International Conference/Workshop on Rice Climate Mitigation and Adaptation

25 March 2024

KASETSART UNIVERSITY
THAILAND

Program BOOK

Rice and Climate Change

Rice in Thailand is one of the main agricultural crops and holds immense significance as a means of ensuring food security and preserving cultural heritage. However, Thai rice farmers in face numerous challenges, such as low income, aging demographics, limited access to water sources, and a heavy reliance on rainwater for cultivation. Moreover, they lack the means to adopt modern and efficient environmentally friendly production techniques. Insufficient income and the sustainability of rice production have emerged as major obstacles to national development, leading to inequality. The looming challenge of global climate change need to be addressed so as not to add more burden to Thai rice farmers, sustain the rice industry and mitigate the impacts on rice production.

Climate change affects rice production by reducing yield due to increase in atmospheric temperature, alterations in precipitation patterns, soil salinity due to sea level rice, extreme weather events such as storms, floods, and droughts. Climate change may also influence the distribution and prevalence of pests and diseases. To address the effects of climate change, mitigation, and adaptation strategies should be initiated which will create awareness and community engagement to introduce and implement innovations that will increase resilience to climate change.

The Thailand Rice Science Research Hub of Knowledge brings together experts to share information on rice climate mitigation, which could be adapted by different sectors of the rice improvement and production. A conference workshop was initiated not only to share information but also to gather thoughts among academes, researchers and stakeholders to come up with a possible ideas and solutions to mitigate the effects of climate change in rice in a wider perspective.

Assoc.Prof.Dr.Siwaret Arikit
Director of Rice Science Center,
Kasetsart University

HUB
of RICE

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General information

Venue

Ruang Khao Grand Conference Hall, Vajiranusorn
Building, Kasetsart University
Bangkhen, Bangkok 10900 THAILAND

Registration Fee

Free of charge

Registration

Please have your QR code ready to scan at the counter. You will then receive your name badge at the registration desks.

Open hours check-in

Monday 25 March 2024 07:30 – 08:30

Poster Prize

2 prizes for the best posters.

General information

สถานที่จอดรถ

อาคารจอดรถบางเขน

อยู่ใกล้อาคารวชิรานุสรณ์ คณะเกษตร
มากที่สุด (550 เมตร)

ข้อมูลอาคารจอดรถทั้งหมด
https://kuparking.ku.ac.th

แผนที่ googlemap
อาคารจอดรถบางเขน

Organizers

Thailand Rice Science Research Hub of Knowledge

Kasetsart University
ku.ac.th

Rice Science Center
dna.kps.ku.ac.th

National Center for Genetic Engineering and Biotechnology (BIOTEC)
www.biotec.or.th

Kasetsart University Research and Development Institute(KURDI)
www3.rdi.ku.ac.th

National Research Council of Thailand (NRCT)
www.nrct.go.th

Ministry of Higher Education, Science, Research and Innovation(MHESI)
www.mhesi.go.th

Rice Department
www.ricethailand.go.th

Sponsors

THE ORGANIZING COMMITTEE GRATEFULLY ACKNOWLEDGES THE FINANCIAL CONTRIBUTION FROM THE FOLLOWING SPONSORS

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Program

International Conference/Workshop on
Rice Climate Mitigation and Adaptation

25 March 2024
08:00 - 12:00

07:30 - 08:30 **Registration**

08:30 - 09:10 **Opening by**

Professor Dr.Soottiporn Chittmittrapap
National Research Council of Thailand (NRCT)

Dr.Wonnop Visessanguan
National Center for Genetic Engineering and Biotechnology (BIOTEC)

Associate Professor Dr.Anuchai Pinyopummin, DVMSc,
Kasetsart University(KU)

09:10 - 09:40

Manipulating stomata to enhance rice stress tolerance
Professor Julie Gray - University of Sheffield, United Kingdom

09:40 - 10:10

Water management and greenhouse gas emissions in temperate rice paddies
Professor Kosuke Noborio - Meiji University, Japan

10:10 - 10:30 **Coffee break**

10:30 - 11:00

GHG mitigation in rice: Pieces of a comprehensive solution
Dr.Bjoern Ole Sander - IRRI, Philippines

11:00 - 11:30

Identification of Salt Tolerant Genes in Rice and Their Mechanisms
Professor Supachitra Chadchawan - Chulalongkorn University, Thailand

11:30 - 11:50

Controlled Environment and High Throughput Plant Phenotyping Systems Solution by PSI
Apiluck Musigkain - Gene plus Co.,Ltd. Thailand

12:00 - 13:00 Lunch *(First Floor)*

25 March 2024
13:00 - 16:15

13:00 - 13:30

Where Less is More: A Path Towards More Water Productive Rice
Professor Apichart Vanavichit - Kasetsart University, Thailand

13:30 - 14:00

Breeding rice varieties suitable for direct seeding
Dr.Shalabh Dixit - IRRI, Philippines

14:05 - 14:50

Group Discussions

1.Physiology *(Sub Meeting Room 2)*
2.Environment *(Ruang Khao Grand Conference Hall (1))*
3.Breeding *(Sub Meeting Room 4)*

