formulations are summarized in Table 2. The oil-loaded niosomes exhibited stronger DPPH radical-scavenging activity than the free oil, with $SC_{50}$ values of 7.45 ± 1.22 and 41.13 ± 2.56 mg/mL, respectively. Vitamin C showed substantially greater activity, with an $SC_{50}$ of 0.66 ± 0.02 mg/mL. The enhanced activity of the niosomal formulation may be attributed to improved dispersion and increased accessibility of lipophilic antioxidant compounds in the aqueous assay system. Similarly, the niosomal formulation retained lipid peroxidation-inhibitory activity, with an $IC_{50}$ value of 7.01 ± 1.17 mg/mL, which was significantly higher to that of the free oil (7.37 ± 0.89 mg/mL). Meanwhile, tocopherol exhibited markedly stronger activity ($IC_{50}$ = 0.075 ± 0.02 mg/mL).

Niosomal encapsulation also enhanced tyrosinase inhibitory activity. The oil-loaded niosomes showed an $IC_{50}$ of 8.77 ± 0.08 mg/mL, compared with 21.93 ± 0.06 mg/mL for the free oil. Although the activity was lower than those of the reference compounds BHT (0.37 ± 0.03 mg/mL) and kojic acid (0.07 ± 0.01 mg/mL), the results suggest that niosomal encapsulation improved the apparent availability of bioactive constituents.

**Table 2** Antioxidant and anti-tyrosinase activities of organic black rice bran oil and loaded niosomes compared to standards

| Sample | lipid peroxidation (TBARs mg/ml) | DPPH inhibition assay ($SC_{50}$ mg/ml) | Tyrosinase inhibition assay ($IC_{50}$ mg/ml) |
|---|---|---|---|
| Organic Black Rice Bran Oil | 7.37±0.89 [a] | 41.13±2.56[a] | 21.93±0.06[a] |
| Loaded Organic Black Rice Bran Oil Niosomes | 7.01±1.17 [b] | 7.45±1.22[b] | 8.77±0.08[b] |
| Vitamin C | - | 0.66±0.02[c] | - |
| Tocopherol | 0.075±0.02[c] | 0.075±0.02[d] | - |
| BHT | - | - | 0.37±0.03[c] |
| Kojic acid | - | - | 0.07±0.01[d] |

[a-d] Means within the same column with different letters (a–d) are significantly different ($p \leq 0.05$) Data points with (*) are significantly different from cream base at $p<0.05$

The cytotoxicity assay further demonstrated that the oil-loaded niosomes showed no apparent cytotoxicity toward skin fibroblast cells under the tested conditions. At 1 mg/mL, cell proliferation increased by approximately 24.96% compared with the control. Collectively, these findings demonstrate that organic purple rice bran oil-loaded niosomes possess favorable physicochemical characteristics, antioxidant and tyrosinase-inhibitory activities, and good preliminary cytocompatibility, supporting their potential for further development as topical skin-care delivery systems.

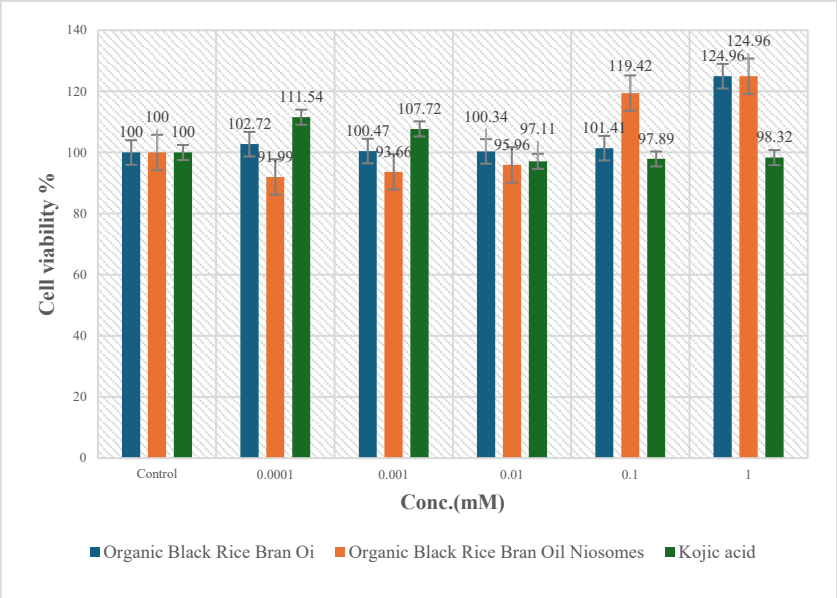


**Figure 3** The percentages of human skin fibroblast viability by resazurin reduction assay of the blank niosomes (a) and organic purple rice bran oi loaded in niosomes (b) (each value represents mean ± SD, $n = 3$)

## Conclusion

This study demonstrated the successful development of organic purple rice bran oil-loaded niosomes using a modified thin-film hydration method combined with high-pressure microfluidization. The optimized formulation exhibited favorable nanoscale characteristics, with a mean particle size of 195.1 ± 1.34 nm, PDI of 0.275, zeta potential of −16.62 ± 0.27 mV, and entrapment efficiency of 69.74 ± 0.05%. The niosomes demonstrated antioxidant, lipid peroxidation-inhibitory, and tyrosinase-inhibitory activities, with no apparent cytotoxicity toward skin fibroblast cells under the tested conditions. These findings support the potential of organic purple rice bran oil-loaded niosomes as a delivery system for topical cosmetic applications. Further studies on formulation stability, skin permeation and retention, reconstructed skin models, and in vivo safety and efficacy are warranted to confirm their practical applicability.

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## References

Ahmed SA, Gogal RM Jr, Walsh JE. A new rapid and simple non-radioactive assay to monitor and determine cell viability. Journal of Immunological Methods. 1994;170(2):211–224.

Chen, S., Hanning, S., Falconer, J., Locke, M., & Wen, J. Recent advances in non-ionic surfactant vesicles (niosomes): Fabrication, characterization, pharmaceutical and cosmetic applications. European Journal of Pharmaceutics and Biopharmaceutics, 2019;144, 18–39

Ito, V. C., and Lacerda, L. G. Black rice (*Oryza sativa* L.**):** A review of its historical aspects, chemical composition, nutritional and functional properties, and applications and processing technologies. *F*ood Chemistry. 2019*;* 301*,* 125304.

Manosroi A, Chutoprapat R, Abe M, Manosroi W, Manosroi J. Anti-aging efficacy of topical formulations containing niosomes entrapped with rice bran bioactive compounds. Pharmaceutical Biology. 2012; 50:208–224.

Manosroi A, Boonpisuttinant K, Winitchai S, Manosroi W, Manosroi J. Free radical scavenging and tyrosinase inhibition activity of physic nut (Jatropha curcas Linn.) seed oil entrapped in niosomes. Current Nanoscience. 2011;7(5):825–829.

Manosroi A, Ruksiriwanich W, Abe M, Sakai H, Manosroi W, Manosroi J. Biological activities of the rice bran extract and physical characteristics of its entrapment in niosomes by supercritical carbon dioxide fluid. The Journal of Supercritical Fluids. 2010;54(2):137–144.

Obeid MA, Khadra I, Mullen AB, Tate RJ, Ferro VA. The effects of hydration media on the characteristics of non-ionic surfactant vesicles (NISV) prepared by microfluidics. International Journal of Pharmaceutics. 2017; 516:52–60.

Zeb, A., and Ullah, F. A. Simple spectrophotometric method for the determination of thiobarbituric acid reactive substances in fried fast foods. Journal of Analytical Methods in Chemistry, 2016, 1-5.

# NKI14094-13-1-4-2-1-SKN-2 : A Promising Black Glutinous Rice Line with High Nutritional Value for Farmers and Consumers in the Future

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## Abstract

Black glutinous rice is well known for its high nutritional value as it is a source of anthocyanin and other antioxidants. Northeastern Thailand is the important region for glutinous rice because it is the stable food for many million people. Many traditional black glutinous rice varieties are grown in the rainfed area in this region mainly used for household consumption and niche market. Kham Noi is the most popular traditional variety because of its outstanding cooking quality and aroma. However, this traditional variety is not resistant to lodging and blast causing a decline in farmers' acceptability, and the current diversity of serotypes of rice blast disease is causing a decline in rice yield. Rice Department has conducted a project funded by Thailand Science Research and Innovation with the objective to develop a photoperiod-sensitive black glutinous variety with blast and lodging resistance, while remaining good cooking quality and high nutritional value, as an alternative variety for local farmers and consumers in Thailand. The breeding program had been conducted from 2014 to 2025 by northeastern rice research center group and successfully resulted in a promising rice line designated NKI14094-13-1-4-2-1-SKN-2 derived from a single cross between a female parent, RGDU10017-1-MAS-49-4-1-NKI-1-2 and a male parent Hawm Phu Kiew. The new rice line is a photoperiod-sensitive rice with the flowering date at 20$^{th}$ October, similar to Kham Noi but it is more resistant to lodging and leaf blast than Kham Noi. The average yield grown at farmer fields was 518kg/rai (3.24 ton/ha), 20 percent higher than Kham Noi. Regarding the physical properties, the rice hull color was black. The brown rice color was purple. It was classified as long grain glutinous rice with a slender shape. The steamed rice was sticky and soft. For grain chemical properties and nutritional value, the total phenolic, flavonoid and vitamin E content is 3,935.03±224.24 mg GAE/kg, 4,212.35±418.37 mg/kg and 79.20±0.53 mg/kg, respectively. The content of anthocyanin, including cyanidin and pelargonidin is 919.49±66.78 mg/kg and 543.02±39.44 mg/kg, respectively. Gamma-oryzanol content is 379.47±3.92 mg/kg. Last but not least, antioxidant content is 3,872.14±102.07 mg AAE/kg. This promising rice line could be promoted as a healthy rice for the niche market and will be submitted to Thailand Rice Variety Board to certify it as a new variety in the future.