14:55 - 15:10 **Coffee break**

15:10 - 16:00

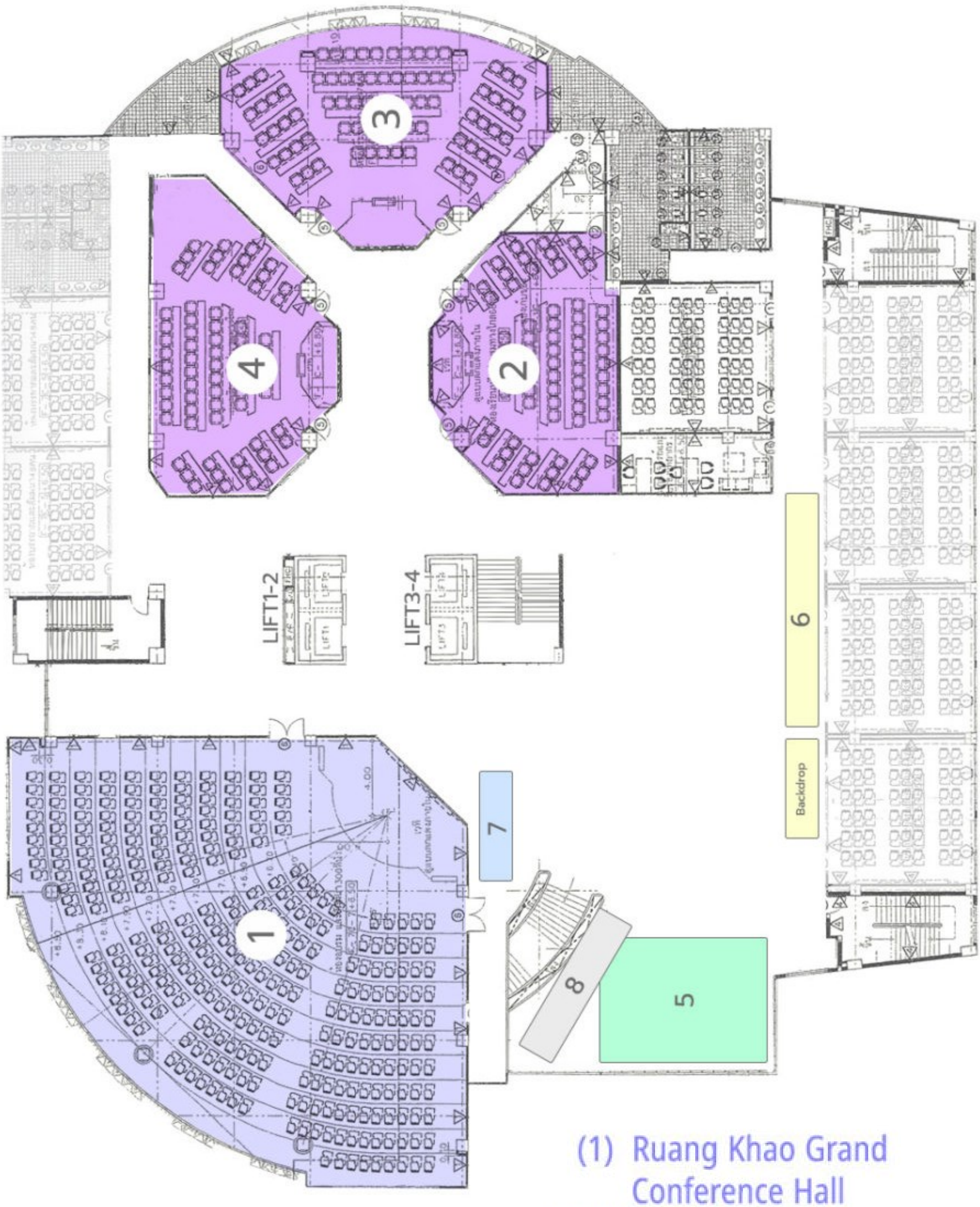
Summary of working group discussions
(Ruang Khao Grand Conference Hall (1))

16:00 - 16:10

Closing by
Dr.Theerayut Toojinda
National Center for Genetic Engineering and Biotechnology (BIOTEC)

2th Floor Plan

Vajiranusorn Building, Kasetsart University



(1) Ruang Khao Grand Conference Hall
(2-4) SUB Meeting Rooms
(5) Sponsor Zone
(6) Poster Session
(7) Registration desk
(8) Coffee Break

Professor Julie Gray

University of Sheffield,
United Kingdom

Professor Julie Gray is the Director of Research and Innovation in the School of Biosciences at the University of Sheffield. She studies plant environmental signalling responses, particularly those that control water use. Her research group have genetically manipulated, or gene edited, barley, wheat, rice and soybean to create new varieties with fewer stomata that have improved drought tolerance and reduced water requirement. Julie is a member of the European Molecular Biology Organisation (EMBO) and was recently awarded a Leverhulme Senior Fellowship.

Manipulating stomata to enhance rice stress tolerance

Julie E. Gray[1]

[1]*University of Sheffield, UK*
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Abstract

Stomata underpin crop productivity by allowing carbon dioxide to enter leaves and water vapour to exit. They open in the light for photosynthesis, and close in the dark or on dehydration. Manipulating the levels of rice epidermal patterning factors produced plants with abnormally low stomatal densities and reduced stomatal conductance. These modified crops have substantially lower levels of water loss and show enhanced drought tolerance. They require less water to grow, and yet maintain seed yields. For example, rice seedlings with approximately half the usual number of stomata, use only 60% of the normal amount of water, are better able to survive drought, and still yield well. Optimisation and adoption of this technology could enhance yields under stressful conditions, reduce agricultural water requirements, help to mitigate the impacts of climate change on food security, and reduce future GHG emissions.