**Keywords:** *Black, Glutinous, Rice, Blast Resistance, Anthocyanin, Anti-oxidants*

# Rice Protein Hydrolysates Derived from Pigmented Leaf and Bran: Nutritional Analysis and Health Benefits

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## Abstract

Using rice biomass as edible products and functional ingredients for humans is novel and could add significant value for farmers. This research aims to analyse the nutritional value and phytochemical properties of protein hydrolysates (PH) derived from vegetative leaves of Rainbow Rice (RBR02) and Riceberry (RB), which express high and low anthocyanin-to-chlorophyll ratios, respectively. The analysis results were compared with RB seed bran, a popular source of PH for rice, which also contains a high anthocyanin content. In proximate analyses, RB bran PH had significantly higher caloric content than both RBR02 and RB leaf PHs. RB bran PH contained significantly higher energy levels from Fat and Carbohydrate than the leaf PHs. Both RBR02 and RB had similar protein content at 20%, while PHs were 30.6% and 28.8%, respectively; RB bran PH had 14% protein (50% lower). Nonetheless, rice leaf and bran PH contained all nine essential amino acids, but differed in relative contents. Aspartic and Glutamic acids, the major amino acids in leaf PHs, were 6.4 and 4.2 g/100 g for RBR02 and 5.5 and 5.0 g/100 g for RB PHs, respectively. In general, RBR02 leaf PH contained higher concentrations of essential amino acids than RB leaf PH, including branched-chain amino acids (BCAA) Leucine, Isoleucine, and Valine; in contrast, Methionine was identified only in RBR02 leaf PH, and only in small quantities. Interestingly, RBR02 leaf PH contained higher Phenolic compounds (55 mg GAE/g) than RB leaf (31 mg GAE/g) and bran PHs (33 mg GAE/g) but had similar flavonoid content (20-22 mg CE/g). The leaf PH contained more p-Coumaric acid (0.117–0.218% w/w) but less Protocatechuic acid than RB bran PH (0.095% w/w). In general, RBR02 and RB Leaf PH shared common polyphenols but in higher quantities, particularly p-Coumarin and Chlorogenic acid. Nonetheless, only RBR02 had interesting levels of the Flavonoid Catechin and shared Rutin with RB bran PH. To understand the functional roles of leaf and bran PH, we performed in vitro analyses to assess inhibition of angiotensin-converting enzyme (ACE) and α-amylase, an important digestive enzyme that converts starch molecules to glucose. RBR02 and RB leaf PH had low IC50 values at 1.05 and 1.15 mg/ml, respectively, whereas RB bran PH had an IC50 of 3.96 mg/ml. However, RB bran PH inhibited α-amylase more effectively than both leaf PHs. RBR02 leaf PH and RB leaf PH showed 51% and 52% inhibition, respectively, at 30 mg/ml, while RB bran PH showed 31% inhibition at 1 mg/ml. This result clearly showed that both leaf PHs were more efficient at inhibiting ACE but less efficient at inhibiting α-amylase than rice bran PH. Further in vivo analyses are needed to confirm their roles in ameliorating hypertension and diabetes.

**Keywords:** *Rice leaf, Functional analysis, Flavonoids and Phenolic compounds*

# Evaluation of Grain Characteristics and Yield Components in $F_2$ Populations Derived from Crosses Between Cultivated and Weedy Rice

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## Abstract

Enhancing genetic diversity is essential for improving yield potential in rice breeding programs. Weedy rice represents a valuable genetic resource due to its substantial genetic variability and potential contribution of favorable yield-related traits. This experiment aimed to evaluate grain characteristics and yield components in $F_2$ populations derived from five crosses between cultivated rice and weedy rice: RD41 × WDR5, RD85 × WDR1, RD95 × WDR3, RD95 × WDR5, and RD97 × WDR5. The evaluated traits included total grains per panicle, filled grains per panicle, spikelet fertility, grain weight per panicle, and 100-grain weight, and awn presence. The results revealed considerable phenotypic variation among the $F_2$ populations. Mean grain weight per panicle ranged from 2.37 to 3.31 g, while 100-grain weight ranged from 2.60 to 2.77 g. The RD95 × WDR5 population exhibited the highest mean grain weight per panicle (3.31 g), filled grains per panicle (119.53), and total grains per panicle (139.30). Meanwhile, RD97 × WDR5 showed the highest mean 100-grain weight (2.77 g). Mean spikelet fertility ranged from 79.63% to 87.41%, with RD85 × WDR1 exhibiting the highest value. Variation in awn presence was also observed among the segregating populations, indicating the segregation of grain morphological traits inherited from the parental lines. These findings demonstrate substantial phenotypic variation in early segregating populations and highlight the potential of weedy rice as a genetic resource for broadening the genetic base of cultivated rice. The observed variation provides opportunities for selecting promising individuals with favorable yield-related traits in subsequent breeding generations.

**Keywords:** *Genetic diversity, Weedy rice, Grain characteristics, Yield components*

# Selection and Evaluation of Black Short Grain Breeding Lines Associated with Yield, Cooking Quality, High Nutrition and Antioxidant Potential Derived from Indica Black Rice x Japonica White Rice

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## Abstract

The combination of the trend of Japanese food consumption with the health benefits of black rice is in high demand for rice consumers in Thailand. For this challenge, incorporation of desirable traits from tropical indica black rice, Riceberry and temperate japonica white rice, Akitakomachi was performed by pedigree selection with maker-assisted selection (MAS). The three candidate lines showed highly favourable agronomic characteristics and a high grain yield, with short grains and good cooking quality, similar to japonica rice, in a tropical climate. In addition, these lines showed black coloration of the pericarp, indicating high nutritional value and phytochemical, antioxidant and antidiabetic activities, similar to those of the Riceberry parent. In terms of the sensory testing of unpolished rice, two breeding lines; 69-1-1 and 72-4-3 showed higher scores than their parents. However, only 69-1-1 was identified as japonica type according to its genetic background. Therefore, this breeding programme can create black short grain rice variety adapted to a tropical environment, similar to japonica-type rice.

**Keywords:** *Anthocyanin, Breeding, Coloured rice (Oryza sativa L.), grain shape*

# From Grain to Green: Stacking Resistance Genes in Colored-Leaf Rice for Organic Biorefinery

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## Abstract

**Introduction and Objectives:** Rainbow Rice (RBR), developed at the Rice Science Center, Kasetsart University, produces colored and striped leaves rich in anthocyanins, dietary fiber, and protein, making it a promising feedstock for green biorefinery and functional ingredients. Leaf-based products, however, demand healthy, pesticide-free foliage, and existing RBR lines remain susceptible to bacterial leaf blight (BLB), blast, and brown planthopper (BPH), which limits organic production. This study aimed to introgress and fix resistance alleles for these three stresses in the homozygous state while retaining the characteristic leaf color patterns, using marker-assisted selection (MAS) and gene pyramiding.

**Materials and Methods:** RBR01, RBR02, and RBR05 served as recurrent parents and were crossed with the donor line PinK+6/RB_3E01. The donor carries genes for blast resistance (TBGI055578_TC_Chr1, TBGI454717, TBGI454800), BLB resistance (SNP_Xa5, SNP_P100Xa21), BPH resistance (Bph_32_2_1223322, OsLecRK3_QBPHR), and submergence tolerance (Sub1C_loci3). It also carries the white-striped leaf trait (OsSAMHD1: wsl1_ch1_503564_G/A), together with loci for alkali spreading value (ALK_ex8_SNP_GC_TT) and aroma (BADH2-3). $BC_1$ and $BC_2$ populations were advanced by self-pollination to the $F_5$ generation, and target genes were selected at each generation using KASP SNP markers.

**Results and Conclusion:** Field evaluation combined with MAS identified 170 advanced lines from the $BC_1F_5$ and $BC_2F_5$ populations that were homozygous for the target genes (12, 59, and 99 lines from RBR01, RBR02, and RBR05, respectively). These lines combine multiple pyramided resistance and tolerance genes with the striped-leaf phenotype, alongside favorable agronomic performance and cooking quality. They are promising materials for developing resilient, organically grown Rainbow Rice for leaf-based functional ingredient production, and will be further evaluated for leaf bioactive compound content.

**Keywords:** *Rainbow Rice, Marker-assisted selection, Gene pyramiding, Disease and insect resistance, KASP markers, Green biorefinery*

# Preparation and Characterization of Sangyod Rice Bran Nano Liposomes for Potential Topical Application

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## Abstract

Sangyod rice bran is a local agricultural resource with potential for development into value-added topical ingredients. This study aimed to prepare liposomes containing Sangyod rice bran extract (SLP) and evaluate their particle characteristics and preliminary physicochemical stability. Rice bran obtained from Phatthalung Province, Thailand, was extracted with propylene glycol using microwave-assisted extraction at 450 W and a material-to-solvent ratio of 1:4 (w/w). Liposomal dispersions were prepared by ethanol injection followed by probe sonication. Blank liposomes and two extract-containing formulations, PG-F1 and PG-F2, were evaluated for particle size, polydispersity index, and zeta potential. PG-F1 was subsequently subjected to six hot–cold cycles, each comprising storage at 45 °C for 24 h followed by 4 °C for 24 h. Mean particle sizes were 205.9 ± 2.81, 227.6 ± 2.48, and 278.7 ± 21.43 nm for blank liposomes, PG-F1, and PG-F2, respectively. Corresponding polydispersity indices were 0.13 ± 0.02, 0.40 ± 0.08, and 0.53 ± 0.09. PG-F1 exhibited a smaller mean particle size and lower polydispersity index than PG-F2. Following thermal cycling, its pH changed from 5.63 ± 0.13 to 5.73 ± 0.22, while viscosity changed from 198.50 ± 5.41 to 203.50 ± 3.21 cP. Within-sample calculations from the stability dataset indicated higher retention of phenolic, flavonoid, and anthocyanin assay responses in PG-F1 than in the free extract. Franz diffusion cell assessment indicated that PG-F1 exhibited approximately 20-fold greater anthocyanin transport than the original extract under the experimental conditions. These preliminary findings support further investigation of SLP for topical formulation development.