Professor Kosuke Noborio

Meji University, Japan

Dr. Noborio, the full professor of Soil and Environmental Physics at Meiji University's School of Agriculture in Japan, boasts a robust academic and research portfolio. After completing his undergraduate and master's studies in agricultural engineering at Ehime University and Tottori University in 1981 and 1987, respectively, he pursued and attained his Ph.D. in soil science at Texas A&M University in 1995. His expertise centers on the dynamics of mass and energy transport within porous media and their interaction with the atmosphere. Over the past decade, Dr. Noborio has spearheaded a research team at Meiji University, focusing on the intricate exchanges of greenhouse gases between the atmosphere and various terrestrial and aquatic ecosystems. His fieldwork spans Japan, Thailand, Malaysia, and the waters of the Pacific and the Sea of Japan. More recently, Dr. Noborio's investigative interests have expanded to include studying gene functions in rice plants under environmental stressors, particularly those related to water scarcity and temperature extremes.

Water management and greenhouse gas emissions in temperate rice paddies

Kosuke Noborio[1], Nurtasbiyah binti Yusof[2], Sunchai Phungern[2,3], Fumitaka Shiotsu[1], Kentaro Yano[1,4], Jonaliza Siangliw[5]

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[2]*Graduate School of Agriculture, Meiji University, Kawasaki, Japan*
[3]*Department of Soil Science, Kastsart University, Kamphaen Saen, Thailand*
[4]*WellGreen-i Co. Ltd., Kawasaki, Japan*
[54]*National Center for Genetic Engineering and Biotechnology (BIOTEC), Kamphaen Saen, Thailand*
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Abstract

The imperative to reduce greenhouse gas (GHG) emissions from agricultural practices is a global concern, with particular attention on rice paddies due to their significant contribution to methane and nitrous oxide emissions. The System of Rice Intensification (SRI), coupled with Alternate Wetting and Drying (AWD) irrigation practices, has emerged as a promising approach to enhance rice productivity while concurrently mitigating GHG emissions. This methodology has gained popularity, especially in tropical regions, for its dual benefits. However, its application in temperate climates, such as in Japan, has often led to a paradox where AWD implementation reduces GHG emissions at the expense of rice yields. This study explores innovative water management strategies within the framework of SRI with AWD in temperate Japanese rice paddies, aiming to reconcile the need for GHG mitigation with the demand for high crop yields. Our research demonstrates that initiating AWD post the tillering phase, while ensuring continuous flooding up to this stage, effectively maintains rice yields without compromising GHG emission reduction. This finding challenges the prevailing notion that AWD's benefits are limited to tropical settings and opens new avenues for its application in temperate regions. Furthermore, the study delves into the genetic underpinnings that may explain the varietal responses to AWD, comparing the Sintanur variety, known for its high yield under AWD in tropical Thailand, with the Akita Komachi (japonica) and IR64 (indica) varieties. Preliminary results reveal distinct RNA expressions in Sintanur, suggesting a genetic basis for its superior performance under AWD conditions. These insights contribute to a better understanding of the differential success of SRI with AWD across climatic zones and highlight the potential for genetic interventions to enhance rice resilience and sustainability.

Dr.Bjoern Ole Sander

IRRI, Philippines

Ole is a Senior Scientist and IRRI's climate change focal point. His research group focuses on greenhouse gas (GHG) emissions and mitigation technologies. He currently leads IRRI's country office in Thailand. Ole completed his PhD at the University of Kiel in 2008. In 2010, he joined IRRI as a Collaborative Research Scientist with Dr. Reiner Wassmann.

As climate change specialist, Ole analyses the GHG balance of different cropping systems. He evaluates different mitigation options through water, fertilizer, and crop residue management. In his inter-disciplinary research, Ole identifies suitable bio-physical but also socio-economic conditions to support dissemination of climate-smart technologies. Incentivizing the adoption of these climate-beneficial technologies and monitoring their uptake have been a particular interest in recent years.

Ole's expertise in agricultural environment and multi-stakeholder engagement further supports the implementation of impactful projects throughout the field of climate change research and climate-smart technologies. Throughout his years with IRRI, Ole has continually worked with various stakeholders in countries within the region to foster the implementation of climate-smart farming practices.

GHG mitigation in rice: Pieces of a comprehensive solution

Bjoern Ole Sander
IRRI, Philippines

Abstract

Rice cultivation is a significant contributor to greenhouse gas (GHG) emissions, particularly methane (CH4), a potent greenhouse gas. This presentation delves into the multifaceted approach required to mitigate GHGs in rice production, focusing on GHG-reducing technologies, Monitoring, Reporting, and Verification (MRV), and the integration of carbon markets.

The first component explores innovative technologies and practices for reducing GHG emissions in rice production. From low-carbon crop management practices to soil amendments and the role of breeding, a spectrum of strategies will be discussed, highlighting their potential to minimize emissions while enhancing productivity and resilience

The second segment examines the critical role of MRV systems in accurately assessing emissions from rice cultivation. Precise monitoring and transparent quantification of emissions lay the groundwork for informed decision-making and targeted mitigation efforts. New MRV tools and the vision of a comprehensive system will be discussed.