**Keywords:** *Sangyod rice bran, Liposomes, Microwave-assisted extraction, Physicochemical stability, Topical application*

## Introduction

Sangyod rice (*Oryza sativa* L.) is a red-pigmented rice cultivar associated with southern Thailand. Its bran provides a potential source of ingredients for value-added applications. Research on Sangyod rice has identified phenolic constituents, including proanthocyanidins, that warrant investigation beyond conventional food uses. Thitipramote et al. [1] reported a total proanthocyanidin content of 1.50 ± 0.16 mg epicatechin equivalents/g extract in a Sangyod rice extract prepared using 70% ethanol. The extract also exhibited 5α-reductase inhibitory activity and promoted hair-related cellular responses and hair regeneration in experimental models. These findings support the cosmetic relevance of Sangyod rice constituents, although they do not directly establish skin-barrier benefits. Furthermore, an evidence relevant to skin-care development has also emerged from comparative studies of Thai pigmented rice. Teeranachaideekul et al. [2] investigated 50% ethanolic extracts of five rice varieties, including Sang-Yod, and evaluated their phytochemical contents and cosmetic-related biological activities. The extracts exhibited antioxidant activity and inhibited advanced glycation end-product formation, collagenase, and elastase in laboratory assays, whereas anti-tyrosinase

activity was comparatively weak. These results provide a rationale for investigating pigmented rice extracts as cosmetic ingredients, while emphasizing that activity varies with rice variety and the endpoint examined. Studies specifically addressing Sangyod rice bran further demonstrate the importance of processing conditions. Aenglong et al. [3] investigated alcalase-assisted production of Sangyod rice bran hydrolysates and showed that incubation time and enzyme concentration affected hydrolysate characteristics and antioxidant activity. Although enzymatic hydrolysates differ from solvent extracts, this study illustrates that the preparation process influences the properties of the resulting ingredient. Complementary evidence of biological activity was reported by Woonnoi et al. [4], who investigated an ethanolic Sangyod rice extract in lipopolysaccharide-stimulated RAW264.7 macrophages and a diabetic rat model. The extract suppressed inflammatory signaling involving Akt, ERK1/2, p38 MAPK, and NF-κB in the cellular model. These preclinical findings support further investigation of Sangyod-derived ingredients but cannot be directly extrapolated to topical efficacy or to extracts prepared using different solvents. The formulation of rice-derived constituents into vesicular carriers offers an additional direction for topical development. Manosroi et al. [5] evaluated rice bran bioactive compounds entrapped in niosomes and incorporated into gel and cream formulations, reporting antioxidant activity and enhanced skin hydration in human assessments. This work provides a precedent for combining rice bran ingredients with vesicular delivery systems. However, it involved a different carrier system and did not establish the performance of Sangyod rice bran liposomes.

Taken together, these studies provide a rationale for investigating Sangyod rice bran as a source of topical ingredients while highlighting the need for formulation-specific characterization. The present study therefore aimed to prepare a propylene glycol extract of Sangyod rice bran using microwave-assisted extraction, incorporate the extract into liposomal dispersions, and evaluate particle size, polydispersity index, zeta potential, and preliminary physicochemical stability under hot–cold cycling. The study represents an initial step toward topical formulation development; improved chemical protection, skin delivery, and skin-barrier performance require separate experimental confirmation.

**Materials and Methods**

Sangyod rice bran (*Oryza sativa* L.) was obtained from Phatthalung Province, Thailand. Propylene glycol (PG), phosphatidylcholine (90%), cholesterol (95%), ethanol (95%), distilled water, and phosphate buffer at pH 7.4 were used for extraction and formulation preparation. Gallic acid, Folin–Ciocalteu reagent, sodium carbonate, quercetin, sodium nitrite, aluminium chloride, and sodium hydroxide were used for phytochemical assays. Potassium chloride and sodium acetate buffers were used for anthocyanin determination.

Preparation of the sang yod rice bran extract was extracted with propylene glycol (PG) at a material-to-solvent ratio of 1:4 (w/w) using microwave-assisted extraction at 450 W. Microwave irradiation was applied intermittently, alternating 1 min of irradiation with 1 min of resting, for a recorded extraction period of 30 min. The temperature was maintained below 80 °C. The extract was filtered through Whatman No. 1 filter paper and stored in light-protective containers at 4 °C until use. Preparation of Sang yod rice bran nano liposome (SLP) was prepared by ethanol injection followed by probe sonication. For formulation PG-F1, 1.2 g of phosphatidylcholine (90%) and 0.2 g of cholesterol (95%) were dissolved in 10 mL of 95%

ethanol. The aqueous phase consisted of 30 mL of phosphate buffer at pH 7.4 and 7 mL of PG extract. The aqueous phase was maintained at 50 °C under magnetic stirring at 600–750 rpm. The lipid phase was slowly injected below the liquid surface, and stirring was continued for 30 min under protection from light. Ethanol was subsequently removed using a rotary evaporator. The dispersion was probe-sonicated at a stated power of 24 W and 100% amplitude for 24 treatment periods of 10 s each, with 1-min resting intervals. An ice bath was used to limit heat accumulation. Samples were centrifuged at 3,000 rpm for 10 min before characterization. Blank liposomes and a second extract-containing formulation, PG-F2, were included for comparison.

The physical properties of samples were evaluated. Briefly, the pH of each sample was measured at 25 °C using a calibrated digital pH meter (Model: SP-2250, Suntex Instruments Co., Ltd., Taiwan) equipped with a Mettler Toledo electrode. The instrument was calibrated with standard buffer solutions (pH 4.0, 7.0, and 10.0) before each use. Measurements were carried out in triplicate, and the values were recorded as mean ± SD. The viscosity of the sample was measured at 25 °C using a rotational viscometer (Model: DVE, Brookfield AMETEK, USA) equipped with spindle No. 61 at 100 rpm. The viscosity values were recorded in centipoise (cP) and expressed as mean ± SD of three measurements. The physical appearance of sample was visually assessed under consistent lighting to observe clarity, homogeneity, and phase separation. The color values were measured using a spectrophotometer (Model: CM-5, Manufacturer: Konica Minolta, Japan) based on the CIE Lab* color system. Measurements were performed in triplicate, and the results were expressed as mean ± standard deviation.

Total phenolic content (TPC) was measured using the Folin–Ciocalteu assay with gallic acid as the reference standard. Sample or standard solution (25 µL) was mixed with 125 µL of 10% Folin–Ciocalteu reagent and incubated in the dark for 5 min. Sodium carbonate solution (10%, 100 µL) was added, followed by incubation in the dark for 30 min. Absorbance was measured at 760 nm, and results were expressed as milligrams of gallic acid equivalents per millilitre of sample (mg GAE/mL). Total flavonoid content (TFC) was determined using an aluminium chloride colorimetric assay with quercetin as the reference standard. Sample or standard solution (25 µL) was mixed with 25 µL of 5% sodium nitrite and [volume] µL of 10% aluminium chloride. After 6 min in the dark, 175 µL of 4% sodium hydroxide was added. Following a further 30-min incubation, absorbance was measured at 510 nm. Results were expressed as milligrams of quercetin equivalents per millilitre (mg QE/mL). Total monomeric anthocyanin content (TAC) was determined by the pH differential method. Separate sample aliquots (0.25 mL) were mixed with 1.75 mL of potassium chloride buffer at pH 1.0 or sodium acetate buffer at pH 4.5. After incubation in the dark for 30 min, absorbance was measured at 510 and 700 nm. Results were expressed as cyanidin-3-glucoside equivalents (C3GE).

The Particle size, PDI, and Zeta Potential of sample were demonstrated. The average droplet size, polydispersity index (PDI), and zeta potential of SLP formulations were determined using dynamic light scattering (Zetasizer Nano ZS, Malvern Instruments, UK) at 25 °C. All measurements were conducted in triplicate, and the results were reported as mean ± SD. The encapsulation efficiency (EE%) of the SLP was evaluated by determining the total anthocyanin content (TAC) using the pH differential method. To disrupt the liposomal, an equal volume of methanol was added (1:1, v/v). An aliquot of 1.5 mL of the disrupted liposomal was transferred into a microcentrifuge tube (1.5 mL capacity) and centrifuged at 15,000 rpm for 90 min at 4 °C. The supernatant was carefully collected for further analysis. The Encapsulation

efficiency (EE%) was calculated using the following equation: EE% = (Encapsulated TAC / Total TAC) × 100.

The stability of the SLP formulations was evaluated under thermal cycling (Hot–Cold Cycle). Briefly, samples were placed in a programmable stability chamber and subjected to alternating storage at 4 ± 2 °C and 45 ± 2 °C every 24 h. One complete cycle consisted of 48 h (24 h at each temperature), and a total of six cycles were performed. After the final cycle, the samples were evaluated for changes in appearance, color, pH, viscosity, droplet size, PDI, and zeta potential to determine thermal stability. Furthermore, *In vitro* permeation of SLP was evaluated using Franz diffusion cells with a cellulose acetate membrane (pore size 0.45 µm). The receptor compartment was filled with phosphate-buffered saline (PBS, pH 7.4) and maintained at 37 ± 0.5 °C under constant stirring (300 rpm). A 1 mL sample of each formulation (ethanolic extract, PG extract, and SLP) was placed in the donor compartment. At predetermined intervals (0.5, 1, 2, 4, 6, 8, and 24 h), aliquots of 1 mL were withdrawn from the receptor compartment and replaced with fresh PBS. TAC content was quantified using pH differential method. The cumulative permeation of TAC was plotted as a function of time, and the release profiles were compared across formulations. Experiments were performed in triplicate, and results were expressed as mean ± standard deviation. The experimental protocol specified analysis of variance followed by Tukey's multiple comparison test using SPSS, with statistical significance defined as $p < 0.05$. Retention percentages were calculated from reported mean concentrations.

## Results and Discussion

### Extract characteristics and phytochemical contents

The PG extract exhibited a pH of 5.50 ± 0.03 and a viscosity of 169.50 ± 4.49 cP. The extraction showed TPC of 6.86±0.23 mg GAE/mL, TFC of 5.93±0.21 mg QE/mL and TAC of 21.40±0.33 mg C3GE/mL extract (Table 1). The phenolic-related responses are consistent with previous investigations of Sangyod-derived preparations [1,3].

### Particle characteristics and preliminary formulation selection

The incorporation of Sangyod rice bran extract was accompanied by increases in mean particle size and polydispersity index relative to blank liposomes. PG-F1 exhibited a mean particle size of 227.6 ± 2.48 nm and a polydispersity index of 0.40 ± 0.08, whereas PG-F2 exhibited corresponding values of 278.7 ± 21.43 nm and 0.53 ± 0.09. The increase in particle size following extract addition may reflect changes in vesicle formation or interactions with formulation components. PG-F1 and PG-F2 exhibited similar, less negative zeta potentials than blank liposomes. This indicates a change in the interfacial environment. PG-F1 was therefore selected for further investigation based on its smaller particle size and lower polydispersity index within the formulations examined. The selected PG-F1 had a reported EE of 85%, suggesting substantial loading of the measured marker.