Lastly, the presentation explores the emerging role of carbon markets in incentivizing GHG mitigation efforts in the rice sector. By providing financial rewards for emission reductions through carbon credits, carbon markets offer a market-based mechanism to promote and support the adoption of GHG-reducing technologies in rice cultivation.

Through a comprehensive examination of MRV systems, GHG-reducing technologies, and carbon markets, this presentation aims to provide insights into the integrated approach necessary for effective GHG mitigation in rice production

Professor Supachitra Chadchawan

Chulalongkorn University, Thailand

Supachitra Chadchawan is a professor at the department of Botany, Faculty of Science, Chulalongkorn University. She is the Head of the Center of Excellence in Environment and Plant Physiology, at the department of Botany, Faculty of Science. She is currently the Director of Bioinformatics and Computational Biology Program, which is the interdisciplinary program under Graduate School of Chulalongkorn University. Her research interests include plant stress physiology and plant productivity enhancement using chitin – chitosan related materials.

Identification of Salt Tolerant Genes in Rice and Their Mechanisms

Supachitra Chadchawan[1,2], Teerapong Buaboocha[2,3], Isabelle M. Henry[4], Luca Comai[4], Monnat Pongpanich[2,5], Kitiporn Plaimas[2,5], Duangjai Suriya-Arunroj[6], Meechai Siangliw[7]

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Abstract

Salt tolerance is controlled by multiple genes and related to various mechanisms. Based on the advancement of high-throughput technology, we can use genomics and transcriptomics data to predict the genes related to salt stress responses and the potential salt tolerant genes in rice. Genome-wide association study of Thai rice cultivars was used to identify salt tolerant genes for example *OsCRN* and *OsCullin*. The time-course transcriptome data from a single rice cultivar can be used to predict the mechanisms in salt tolerance and also predict the novel salt tolerant genes for example *OsOBP4*, which encodes the transcription factor involving in root development, flowering time and protection of photosynthesis system during salt stress. The combination of transcriptomic and genomic data can also be used to predict the salt tolerant genes, effectively. Using these data from chromosome substitution line 16 (CSSL16) and analyzed the transcriptomic data by gene co-expression network, two-state co-expression with clustering coefficient, and weighted gene co-expression network, *OsBTBZ1* and *OsERD4* were predicted to be involved in salt tolerance. Validation for the functions of these predicted genes were performed by using the complementation of the *Arabidopsis* mutant lines with the predicted rice genes.

Professor Apichart Vanavichit

Kasetsart University, Thailand

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

Where Less is More: A Path Towards More Water Productive Rice

Apichart Vanavichit[1] Chutima Phunthong[1], Mutiara K. Pitaloka[1], Cattleya Chutteang[2], Siriphat Ruengphayak[1], Siwaret Arikit[1,2],

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

Abstract

Rice is among the least water-use-efficient crops, and rice plants utilise most of their water uptake for transpirational cooling via stomata. To improve water-use efficiency (WUE) in rice, reducing stomatal density (*sd*) and size (*sz*) could help optimise transpiration and photosynthesis. We first initiated a non-GM breeding by isolating stomatal mutants from a large-scale, fast-neutron, stabilised mutant population derived from Jao Hom Nin (JHN), a Thai pigmented cultivar. Here, two series of purple rice stomata mutants: the Stomatal Model Mutant (SMM) identified microscopically on flag-leaves (Pitaloka et al., 2022) and the Drought-selected Model Mutant (DMM) generated through two rounds of screening under severe water stress, between -60 to -80 Ψ_m, right before the R_{1-2} reproductive stage. The three selected DMMs displayed intermediae to low *sd* (618–697 sd/mm^2), spanning a more comprehensive range than the low-density stomata mutant (JHN 8756 (LD, 650 sd/mm^2)). Compared to JHN WT and other SMM mutants, DMMs and LD displayed greater resilience with fewer penalties on shoot dry weight (SDW) and improved water use efficiency towards more restricted water conditions similar to alternate wetting and drying (AWD at 42 mm/plant). These low-to-intermediate density stomatal mutants could perfectly align SDW with enhanced WUE under restricted water conditions. Unexpectedly, we did not find strong correlations between *sd* vs SDW and *sd* vs WUE. We postulated that stomatal density *per se* was not the major player in improving shoot biomass and WUE under restricted water conditions. We predicted that resistance to abiotic stresses, including drought and heat, could support stomatal functioning under such restrictive irrigation as AWD.

Dr.Shalabh Dixit

IRRI, Philippines

Shalabh is a plant breeder with extensive experience in developing rice varieties for stress-prone ecosystems. These include drought and flood-prone ecosystems and direct-seeded rice systems. I currently lead the Direct-seeded and Upland rice (DSR) breeding program and Breeding activities for Southeast Asia.

Breeding Tomorrow's Rice: Advancing Direct-Seeded Cultivation with IRRI

Authors: Dixit S*, Heredia MCC, Argayoso MA, Ponce K
International Rice Research Institute, Los Baños, Laguna, Philippines.
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Abstract

Direct-seeded rice (DSR) cultivation occupies a significant portion of global rice production, relying heavily on outdated practices and varieties. In response to contemporary challenges like climate change, water scarcity, and labor shortages, adopting mechanized dry DSR presents a promising strategy for improving sustainability in rice farming. This method offers benefits such as reduced water usage, lower greenhouse gas emissions, and decreased production costs, contributing to environmental preservation and economic viability.