**Figure 1.** Appearance of Sangyod rice bran extract (left), blank liposomes (middle), and Sangyod rice bran extract-loaded nanoliposomes (right).

## Preliminary physical and physicochemical stability

Following six hot–cold cycles, PG-F1 exhibited relatively small numerical changes in pH and viscosity. Its pH increased from 5.63 ± 0.13 to 5.73 ± 0.22, while viscosity increased from 198.50 ± 5.41 to 203.50 ± 3.21 cP (Table 2). Furthermore, for PG-F1, L* decreased from 4.56 ± 0.03 to 4.16 ± 0.33, a* increased from 20.40 ± 0.05 to 22.30 ± 0.22, and b* decreased from 7.18 ± 0.06 to 6.12 ± 0.36. These shifts indicate reduced lightness, an increased red component, and a reduced yellow component. The experimental report described these changes as statistically non-significant. These observations provide preliminary information on formulation behavior under alternating temperature conditions. In addition, PG-F1 retained 94.6%, 91.1%, and 97.9% of its initial phenolic, flavonoid, and anthocyanin assay responses, respectively (Table 3). The corresponding values for the free extract were 49.9%, 52.6%, and 88.0%. These patterns are consistent with a possible formulation-related protective contribution.

**Table 1. Initial particle characteristics of liposomal formulations**

| Formulation | Particle size (nm) | PDI | Zeta potential (mV) |
|---|---|---|---|
| Blank liposomes | 205.9 ± 2.81 | 0.13 ± 0.02 | −30.43 ± 1.90 |
| PG-F1 | 227.6 ± 2.48 | 0.40 ± 0.08 | −18.66 ± 3.46 |
| PG-F2 | 278.7 ± 21.43 | 0.53 ± 0.09 | −18.23 ± 0.94 |

**Table 2. Selected physicochemical properties before and after thermal cycling**

| Property | Blank, initial | Blank, after cycling | PG-F1, initial | PG-F1, after cycling |
|---|---|---|---|---|
| pH | 5.30 ± 0.05 | 5.23 ± 0.15 | 5.63 ± 0.13 | 5.73 ± 0.22 |
| Viscosity (cP) | 143.50 ± 4.49 | 153.70 ± 3.34 | 198.50 ± 5.41 | 203.50 ± 3.21 |
| Particle size (nm) | 205.9 ± 2.81 | 215.9 ± 1.31 | 227.6 ± 2.48 | 236.3 ± 3.58 |
| Zeta potential (mV) | −30.43 ± 1.90 | −31.23 ± 1.90 | −18.66 ± 3.46† | −17.86 ± 2.45 |

**Table 3. Phytochemical contents and apparent retention after thermal cycling**

| Assay | Sample | Initial | After cycling | Retention (%) |
|---|---|---|---|---|
| TPC (mg GAE/mL) | Free PG extract | 6.86 ± 0.23 | 3.42 ± 0.53 | 49.9 |
| TPC (mg GAE/mL) | PG-F1 | 1.48 ± 0.03 | 1.40 ± 0.03 | 94.6 |
| TFC (mg QE/mL) | Free PG extract | 5.93 ± 0.21 | 3.12 ± 0.13 | 52.6 |
| TFC (mg QE/mL) | PG-F1 | 1.35 ± 0.40 | 1.23 ± 0.33 | 91.1 |
| TAC (mg C3GE/mL) | Free PG extract | 21.40 ± 0.33 | 18.84 ± 0.15 | 88.0 |
| TAC (mg C3GE/mL) | PG-F1 | 4.30 ± 0.03 | 4.21 ± 0.35 | 97.9 |

## Preliminary delivery observations

The liposomal formulation showed a reported approximately 20-fold increase in anthocyanin transport compared with the original extract under the experimental conditions (Fig. 2). This enhancement may involve interactions between liposomal phospholipids and stratum corneum lipids, facilitating the transfer of released constituents into the skin. Previous studies demonstrated that liposomal formulations enhanced skin penetration of both encapsulated and non-encapsulated hydrophilic markers [7]. However, this does not necessarily involve intact vesicles crossing the skin: microscopy studies suggest that liposomes can disintegrate and mix with superficial skin lipids, promoting delivery of their contents [8].

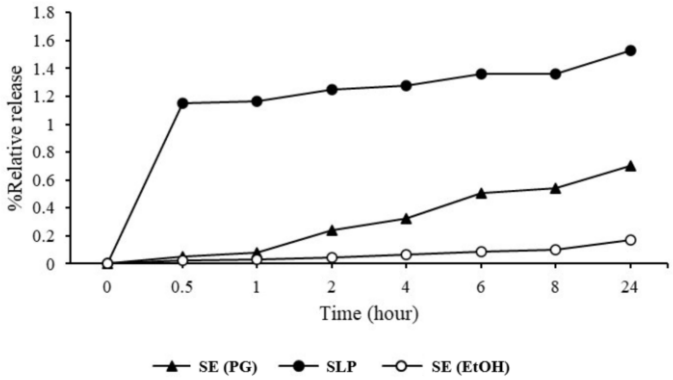


**Figure 2.** *In vitro* permeability study using Franz Diffusion Cells. The % Relative release of Anthocyanin from different samples over 24 hours. SE (PG) is a Sangyod rice bran extracted with Propylene glycol using MAE method, SLP is a Sangyod Rice Bran Nano-Liposome, and SE (EtOH) is a Sangyod rice bran extracted with ethanol using maceration method.

Overall, the findings identify PG-F1 as a candidate for further formulation development. The contribution of this work lies in connecting a local rice-bran resource with liposomal ingredient development. Demonstration of improved skin delivery, moisturizing performance, economic value, or environmental benefit will require additional evidence appropriate to each outcome.

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## References

1. Thitipramote, N., Imsonpang, S., Sukphopetch, P., Pradmeeteekul, P., Nimkamnerd, J., Nantitanon, W., and Chaiyana, W. (2022). Health benefits and safety of red pigmented rice (Oryza sativa L.): In vitro, cellular, and in vivo activities for hair growth promoting treatment. *Cosmetics*, 9(6), 111. https://doi.org/10.3390/cosmetics9060111
2. Teeranachaideekul, V., Wongrakpanich, A., Leanpolchareanchai, J., Thirapanmethee, K., and Sirichaovanichkarn, C. (2018). Characterization, biological activities and safety

evaluation of different varieties of Thai pigmented rice extracts for cosmetic applications. *Pharmaceutical Sciences Asia*, 45(3), 140–153. https://doi.org/10.29090/psa.2018.03.140

3. Aenglong, C., Woonnoi, W., Tanasawet, S., Klaypradit, W., and Sukketsiri, W. (2024). Impact of time and enzyme concentration on Sangyod rice bran hydrolysate: Phytochemicals, antioxidants, amino acids, and cytotoxicity. *Rice*, 17, 13. https://doi.org/10.1186/s12284-024-00692-1
4. Woonnoi, W., Thipart, K., Hanchang, W., Saetan, J., Tanasawet, S., Moolsup, F., Suttithumsatid, W., Wongtawatchai, T., and Sukketsiri, W. (2025). Sangyod rice extract attenuates vascular inflammation and injury in a rat model of diabetes by modulating the Akt/MAPK signaling pathway. *Advances in Pharmacological and Pharmaceutical Sciences*, Article 1169062. https://doi.org/10.1155/adpp/1169062
5. Manosroi, A., Chutoprapat, R., Sato, Y., Miyamoto, K., Hsueh, K., Abe, M., Manosroi, W., and Manosroi, J. (2011). Antioxidant activities and skin hydration effects of rice bran bioactive compounds entrapped in niosomes. *Journal of Nanoscience and Nanotechnology*, 11(3), 2269–2277. https://doi.org/10.1166/jnn.2011.3532
6. Lee, J., Durst, R. W., and Wrolstad, R. E. (2005). Determination of total monomeric anthocyanin pigment content of fruit juices, beverages, natural colorants, and wines by the pH differential method: Collaborative study. *Journal of AOAC International*, 88(5), 1269–1278. https://doi.org/10.1093/jaoac/88.5.1269
7. Verma, D. D., Verma, S., Blume, G., & Fahr, A. (2003). Liposomes increase skin penetration of entrapped and non-entrapped hydrophilic substances into human skin: A skin penetration and confocal laser scanning microscopy study. *European Journal of Pharmaceutics and Biopharmaceutics,* 55(3), 271–277. https://doi.org/10.1016/S0939-6411(03)00021-3. PubMed
8. Dreier, J., Sørensen, J. A., & Brewer, J. R. (2016). Superresolution and fluorescence dynamics evidence reveal that intact liposomes do not cross the human skin barrier. *PLOS ONE*, 11(1), e0146514. https://doi.org/10.1371/journal.pone.0146514. PubMed



SECTION

# PS6

## Agri-tech

Digital agriculture, sensing, automation and data-driven rice farming

Poster 8

# Effect of Irrigation-Water Total Dissolved Solids on Establishment, Vegetative Growth, and Grain Yield of Rice (*Oryza sativa* L. cv. RD41) under Field Conditions in the Chao Phraya Basin, Thailand

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## Abstract

This study examined the effects of irrigation-water total dissolved solids (TDS) on the establishment, vegetative growth, and grain yield of rice (*Oryza sativa* L. cv. RD41) in the Chao Phraya Basin, Thailand. A field experiment was conducted using three irrigation treatments: normal water (250–400 ppm TDS), high TDS (400–550 ppm), and simulated seawater intrusion (2,000–2,200 ppm). Increasing TDS delayed germination and lowered the final germination rate from 97.6% to 90.2%. By 35 days after sowing, key growth metrics were negatively impacted. Compared to the control, high TDS and simulated seawater intrusion reduced plant height by 13.0% and 18.1%, leaf count by 17.9% and 26.9%, and tiller number by 16.3% and 25.3%, respectively. These early growth penalties directly led to lower productivity. Grain yield declined by 10.8% under high TDS and 20.5% under simulated seawater intrusion. The harvest index also fell from 0.46 to 0.40 and 0.36, respectively. Notably, measurable yield penalties occurred even at a moderate TDS level of 400–550 ppm, despite no visible signs of canopy injury. These findings provide strong field-scale evidence that even low-level increases in irrigation-water TDS can significantly impair rice establishment and reduce grain yield. Therefore, routine monitoring of canal-water TDS is recommended as a crucial tool for managing dry-season salinity risk in the lower Chao Phraya Basin.