However, the widespread adoption of mechanized dry DSR faces obstacles, mainly due to the need for suitable rice varieties. Research at the International Rice Research Institute (IRRI) has identified nine essential traits for successful rice cultivation in DSR systems, addressing various growth stages and stressors.

To tackle breeding challenges in DSR, IRRI is establishing a founder panel of elite breeding lines to characterize their traits and breeding values. By employing genomic selection and a closed pool of elite cultivars, IRRI aims to accelerate genetic improvements in DSR, utilizing rapid generation advancement techniques and parental recycling strategies.

Overall, the shift towards mechanized dry DSR represents a significant change in rice cultivation, promising enhanced sustainability and profitability. Through targeted breeding efforts and advanced genomic selection, IRRI aims to lead the advancement of DSR technologies, ensuring food security amidst changing environmental and agricultural conditions.

Poster session

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Some agronomic characteristics of landrace rice varieties and adaptation of farmers community for rice utilization by wisdom, and culture through BCG Economic Model

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Abstract

Landrace rice varieties were grown in farmer fields, Udon Thani Province, Thailand. They could be divided into 3 groups i.e. white glutinous rice, colored glutinous rice, and non-glutinous rice. All landrace rice varieties were grouped into medium height with 100-130 cm. and had moderate tillering with 9-14 shoots per plant. The farmers prefer varieties with erect type tillers. Most varieties have green leaves except the purple glutinous variety. All varieties have average panicle length between 23.4-28.3 cm. Some varieties have harvesting period shorter than RD 6 and higher yields than RD 6. Rice plants grow and adapt well in low-fertility soils. Landrace rice has been preserved through the wisdom and culture of farmers community. Rice grain is processed into various snacks and foods such as ‘Khao Mao’ or ‘Kanom Nang Led’ and are sold to increase income for the household. However, climate change is affecting the quality and quantity of rice production and affecting the income of farmers. Adaptation of farmers community was promoted by developing the sticky rice growing community of Udon Thani Province towards a creative economy through community tourism with the BCG Model. Not only rice grains can be processed to add value, but every part of the rice and rice fields can be processed into products such as food, drinks, clothes, hats, bags, and notebooks. These products are sold to tourists at community tourism based on rice culture and farmer lifestyles.

Eye structure and its alteration of the brown plant hopper *Nilaparvata lugens* (Stål) (Hemiptera: Delphacidae) caused by the infected *Cordyceps fumosorosea*

Peerasak Bunsap[1], Sinlapachai Senarat[2], Seree Niyomdecha[2] and Narit Thaochan[1,*]

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Abstract

The brown planthopper, *Nilaparvata lugens* (Stål), (Hemiptera: Delphacidae) is a major destructive rice pest, as namely designed "BPH", in Asian area particulary Thailand. This situation might be related to the environmental and the climate changes. A comprehensive overview of the insect controls in the rice fields has been focused by using entomopathogenic fungi, as a parasitic microorganism, specifically *Cordyceps fumosorosea*. The present study was to investigate the eye structure and its alteration of BPH after they were exposed to *C. fumosorosea*. To gain insight into the host-pathogen interaction at the histological level, all adult samples were collected at 0, 12, 24, 36, 48, 72, 84, 108 and 120 hrs post-inoculation. They were fixed with Davidson's fixative for 36-48 hrs, which they were processed by using a standard histological method. A paired compound eyes with the ommatidia as a regular pattern of BPH was observed to be a common pattern of BPH. Various cell types of the ommatidium were classified and included the crystalline cone and the photoreceptor cells (or retinular cells). The study intriguingly revealed that degenerative features were observed in certain crystalline cones as early as 36 hours post-inoculation. This degeneration was notably exacerbated, with significant loss of eye structure occurring between 60 to 120 hrs post- inoculation, a trend that corresponded with the escalation of fungal populations. Remarkably, this represents the first documented instance where the fungi, induced by the eye histopathology of BPH at 36 hrs post- inoculation, have been utilized. The application of these findings has been instrumental in controlling BPH populations in rice cultivation in Thailand, offering a promising avenue for enhancing agricultural productivity. This pioneering approach underscores the potential of targeted biological control measures in the sustainable management of agricultural pests.

Keywords: Entomopathogenic fungi, eye histopathology, ommatidium, Rice field

Cis-acting elements on BADH2 promoter and their potential roles in rice responses to environmental stimuli

Parichart Burns, Wintai Kamolsukyunyong, Burin Thunnom, Yeetoh Dabbhadatta, Ratree Koohapitakthum, Wasin Poncheewin, Samart Wanchana and Vinitchan Ruanjaichon

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Abstract

Betaine aldehyde dehydrogenase 2 (BADH2) is an enzyme that catalyses the oxidation of aminoaldehydes to carboxylic acids. BADH2 preferentially converts γ-aminobutyraldehyde (GAB-ald) into gamma-aminobutyric acid (GABA). In the absence of BADH2, GAB-ald is converted to 2-acetyl-1-pyrroline (2AP). The 2AP molecule in rice grain is an important factor contributing to the aroma of aromatic rice. There were reports of SNPs and indels in exons 2, 7, 12, 13 and 14 associated with aromatic rice varieties. The nucleotide polymorphisms could lead to premature termination or alter the 3D structure of the enzyme and its subsequent functionality. However, little is known about the mechanism of fine-tuning the level of 2AP production. In this study, the presence of cis-acting elements in 300 base pairs upstream of the coding region of BADH2 in aromatic and non-aromatic rice was investigated using PLANT CARE (https://bioinformatics.psb.ugent.be/webtools/plantcare/html/), PLACE (https://www.dna.affrc.go.jp/PLACE/?action=newplace) and TSSP (http://www.softberry.com/berry.phtml?topic=tssp&group=programmes&subgroup=promoter). Several cis-acting elements for abscisic acid (ABA) signalling, plastid regulation, light and dehydration responses were identified, including BOXIINTPATPB (ATAGAA), DRE2COREZMRAB17 (ACCGAC) and BOXCPSAS1 (CTCCCAC). The results suggest that BADH2 can be fine-tuned by pre-transcriptional regulation and consequently 2-AP production.

Improvement of the 2-Acetyl-1-Pyrroline (2-AP) Content and Maintain of Grain Yield in Aromatic Rice using Shading and Alternate Wetting and Drying Irrigation Management during the Grain Filling Stage

Noynay, J. [1], Chutteang, C. [2] and Malumpong, C.[2]

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Abstract

Aromatic rice is highly sensitive to abiotic stress, which reduces crop yield and grain quality. However, abiotic stress may increase the 2-acetyl-1-pyrroline (2-AP) that is a major component for aromatic in rice grains. This study aimed to increase the 2-AP content of aromatic rice cultivars using AWD and shading during the grain-filling stage without affecting yield and quality. The factorial experiment using the two water regimes and shade conditions: Continuous Flooding- No shade (CN), Continuous Flooding- Shaded (CS), AWD-No shade (AN) and AWD-Shaded (AS) with two aromatic Thai rice cultivars (Hom Malaiman and Pathumthani1) were replicated three times in the dry (DS) and wet season (WS) 2023. Results showed that the 2-AP and proline contents of PTT1 significantly increased under AS compared to control and other treatments, while HMM resulted to a decrease in 2-AP content and no effect on proline content at DS. It is also observed that proline content is relatively higher in DS compared with WS due to higher temperature and lower relative humidity. Shading has significantly affected the gas exchange rate in each treatment. The increase in photosynthetic rate (Pn) under AN is attributed to the increased yield. HMM significantly increased yield under AN in both seasons compared with other treatments, while PTT1 significantly decreased yield under CS in both seasons but increased under AN in DS. The seed set percentage and filled grains were reduced under shaded conditions for both cultivars. The amylose content significantly decreased under AS, while chalkiness significantly increased in CS and AS compared with control in both seasons. It was concluded that PTT1 responds positively to the combination of AWD and shaded conditions to increase 2-AP content without yield loss. The varietal differences of the cultivars under low light stress and mild drought may contribute to the final 2-AP content outcome.

Rice Breeding for Heat Tolerance with Combined Biotic and Abiotic Stress Resistances by MAS Pedigree Selection

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Abstract

Global warming causes surface temperatures to rise which causes droughts, floods and severe insect disease outbreaks which resulted in a decrease in the grain yield of rice. Therefore, this study was to improve rice heat tolerance during reproductive stage and combines biotic and abiotic stress resistances from PinKaset+4 into new breeding lines. The Pinkaset+4 was crossed with heat tolerance variety namely Kimhunt. The progenies from each generation were selected by pedigree selection with MAS under the critical temperature at 42°C in controlled greenhouses. The 296 of F_2 generation were started to select high seed set over 50% and using MAS to select resistance genes from PinKaset+4. The result showed that phenotypic segregation of seed set had a right skewed continuous distribution and only six plants were found to have a percentage of seed set more than 50%. The plant with the highest seed set was 61.2%, while 72 plants had no seed set (0%). In addition, the Kimhant had 59% of seed set and the PinKaset+4 had 6% of seed set. MAS were tested for six plants and found that these plants contained brown plant hopper (*Bph3, TPS*), blast (*Pi-ta*), bacteria leaf blight (*Xa21, Xa5*), flood tolerance (*Sub1C*), aroma (*badh2*), gelatinization temperature (*SSIIa*), and starch type (wx^a) in both homozygous and heterozygous. After that, all six selected lines were planted in the F_3 generation with 50 plants of each line and 35 selected plants were able to produce seed set under high temperatures more than 70% with contained all MAS in homozygous and heterozygous. In F_4 generation, the 9 lines that were able to produce seed set under high temperatures more than 70% and detected all MAS in the homozygous and heterozygous were selected and it continue to evaluate in both controlled greenhouse and paddy field conditions in F_5 generation.