**Keywords:** *Rice establishment, Grain yield, Total dissolved solids (TDS), RD41, Irrigation-water salinity*

# Classification of Thai Rice Types under Postharvest Conditions Using an Electronic Nose and Machine Learning

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## Abstract

This study presents a metal-oxide-semiconductor (MOS) electronic nose for classifying four classes of Thai milled rice based on odor characteristics. The system consisted of eight gas sensors. Five features were extracted from each sensor: reference resistance, late mean, late median, late standard deviation, and response range, resulting in a 40-dimensional feature vector. A balanced dataset of 40 measurements was obtained, with 10 measurements per rice class. Principal component analysis (PCA) was used to reduce the feature dimension to three and five principal components before classification using a radial basis function support vector machine (RBF-SVM). The PCA-3 model achieved 62.50% validation accuracy, 54.17% macro precision, and 62.50% macro recall. The PCA-5 model improved the performance to 87.50% accuracy, 91.67% macro precision, and 87.50% macro recall. These results demonstrate that the proposed E-nose combined with PCA and SVM can effectively discriminate rice samples differing in rice type, harvest period, and processing condition, showing potential as a rapid and low-cost method for rice classification.

**Keywords:** *Electronic nose, Machine learning, Gas sensor*

## 1. Introduction

Rice (*Oryza sativa* L.) is one of the most important staple foods worldwide, particularly in Asia. Its quality is influenced by physical characteristics as well as aroma, which originates from a complex mixture of volatile organic compounds (VOCs). Rice VOC profiles can vary with cultivar, processing method, and storage conditions (Hu et al., 2020). In particular, changes in aroma-active compounds such as 2-acetyl-1-pyrroline, hexanal, octanal, and nonanal have been observed during storage (Zhao et al., 2020). Conventional aroma analysis using sensory evaluation or gas chromatography–mass spectrometry (GC–MS) can provide detailed information but generally requires expensive equipment, skilled personnel, and considerable analysis time.

An electronic nose (E-nose) provides a rapid and low-cost alternative by using an array of cross-sensitive gas sensors to generate characteristic odor fingerprints. Previous studies have demonstrated the application of MOS-based E-noses for rice identification and quality assessment. Timsorn et al. (2017) successfully applied a portable E-nose to detect adulteration of Thai Jasmine rice with white rice, while Aznan et al. (2022) demonstrated that E-nose measurements combined with machine-learning techniques could effectively classify different commercial rice types. Moreover, Rahimzadeh et al. (2019) showed that MOS sensor responses can detect aroma changes associated with rice aging during storage. These studies indicate that E-nose responses contain useful information related to rice type and postharvest condition.

In this study, an E-nose consisting of eight MOS gas sensors was developed to classify four classes of Thai milled rice: (A) white rice harvested in April 2026, (B) Mali rice harvested in June 2026, (C) Mali rice harvested in September 2025, and (D) parboiled rice harvested in June 2026. Five features were extracted from each sensor response and reduced using principal component analysis (PCA) before classification using a support vector machine (SVM). The objective was to evaluate whether the proposed E-nose could discriminate rice samples differing in rice type, harvest period, and processing condition, providing a potential rapid and low-cost approach for rice classification and postharvest quality assessment.

## 2. Materials and methods

### 2.1 Electronic nose system

The electronic nose (E-nose) was developed using an array of eight metal-oxide-semiconductor (MOS) gas sensors summarized in Table 1. Since each sensor has different sensitivity to volatile compounds, the combined responses of the eight sensors provide a characteristic odor fingerprint of each rice sample. During measurement, airflow through the E-nose system was regulated to maintain consistent gas-delivery conditions for all experiments.

**Table 1**. Gas sensor selection for E-nose system

| No. | Sensor model | Sensible gas |
|---|---|---|
| S1 | MQ137 | Ammonia |
| S2 | MQ138 | Volatile organic compounds |
| S3 | TGS822 | Alcohol |
| S4 | TGS2600 | Air contaminants |
| S5 | TGS2602 | VOCs and odorous air contaminants |
| S6 | TGS2610 | Liquefied petroleum gas |
| S7 | TGS2616 | Hydrogen |
| S8 | TGS2620 | Ethanol and organic solvent |

### 2.2 Rice odor measurement procedure

Figure 1 illustrates the airflow configuration and operating sequence of the developed E-nose system. Ambient air is first passed through a filter and supplied by an air pump, while a flow regulator maintains a constant airflow rate of 1 liter per minute. Each measurement cycle consists of two consecutive phases: a fresh air-in phase and an odor-sniffing phase. During the fresh air-in phase, valve 1 and valve 2 directs filtered fresh air into the gas-sensor chamber for 180 s, while the sample path is isolated. This period allows the eight MOS gas sensors to stabilize under the same reference-air condition. The sensor resistance measured during this phase is used to determine the referenced resistance, $R_0$, for each individual sensor. Establishing $R_0$ before odor exposure reduces the influence of differences in the nominal resistance and baseline level among the sensors.

After the reference phase, the airflow path is switched by valves 2 and 3 so that the regulated air passes through the container containing 20 grams of rice. The air carries volatile organic compounds released from the rice sample into the gas-sensor chamber, initiating the odor-sniffing phase, which lasts for 120 seconds. Exposure to the rice volatiles changes the resistance of each MOS sensor according to its sensitivity. The measured sensor resistance during odor exposure, $R_S$, is then normalized with respect to its corresponding referenced resistance $R_0$, producing a normalized sensor response $\tilde{R}_S$ as,

$$\tilde{R}_S = \frac{R_S - R_0}{R_0} \quad (1)$$

This normalization reduces sensor-to-sensor baseline variation and allows the temporal response patterns of the eight sensors to be compared and subsequently used as the odor pattern for machine-learning classification. Sensor signals are recorded continuously during both phases at a sampling interval of 0.5 second.

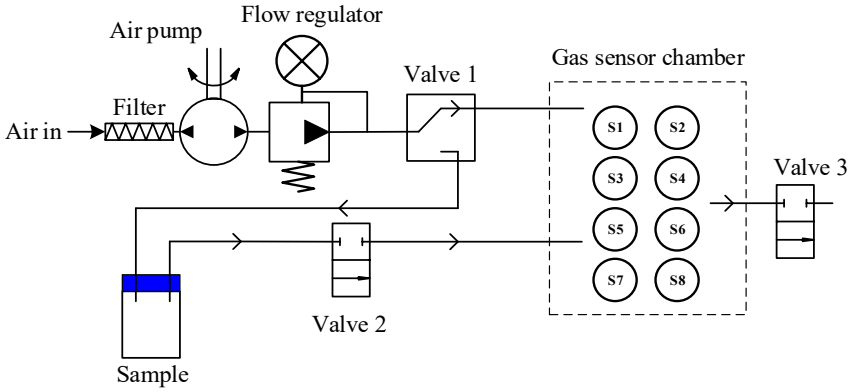



**Figure 1. Schematic diagram of the E-nose airflow system and odor-sampling process**

## 2.3 Dataset organization

The dataset consisted of 40 independent E-nose measurements from four balanced rice classes (A–D), with 10 measurements per class. For each class, eight measurements were randomly selected for training and two for validation, resulting in 32 training samples (80%) and 8 validation samples (20%) summarized in Table 2. The split was performed at the complete measurement-run level to avoid data leakage between training and validation sets.

**Table 2**. Dataset distribution for the four rice classes

| Rice class | Description | Training | Validation | Total |
|---|---|---|---|---|
| A | White rice, Apr. 2026 | 8 | 2 | 10 |
| B | Mali rice, Jun. 2026 | 8 | 2 | 10 |
| C | Mali rice, Sep. 2025 | 8 | 2 | 10 |
| D | Parboiled rice, Jun. 2026 | 8 | 2 | 10 |
| Total | | 32 | 8 | 40 |

## 2.4 Feature extraction

For each gas sensor, five features were extracted to characterize the rice odor response, as shown in Figure 2: reference resistance ($R_0$), late mean ($S_L^a$), late median ($S_L^b$), late standard deviation ($S_L^c$), and response range ($S_L^d$). $R_0$ represents the baseline sensor resistance measured during the fresh-air phase, while the $S_L^a$ and $S_L^b$ describe the stabilized sensor response near the end of the odor-sniffing period. The $S_L^c$ indicates the variability or stability of the sensor response during this period, and $S_L^d$ represents the overall response excursion between the maximum and minimum normalized signals. All feature computation is summarized in Table 3**.** Together, these features capture the baseline condition, steady-state response level, signal stability, and response magnitude of each sensor, providing a compact

feature set for classification of the four rice odor classes. For total 8 gas sensors, this thus constitutes 40-dimensional feature vector for odor pattern representation.

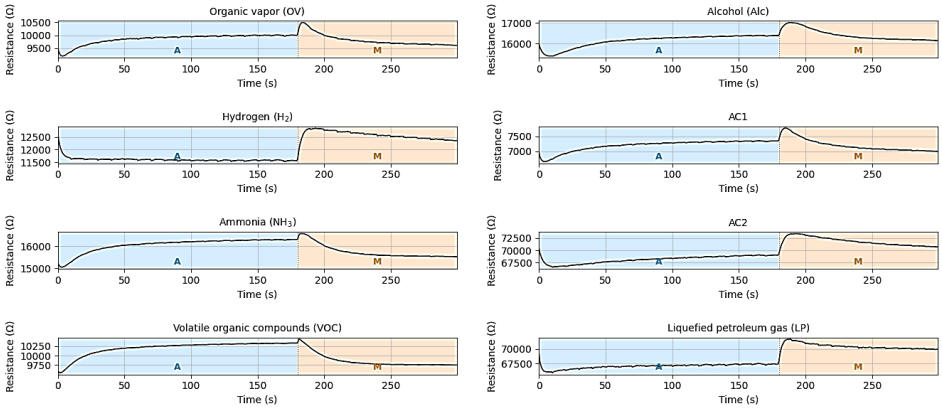



**Figure 2. Fresh air-in phase (blue) and an odor-sniffing phase (orange) in odor-sampling process.**

**Table 3. Extracted E-nose features and their descriptions**

| No | Feature computation | Description |
|---|---|---|
| 1 | $R_0 = \frac{1}{N_L}\sum_{k\in L} R_S^k$ | Baseline sensor resistance measured during the fresh-air phase. |
| 2 | $S_L^a = \frac{1}{N_L}\sum_{k\in L} \tilde{R}_S^k$ | Average normalized sensor response during the final part of the odor-sniffing phase. |
| 3 | $S_L^b = \underset{k\in L}{median}(\tilde{R}_k^S)$ | Median normalized response during the final part of the odor-sniffing phase. |
| 4 | $S_L^c = \sqrt{\frac{1}{N_L - 1}\sum_{k\in L}(\tilde{R}_k^S - S_L^a)^2}$ | Variation of the sensor response during the final odor-sniffing period. |
| 5 | $S_L^d = \max_{k\in L}(\tilde{R}_k^S) - \min_{k\in L}(\tilde{R}_k^S)$ | Difference between the maximum and minimum normalized |