Pedigree Selection for Short Grain and Long Grain Rice derived from Khao Dawk Mali105 x Koshihikari

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Abstract

The type of rice that Thai people prefer to consume the most is jasmine rice especially Khao Dok Mali 105 (KDML105). However, since the urban consumption behavior is quite diverse, Japanese food has become popular in Thailand and the japonica type is starting to become important in Thai rice market. Therefore, the breeding program was started by using KDML105, an indica rice with long and slender shape of grain crossed with Koshihikari, a japonica rice with short and bold shape grain. The F_2 population allowed genetics segregate of the grain size and shape and other agronomic traits. The grain size and shape were distributed as normal distribution in F_2, which is a quantitative inheritance controlled by polygenes. After that, the grain size and shape were selected for 2 groups including long slender grain and short bold grain. Pedigree selection was used in this breeding program from F_2 until F_6. Afterward, the 20 and 24 plants from F_2, were selected according in the standard of Thai and Japanese rice. In F_4 generation, the 5 long grain lines and 2 short grain lines were selected together with good plant type including plant height is between 90-140 cm, resistance to diseases and insects, no awn and produce yield more than 700 kg/rai. These candidate lines will be yield trialed in F_5 and F_6 generation to evaluate yield and cooking quality in rainy and dry seasons in 2024.

Keyword: grain shape, pedigree selection, indica rice, japonica rice

Implementation of The Staining Technique and Image Analysis Approach for Detecting Cadmium Accumulation in Rice

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Abstract

The growing environmental concern surrounding cadmium accumulation in rice plants, primarily stemming from water source contamination, underscores the limitations of conventional cadmium detection methods such as atomic absorption spectrophotometry (AAS). These methods pose challenges, particularly for extensive data analysis, due to their complexity and the limited accessibility of equipment. In response, our study proposes an efficient and accessible method, emphasizing batch analysis, to address these challenges and improve cadmium detection in rice plants. Our novel technique utilizes a staining approach with specific staining chemicals that induce a distinct red coloration upon interaction with cadmium in plant tissues. Subsequently, computational image analysis software is employed for quantitative assessment of cadmium content based on the stained samples. This alternative approach not only simplifies the complexities associated with traditional detection methodologies but also highlights its practical scalability and wider applicability. To validate the efficacy of our staining method for large-scale screening, we conducted hydroponic experiments involving the cultivation of 244 Thai rice varieties in cadmium-contaminated solutions, comparing the results with standard measurements. Given the challenges posed by traditional techniques, the development of a rapid cadmium detection method is crucial for ensuring effective environmental monitoring and food safety.

Root phene for enhancing salt tolerance in rice (Oryza sativa L.).

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Abstract

Salinity stress poses a severe threat to global rice production, significantly reducing yields. While the impact on shoot traits is well-documented, the scarcity of information on roots presents a critical gap. Our study addresses this gap by evaluating the response of rice roots (Oryza sativa L.) to salinity stress, encompassing both low and high salinity levels (50 and 100 mM NaCl). We compared two popular commercial Thai rice varieties: Khao Dawk Mali 105 (KDML105) and Pathum Thani 1 (PTT1), in a pot system during the vegetative phase (60 days). KDML105 is more sensitive than PTT1, exhibiting a significant reduction in shoot biomass by 63%. Interestingly, PTT1 showed an increase in root architectural traits, particularly small lateral root length, alongside better growth performance and lower Na+ accumulation in both shoot and root compared to KDML105 under high salinity stress. However, in a hydroponic system, we assessed six rice cultivars, including KDML105, PTT1, DH103, DH212, Pokkali, and IR29, to evaluate root responses. Root architectural traits' response to salinity stress was not observed during the seedling phase (21 days) across the six rice cultivars, except for Pokkali (tolerance check), which displayed a significant decrease in root density of approximately 30% under salinity stress. This contrasting result led to the hypothesis that the difference in Na+ distribution in the soil media and root placement might influence Na+ uptake in the soil. Therefore, we employed a rootbox system to test the effect of root distribution on salinity stress using two rice cultivars with the same genetic background but differing in root distribution: chromosome segment substitution lines (CSSL) of KDML105, including CSSL24 (shallow) and CSSL46 (deep). In the rootbox system, salt accumulates at high levels on the soil surface and gradually increases in depth (60 cm) due to leaching. Consequently, this situation resulted in shallower rice roots, even in deep-rooting cultivars. CSSL24 exhibited a better yield than CSSL46 due to a larger amount of roots at 18-24 cm than CSSL46 under salinity treatment. Further explanation of this response necessitates a comparison of Na+ content between cultivars. Our research could provide fundamental insights into rice root responses, aiding in the selection of target root phenotypes to enhance salinity tolerance in rice.

Keyword: Salinity stress, Root response, Rice

Identification of adaptive root responsive genes associated with root penetration ability through compacted soil in rice diversity panel (*Oryza sativa* L.) using QTL-seq