## 2.5 Machine learning for rice odor classification

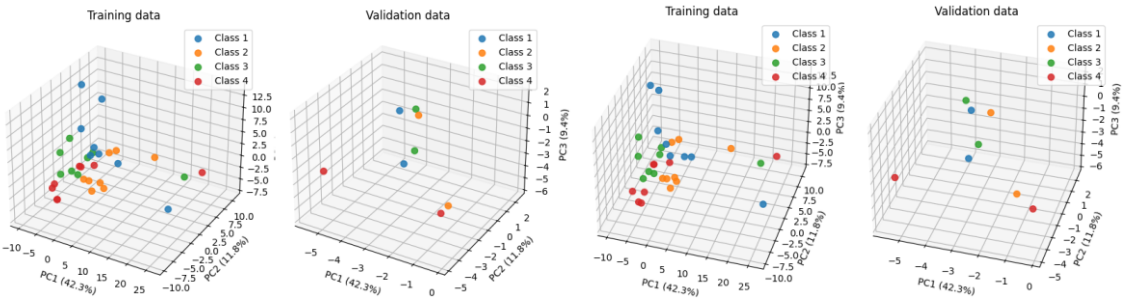
For each measurement, five features were extracted from each of the eight gas sensors, resulting in a 40-dimensional feature vector. To reduce feature redundancy and improve the efficiency of classification, PCA was applied before classification. Two reduced feature sets were investigated by retaining the first three principal components and the first five principal components. These principal components represent linear combinations of the original sensor features that preserve the major variations in the E-nose measurements while reducing the dimensionality from 40 to 3 and 5, respectively.

The PCA-reduced features were subsequently classified using a support vector machine (SVM). A radial basis function (RBF) kernel was selected to handle possible nonlinear relationships among the odor patterns of the four rice classes. The SVM parameters were set to $C = 1.0$ and $\gamma = 0.1$. The penalty parameter (C) controls the trade-off between maximizing the decision margin and minimizing classification errors, whereas the $\gamma$ determines the influence of individual training samples in the RBF kernel. Multi-class classification was performed to distinguish rice Classes A, B, C, and D.

## 3. Results and Discussion

### 3.1 PCA component visualization

The original 40-dimensional feature vector was reduced using PCA to three and five principal components. The first three components explained 42.3%, 11.6%, and 9.4% of the total variance, respectively, for a cumulative variance of 63.3%. The 3D PCA plots in Figure 3 show partial separation among the four rice classes, although some overlap remains. The additional fourth and fifth principal components therefore retain useful information that is not visible in the three-dimensional representation.




(a) (b)

**Figure 3. (a) PCA components of the first three components. (b) PCA components of the five three components.**

### 3.2 Rice odor classification result

The PCA-reduced features were classified using an RBF-SVM, and the classification results are summarized by the confusion matrices in Figure 4. For PCA-3, the training dataset achieved an overall accuracy of 81.25%, with macro-average precision and recall of 81.61% and 81.25%, respectively. Validation performance decreased to 62.50% accuracy, with macro precision of 54.17% and macro recall of 62.50%. Classes C and D were correctly identified with 100% recall, whereas Class B achieved 50% recall and both Class A validation samples were misclassified. For PCA-5, the training accuracy remained at 81.25%, with macro precision of 80.70% and recall of 81.25%. However, validation performance improved substantially to 87.50% accuracy, 91.67% macro precision, and 87.50% macro recall. Classes B, C, and D achieved 100% recall, while one Class A sample was misclassified as Class D. The improvement from PCA-3 to PCA-5 indicates that the fourth and fifth principal components retained additional discriminative information that was useful for separating the rice odor patterns.

Overall, the developed eight-sensor E-nose successfully captured characteristic odor information from the four Thai milled rice classes. Combining five statistical features from each sensor with PCA and SVM reduced the original 40-dimensional feature space while preserving useful classification information. Among the two configurations, PCA-5 + SVM provided the best validation performance, suggesting that five principal components offered a more informative representation of the sensor data than three principal components. Nevertheless, the validation set contained only eight independent measurements, so each misclassification changed the overall validation accuracy by 12.5 percentage points. Therefore, future work should include more independent samples and repeated cross-validation to obtain a more reliable estimate of the model's generalization performance.

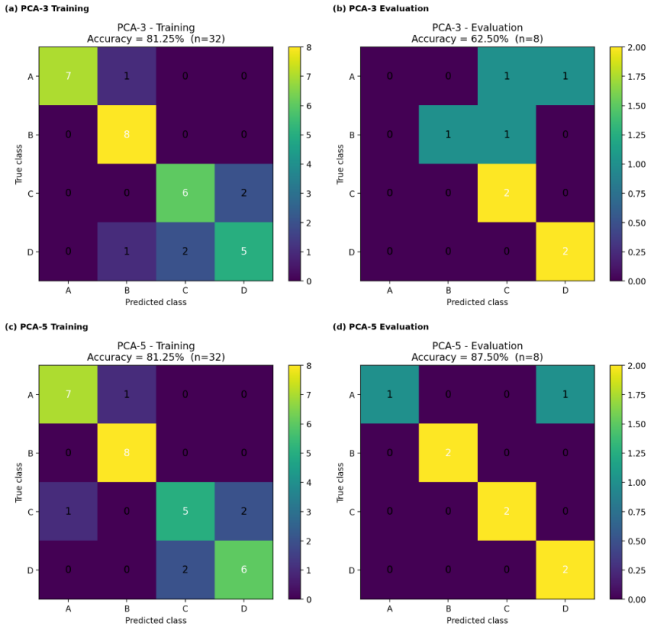



**Figure 4. Confusion matrices of the RBF-SVM classification using PCA-3 and PCA-5 features for the training and validation datasets.**

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## References

Aznan, A., Gonzalez Viejo, C., Pang, A., Fuentes, S., 2022. Rapid assessment of rice quality traits using low-cost digital technologies. Foods 11, 1181. https://doi.org/10.3390/foods11091181.

Hu, X., Lu, L., Guo, Z., Zhu, Z., 2020. Volatile compounds, affecting factors and evaluation methods for rice aroma: A review. Trends Food Sci. Technol. 97, 136–146. https://doi.org/10.1016/j.tifs.2020.01.003.

Rahimzadeh, H., Sadeghi, M., Ghasemi-Varnamkhasti, M., Mireei, S.A., Tohidi, M., 2019. On the feasibility of metal oxide gas sensor based electronic nose software modification to characterize rice ageing during storage. J. Food Eng. 245, 1–10. https://doi.org/10.1016/j.jfoodeng.2018.10.001.

Timsorn, K., Lorjaroenphon, Y., Wongchoosuk, C., 2017. Identification of adulteration in uncooked Jasmine rice by a portable low-cost artificial olfactory system. Measurement 108, 67–76. https://doi.org/10.1016/j.measurement.2017.05.035.

Zhao, Q., Xue, Y., Shen, Q., 2020. Changes in the major aroma-active compounds and taste components of Jasmine rice during storage. Food Res. Int. 133, 109160. https://doi.org/10.1016/j.foodres.2020.109160.

# Rice Growth and Yield with Biostimulants at Reduced Seeding Rates in Southern Vietnam

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## Abstract

A field experiment evaluated C-WEED AA (*Ascophyllum nodosum* extract) and Seamel ZEN (*Solieria chordalis* extract) as components of reduced-seed management programs for OM5451 rice in Cu Chi, Ho Chi Minh City, Vietnam. The reported trial period was November 2023 - February 2024. Seven treatments were arranged in a randomized complete block design with four replications and 30 m² - plots. The treatment protocol specified seed reductions of 15% (reduction of 3.3kg/1000m$^2$) and 30% (reduction of 6.6kg/1000m$^2$) relative to the full-seed control (22kg/1000m$^2$). Products were applied at 1 days after sowing, with selected treatments receiving a second application at 12 days. Grain yield ranged from 6.06 to 7.14 t/ha, compared with 6.49 t/ha in the control, with no significant overall treatment difference (P = 0.10). At 15% seed reduction, single applications of C-WEED AA and Seamel ZEN yielded 7.14 and 6.60 t/ha, respectively. At 30% seed reduction, both two-application programs yielded 6.77 t/ha. Tiller density, plant height, SPAD readings, filled-grain percentage and thousand-grain mass showed no significant treatment differences. The combined biostimulant and reduced-seed programs sustained crop growth, and four programs had numerically higher yields than the full-seed control. These findings support their potential for seed-saving management consistent with the productivity objectives of Sustainable Rice Platform standard. The results describe combined management programs rather than the independent contribution of biostimulants.

**Keywords:** *OM5451, Direct-seeded rice, Seeding rate, Biostimulants, Grain yield*

## Introduction

Seeding rate influences crop establishment, competition and yield formation in direct-seeded rice. Reducing seed use can lower the quantity of planting material required, but the agronomic response depends on establishment and field management. In Cambodian field experiments, drilled rice at 60-80 kg seed/ha produced yields and gross margins comparable to hand-broadcast rice at 180 kg/ha under the tested management conditions (Onwuchekwa-Henry et al., 2022). These results support evaluating seeding rate together with the accompanying crop management program.

Biostimulants may be integrated into rice management to support crop growth and yield. Sharma et al. (2017) reported rice yield responses to seaweed-based biostimulants under field conditions. In the present trial, C-WEED AA and Seamel ZEN were evaluated at early crop establishment with reduced seed quantities. Growth observations and grain yield were used to assess the performance of these programs relative to the full-seed control.

Efficient use of seed while maintaining productivity is relevant to Sustainable Rice Platform (SRP) cultivation. The SRP Standard for Sustainable Rice Cultivation, Version 2.2, includes requirements for pure quality seeds and records of agricultural inputs and crop performance (SRP, 2023). Evidence on reduced-seed programs can inform locally adapted crop establishment decisions within this management framework.

This study evaluated rice growth, grain filling and grain yield under management programs combining Olmix company commercial product from *Ascophyllum nodosum* extract (C-WEED AA) or *Solieria chordalis* extract (Seamel ZEN) with reduced seeding rates in southern Vietnam. The practical comparison was between these programs and a full-seeding-rate control without biostimulants. The experiment also compared single and repeated product applications at the intermediate seeding rate.

## Materials and Methods

### Site and experimental design

The trial was organized by Nong Lam University at Trang Lam Hamlet, Trung Lap Ha Commune, Cu Chi District, Ho Chi Minh City, Vietnam. The reported trial period was November 2023 - February 2024. Rice cultivar OM5451 was used in a randomized complete block design with seven treatments and four replications, giving 28 plots. Each plot measured 5 × 6 m (30 m²). Sowing time, water management, fertilization and crop protection practices (herbicide, insecticide, fungicide) were common to all treatments, apart from the assigned seed quantities and biostimulant applications.

### Treatments and application

The treatment protocol defined three seed levels: 100% for the control and 85% or 70% for biostimulant-treated plots, corresponding to planned seed reductions of 15% and 30%. These protocol-defined percentages are used to identify the treatments throughout the paper. T1 to T4 used 85% seed quantity, T5-T6 used 70%, and T7 (control) received the full seed quantity without biostimulants (Table 1).

**Table 1. Seed quantities and biostimulant applications in the seven treatment programs**

| Treatment | Seed quantity | Seed reduction | Application at 1 DAS | Application at 12 DAS |
|---|---|---|---|---|
| T1 | 85% (18.7kg/1000m$^2$) | 15% (3.3kg/1000m$^2$) | C-WEED AA 1 mL/L | C-WEED AA 2 mL/L |
| T2 | 85% (18.7kg/1000m$^2$) | 15% (3.3kg/1000m$^2$) | C-WEED AA 1 mL/L | None |

| Treatment | Seed quantity | Seed reduction | Application at 1 DAS | Application at 12 DAS |
|---|---|---|---|---|
| T3 | 85% (18.7kg/1000m$^2$) | 15% (3.3kg/1000m$^2$) | Seamel ZEN 2 mL/L | None |
| T4 | 85% (18.7kg/1000m$^2$) | 15% (3.3kg/1000m$^2$) | Seamel ZEN 2 mL/L | Seamel ZEN 2 mL/L |
| T5 | 70% (15.4kg/1000m$^2$) | 30% (6.6kg/1000m$^2$) | C-WEED AA 1 mL/L | C-WEED AA 2 mL/L |
| T6 | 70% (15.4kg/1000m$^2$) | 30% (6.6kg/1000m$^2$) | Seamel ZEN 2 mL/L | Seamel ZEN 2 mL/L |
| T7 | 100% (22kg/1000m$^2$) | 0% | No biostimulant | No biostimulant |

DAS, days after sowing. Seed quantity and reduction follow the treatment protocol, with the full-seed control defined as 100%.

The first biostimulant application was scheduled for 1 DAS, mixed with the pre-emergence herbicide. Selected treatments received a second application on 12 DAS. Spray volume was 360-400 L/ha using a 20-L electric knapsack sprayer. At this volume, concentrations of 1 and 2 mL/L correspond to calculated product rates of 0.36-0.40 and 0.72-0.80 L/ha per application, respectively.

**Measurements and statistical analysis**

Growth observations used fixed 0.4 × 0.5 m quadrats (0.2 m²); two observation points per replicate plot were specified in the field protocol. Tiller density and plant height were recorded at 20, 55 and 86 DAS, with the last observation identified as harvest in the results tables. Leaf photosynthesis was measured at 20 and 55 DAS using a SPAD-502 Plus meter. Reproductive observations included filled and unfilled grains per panicle and thousand-grain mass. Grain yield was determined by harvesting the whole 30 m² plot. Grain yield and thousand-grain mass ($P_{1000}$) were reported on a 12% moisture basis.

The trial analysis used analysis of variance after screening for outliers, with an LSD procedure at $\alpha = 0.05$ in the Agricola package for R 4.1.0. Treatment means, overall P values and coefficients of variation (CV) are presented as reported. Numerical comparisons are described separately from statistically significant treatment differences.

**Results and Discussion**

**Vegetative growth and leaf greenness**

Tiller density did not differ significantly among treatments at 20, 55 or 86 DAS (P = 0.52, 0.96 and 0.86, respectively). Mean density ranged from 952.5 to 1182.5 tillers/m² at 20 DAS and from 755.0 to 822.5 tillers/m² at 55 DAS. At harvest, treated plots had 556.3-615.6 tillers/m², compared with 670.0 tillers/m² in the control (Table 2). The reduced-seed programs maintained tiller populations without a significant treatment difference.

Plant height also showed no significant treatment effect at 20, 55 or 86 DAS (P = 0.70, 0.84 and 0.49). Final height ranged from 69.3 to 72.1 cm. SPAD readings ranged from 32.2 to 38.4 at 20 DAS and from 30.9 to 34.5 at 55 DAS, with no significant differences at either observation (P = 0.10 and 0.32). At 55 DAS, five of the six biostimulant treatments had numerically higher SPAD readings than the control. Together, these measurements show that crop growth and leaf greenness were sustained under the reduced-seed programs. They provide indicators of crop condition rather than a direct measure of disease resistance or recovery from herbicide injury.

**Table 2. Tiller density and plant height at harvest and SPAD readings during crop growth**

| Treatment | Tillers/m² 86 DAS | Height (cm) 86 DAS | SPAD 20 DAS | SPAD 55 DAS |
|---|---|---|---|---|
| T1 | 556.3 | 70.1 | 38.4 | 33.9 |
| T2 | 603.8 | 72.1 | 32.2 | 34.5 |
| T3 | 591.3 | 71.6 | 34.9 | 32.3 |
| T4 | 596.9 | 69.3 | 36.1 | 33.4 |
| T5 | 611.9 | 71.5 | 35.9 | 30.9 |
| T6 | 615.6 | 69.7 | 35.3 | 33.5 |
| T7 | 670.0 | 70.6 | 35.8 | 31.4 |
| P value | 0.86 | 0.49 | 0.10 | 0.32 |
| CV % | 17.64 | 3.06 | 7.17 | 7.29 |

Reported treatment means from four replicated plots; treatment definitions are in Table 1. CV, coefficient of variation. All overall treatment tests were non-significant at $\alpha = 0.05$.

## Grain filling and grain yield

Filled grains ranged from 87.4% to 92.1%, with no significant treatment effect ($P = 0.55$). T3 had the highest numerical filled-grain percentage, 4.7% points above the control, followed by T5 at 90.7%. $P_{1000}$ parameter varied little, from 22.9 to 23.4 g ($P = 0.91$). Grain filling and $P_{1000}$ mass were maintained under the reduced-seed programs, with numerical improvements in filled-grain percentage in several treatments (Table 3).

**Table 3. Grain filling, thousand-grain mass and grain yield**

| Treatment | Filled grains % | $P_{1000}$ (g) | Grain yield t/ha |
|---|---|---|---|
| T1 | 87.4 | 23.0 | 6.06 |
| T2 | 90.4 | 23.3 | 7.14 |
| T3 | 92.1 | 23.1 | 6.60 |
| T4 | 87.7 | 22.9 | 6.31 |
| T5 | 90.7 | 23.2 | 6.77 |
| T6 | 89.2 | 23.4 | 6.77 |
| T7 | 87.4 | 23.3 | 6.49 |
| P value | 0.55 | 0.91 | 0.10 |
| CV % | 4.52 | 2.45 | 7.32 |

Yield and grain mass were reported at 12% moisture. Values are treatment means. The yield P value and CV refer to the reported plot-yield analysis. No overall treatment difference was significant at $\alpha = 0.05$.

Grain yield ranged from 6.06 to 7.14 t/ha, with an overall treatment P value of 0.10 and CV of 7.32%. T2, receiving one C-WEED AA application with 15% seed reduction, had the highest mean yield, 7.14 t/ha compared with 6.49 t/ha in T7. The corresponding single Seamel ZEN application, T3, yielded 6.60 t/ha. At 30% seed reduction, both two-application programs (T5 and T6) yielded 6.77 t/ha. Thus, the mean yields of T2, T3, T5 and T6 were numerically above the full-seed control while using less seed according to the treatment protocol.

At the intermediate seed rate, repeated applications did not show a numerical advantage. T1 yielded 6.06 t/ha compared with 7.14 t/ha in T2, while T4 yielded 6.31 t/ha compared with 6.60 t/ha in T3. Both remained within the non-significant overall treatment comparison. The results identify the single-application programs at 15% seed reduction and the two-application programs at 30% reduction as the combinations with numerical yields equal to or above the control in this experiment.

### Seed saving and relevance to SRP cultivation

The agronomic objective was to reduce seed inputs while sustaining rice growth and yield. Under the tested conditions, the biostimulant programs at protocol-defined 15% and 30% seed reductions maintained growth, grain filling and grain mass, with no significant overall yield difference. These observations support the use of the tested combinations as candidate seed-saving programs. Their value is the combination of lower seed input and sustained crop performance, rather than a demonstrated increase in every growth variable.

This seed-saving objective is consistent with maintaining productivity in SRP-oriented rice cultivation. SRP Version 2.2 requires pure quality seeds suitable for local conditions (Requirement 9) and records of inputs and production (Requirement 2) (SRP, 2023). Integrating the tested programs with these practices would allow seed use and crop performance to be followed at farm level. The 15% and 30% reductions are the trial's treatment levels; SRP Version 2.2 does not prescribe these percentages as universal targets.

The statistical results apply to the combined seed-rate and biostimulant programs. The absence of untreated reduced-seed controls prevents separation of the two factors, and the non-significant yield test does not establish formal equivalence. Within that scope, the trial provides evidence of sustained rice performance with the tested reduced-seed programs.

### Conclusion

Grain yield did not differ significantly among C-WEED AA and Seamel ZEN programs with protocol-defined seed reductions of 15% and 30% and the full-seed control. At 15% seed reduction, single applications yielded 7.14 and 6.60 t/ha, respectively; at 30% reduction, both two-application programs yielded 6.77 t/ha, compared with 6.49 t/ha in the control. The programs sustained measured crop growth and grain development. The results support their potential as seed-saving options within locally adapted, SRP-oriented rice management.

### Acknowledgements

We acknowledge Dr. Nien Nguyen Chau of Nong Lam University for organizing the field experiment and for compiling the trial report. The experiment evaluated C-WEED AA and Seamel ZEN in an Olmix trial program.

### References

1. Onwuchekwa-Henry, C. B., Van Ogtrop, F., Roche, R., and Tan, D. K. Y. (2022). Seeding rate, fertiliser and herbicide effects on canopy growth and productivity of direct-seeded rice (DSR) under different management practices. Field Crops Research, 284, 108565. https://doi.org/10.1016/j.fcr.2022.108565
2. Sharma, L., Banerjee, M., Malik, G. C., Gopalakrishnan, V. A. K., Zodape, S. T., and Ghosh, A. (2017). Sustainable agro-technology for enhancement of rice production in the red and lateritic soils using seaweed based biostimulants. Journal of Cleaner Production, 149, 968–975. https://doi.org/10.1016/j.jclepro.2017.02.153
3. SRP (2023). The SRP Standard for Sustainable Rice Cultivation (Version 2.2). Sustainable Rice Platform, Bangkok. https://sustainablerice.org/resources/

# Biological Methane Mitigation through Methanotrophic PGPR Coupled with Real-Time Sensor-Based Monitoring for Sustainable Rice Production

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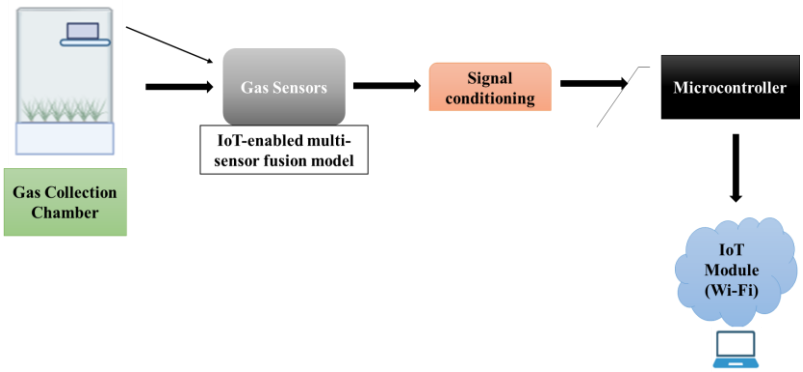
## Abstract

Methane ($CH_4$) emissions from flooded rice ecosystems are a major contributor to agricultural greenhouse gas emissions, necessitating sustainable mitigation strategies and efficient field-level monitoring. This study evaluated an integrated approach combining plant growth-promoting rhizobacteria (PGPR), drip irrigation, and organic amendments (i.e. biochar and farmyard manure) to mitigate methane emissions while improving rice performance. A field experiment was conducted using rice variety Anna 4 at VIT Farm, Vellore, Tamil Nadu, India, under different irrigation and microbial amendment strategies. Methane and nitrous oxide ($N_2O$) fluxes were monitored at key crop growth stages using gas chromatography, alongside the development and evaluation of an IoT-enabled sensor chamber for real-time greenhouse gas monitoring. The sensor system demonstrated 92% accuracy compared with the reference measurements. Sensor system enabled timely detection of treatment-associated changes and provided a practical approach for field-level assessment of biological methane mitigation. The integrated treatment combining drip irrigation, PGPR, biochar, and farmyard manure recorded the 66 % reduced methane flux, whereas the flood-irrigated control exhibited the highest emissions. The integrated treatment also improved rice growth and physiological performance. Although $N_2O$ emissions varied with irrigation and amendment strategies, integrated management showed potential to balance crop productivity and greenhouse gas mitigation. Overall, the integration of microbial interventions, resource-efficient irrigation, and sensor-based monitoring offers a promising strategy for advancing precision greenhouse gas management and sustainable, low-emission rice cultivation.




Block diagram of sensor unit

**Keywords:** *Methanotrophic PGPR, Methane mitigation, Rice cultivation, Greenhouse gases, Climate-smart agriculture*

# Development of an Integrated Web-Based Rice DNA Marker Database System for Rice Breeding and Marker-Assisted Selection

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## Abstract

DNA markers are essential tools for identifying and selecting desirable traits in rice breeding. Although extensive marker data have been generated by rice breeding and research programs in Thailand, the absence of a centralized, interoperable database has constrained their management, retrieval, and use. This study developed the Rice DNA Marker Database System (R-DNAM), a web-based platform for the systematic management, visualization, and exchange of rice DNA marker information to support marker-assisted selection (MAS) and varietal improvement. R-DNAM integrates seven data domains: rice gene information, single-nucleotide variants (SNVs) from whole-genome resequencing, SNP analyses and primer information, validated DNA markers, published SSR and SNP markers, candidate and cataloged markers. The database currently holds 296 SNP primer sets, 982 published primer marker records, 51 candidate markers, 17 cataloged markers, and 18 experimentally validated primer records. An integrated JBrowse2 genome browser displays marker positions on the rice reference genome. RESTful APIs allow external systems to retrieve marker data in JSON format, using the G.S. Number as the primary identifier. Integration with the Rice Passport portal links marker data to genetic characteristics, agronomic traits, seed quality, disease and insect resistance, and nutritional composition. R-DNAM thus provides an interoperable resource for MAS, molecular breeding, and data-driven rice variety development in Thailand. The system is available at https://rdnam.trsi-app.ricethailand.go.th.

**Keywords:** *Rice DNA marker database, Rice Passport, Marker-assisted selection, Web application, API integration*

# Development of Remote Sensing Indices and Regression Models for Rice Yield Forecasting in Lampang 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 Lampang Province, Thailand. The research focuses on enhancing rice yield monitoring across 60 sites within this region during the 2021 growing season by integrating satellite-based remote sensing data with field survey information. Collaboration 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, including ARVI, BI, EVI, GNDVI, NDVI, SAVI, and others, throughout the rice growth cycle. The results indicate that the average rice yield in Lampang Province was 1,012 kg/rai, with a minimum of 900 kg/rai and a maximum of 1,200 kg/rai. Seven indices showed highly significant associations with rice yield, with BI, GEMI, and GNDVI demonstrating the strongest associations ($R^2$ values of 0.617, 0.613, and 0.562, respectively). The multiple regression model achieved an $R^2$ value of 0.965, with a statistically significant relationship ($p < 0.05$). These relationships were used to develop a linear regression model for forecasting rice yield in Lampang Province.

**Keywords:** *Remote Sensing, BI, GEMI, GNDVI*

# Preliminary Electrochemical Investigation of Fenobucarb Using Screen-Printed Electrodes for Pesticide Screening in Rice

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## Abstract

Ensuring rice safety is essential for protecting public health and supporting sustainable agricultural production. Pesticide residues remain a significant concern, highlighting the need for rapid, accessible, and cost-effective analytical methods for food safety monitoring. Electrochemical sensing offers a promising approach owing to its potential for miniaturization, portability, and integration into on-site screening platforms. This study investigates the electrochemical behavior of fenobucarb, a carbamate insecticide, using screen-printed electrodes as an initial step toward developing a sensing platform for pesticide residue screening in rice. Cyclic voltammetry (CV) and square-wave voltammetry (SWV) were employed to evaluate the electrochemical response of fenobucarb using screen-printed carbon electrodes (SPCEs) and screen-printed graphene electrodes (SPGrEs). Measurements were conducted using 100 µM fenobucarb in phosphate-buffered saline (PBS, pH 7.0), with PBS serving as the background control. Preliminary results demonstrated distinguishable current responses in the presence of fenobucarb compared with the background electrolyte for both electrode types. SWV measurements revealed a prominent electrochemical signal at approximately 0.55 V versus Ag/AgCl, while CV measurements also exhibited measurable electrochemical responses under the investigated conditions. These findings provide preliminary evidence of the electrochemical detectability of fenobucarb using screen-printed electrodes. Further investigations are required to establish concentration-dependent responses, analytical sensitivity, repeatability, selectivity, and potential matrix interferences. Validation using rice extracts will also be essential to assess the practical applicability of the proposed approach. Overall, this study provides an initial foundation for developing accessible electrochemical sensing technologies for pesticide residue screening and future rice safety monitoring.

**Keywords:** *Fenobucarb, Electrochemical sensing, Screen-printed electrodes, Pesticide screening, Rice safety*

# Safeguarding Rice from Heavy-Metal Risks: Community-Based Risk Management, Safety Verification, and Social Value in Chiang Rai, Thailand

**Kanyanat Sirithunya[1], Vinitchan Ruanjaichon[2], Srisawat Khanthong[2], Chanakarn Wongsaprom[2], Phongthep Saitanmettajit[1], Adisak Jumaueai[1], Manoch Kumpanalaisatit[1], Surakiat Kumpanalaisatit[1], Hathaichanok Pattaampan[1], Suraphon Chaiwongsar[1]***

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## Abstract

Heavy-metal and arsenic risks in rice-growing watersheds raise concerns regarding food safety, consumer health, and farmers' market access. This study evaluated a community-based approach to preventive heavy-metal risk management and rice safety verification in Mae Sai District, Chiang Rai Province, Thailand. The initiative involved 31 rice farmers cultivating 884 rai (141.4 ha), including 26 farmers (83.87%) participating in targeted heavy-metal risk management. Interventions included vetiver grass barriers, biochar application, and farmer training in rapid screening and contamination risk management. Heavy-metal testing was conducted on paddy and milled rice samples to assess compliance with applicable safety criteria. The reported analytical results indicated that the tested rice samples complied with the referenced heavy-metal standards, providing evidence of product safety within the scope of sampling. Potential economic and social benefits were further evaluated using a scenario-based Social Return on Investment (SROI) approach. Based on an estimated annual paddy production of 961.79 tonnes, a hypothetical 20% at-risk production scenario and a THB 1/kg financial loss proxy yielded a potential avoidable market loss of THB 192,358 annually. Additional health-risk modeling estimated potential avoided healthcare costs of THB 256,478 annually. These modeled values do not represent realized savings or measured reductions in disease incidence. The findings suggest that integrating preventive soil and water management, farmer participation, and rice safety verification can strengthen food safety assurance and market resilience in potentially vulnerable agricultural watersheds. Continued quantitative monitoring is required to determine the effectiveness of individual interventions in reducing heavy-metal concentrations.

Keywords**:** Heavy metals; Arsenic; Rice food safety; Safety verification; Community-based risk management

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