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Abstract

Typically, many agricultural areas have been becoming modern agriculture, where heavy machinery and equipment have been intensively used. Local farmers' practices require mechanical equipment due to increasing crop intensity and reducing labor. Meanwhile, heavy machinery loads result in soil compaction, which has been affecting plant growth, which influence plant yield. Recently, researchers reported that stunning root growth under compacted soil is directly contributed by restricted ethylene diffusion and the crosstalk between auxin, ABA, and ethylene. This study aims to screen and evaluate root-responsive characteristics under ethylene treatment and to identify genomic regions associated with root sensitivity to compaction. Firstly, the ethylene chamber system was used to evaluate the ethylene sensitivity in the root among Thai rice accessions. The phenotypic variation in root length reduction between control and ethylene treatment was high among 275 rice accessions, ranging from 22.5-87.4%. The results of the genome-wide association study (GWAS) identified two SNPs on chromosome 10 that are strongly associated with the trait, with a cut-off threshold ($-\log P$) of 5. The results of the haplotype analysis showed that one haplotype in LOC_Os10g02970 (*OsLRR-RLK2*) was associated with the reduction in small root length. Subsequently, we developed a bi-parental population by crossing Dharia and PTT and used the F_2 progeny to perform QTL-seq for root penetrating ability (RPA) under a hard gel system. As a result, 24 significant QTLs were identified for RPA. Twelve promising candidate genes for RPA were identified based on annotation and literature mining. These include mitochondrial iron transporter gene (*OsMIT)* associates with reprogram primary and secondary metabolism in rice root. The results in this study pave the way for further research into the genetic mechanism of root penetration ability in rice at the seedling stage and could be used as breeder-friendly markers in future breeding programs.

Identification of Genetic Loci Associated with Grain Protein Content (GPC) in Rice (*Oryza sativa* L.) by Genome-Wide Association Study (GWAS)

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Abstract

Rice (*Oryza sativa* L.) is the most important source of energy and nutrition (carbohydrate and protein) for human beings. The effects of climate change on rice production are complex and affect various aspects of rice growth and grain quality. The grain protein content (GPC) of rice is a crucial factor that determines nutritional, cooking, and eating qualities, and can be affected by climate change. Understanding GPC traits in rice and their underlying genetic determinants remains a scientific challenge. To identify genes associated with GPC, grain proteins from 210 indica rice varieties were extracted from Thai rice germplasm and analyzed using the Bradford's method. The association between phenotypes and genotypes was investigated by a Genome-Wide Association Study (GWAS) analysis using multi-models. We identified 9 quantitative trait loci (QTLs) on chromosomes 2, 6, 7, 8, 9, 11 and 12 associated with the trait. Among them was a QTL on chromosome 7 (*qGPC7*), which was commonly detected by all models. Based on linkage disequilibrium (LD) for significant SNPs, 27 genes are in the range within a 400-kb window. Among them, eight genes contain functional SNPs with moderate effects. Expression profiles based on the RiceXpro database indicate that five candidate genes were highly expressed exclusively in rice endosperm. The results of the co-expression network analysis (RiceFREND database) showed that four candidate genes, *Os07g0213600*, *Os07g0213800*, *Os07g0214100*, and *Os07g0214300,* interacted with the *GLUD1*, *13 kDa prolamin*, *OsGluC-1*, and *Prolamin precursor* genes. Therefore, these candidate genes may have a high potential to be associated with the GPC trait in rice. The results of this study provide insight into the genetic regulatory network of protein synthesis and accumulation in rice endosperm, which may be useful for rice breeding programs to improve grain protein content.

Quantitative Trait Locus (QTLs) Mapping for Rice Stomatal Mega-Papillae Using QTL–seq and Genome-Wide Association Studies

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Abstract

Rice, the world's second largest cereal, plays a crucial role in human food security. Climate change is affecting rice production, particularly through water shortages. Similar to other plants, rice uses stomata to maintain the balance between CO_2 uptake and water loss depending on climatic conditions. Unique to rice are special epidermal protrusions on the subsidiary, the so-called papillae. We have observed a large number of papillae on the stomata of subsidiary, known as "mega-papillae", which partially cover the stomata. This structure potentially enhances water use efficiency. However, the genetic components that control the development of mega-papillae are still undiscovered. In this study, we identified quantitative trait loci (QTLs) that control mega-papillae development. We performed QTL-seq analysis in the F_2 population of Pathum Thani 1, a variety with normal papillae, and Dharia, a variety with mega-papillae, and identified 6 QTLs distributed on chromosomes 3, 5, 7, 9 and 11 based on the delta SNP index. In addition, genome-wide association studies (GWAS) for QTL identification were performed with a diversity panel, resulting in the identification of seven associated regions on chromosomes 2, 4, 5, 10 and 11. The most promising QTL is located on chromosome 5, which is stable in both the QTL-seq and GWAS approaches. This candidate QTL could be useful in future breeding programs to improve mega-papillae trait and thus water use efficiency.

Comparative Transcriptome Profiling of Resistant and Susceptible Rice Genotypes to *Xanthomonas oryzae* pv. *oryzicola* Reveals Key Genes for Bacterial Leaf Streak Resistance

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Abstract

Rice is consumed by almost half of the world's population as one of the most important staple foods. Like other crops, rice production is limited by external stress factors such as disease. There are two major bacterial diseases affecting rice, namely, bacterial leaf blight (BLB) and bacterial leaf streak (BLS). The latter can cause yield losses of up to 32%. BLS is a disease caused by gram-negative bacteria called *Xanthomonas oryzae* pv. *oryzicola* (*Xoc*). Resistance to BLS disease is controlled by quantitative trait loci (QTL); at least 20 QTLs have already been unlocked. However, in the course of climate change and bacterial evolution, the resistance genes can be broken down. Therefore, stable, and broad-spectrum resistance genes are desirable. With the help of next-generation sequencing (NGS), expression analysis for the trait of interest can be easily performed. In this experiment, RNA-seq was performed on two resistant varieties (DV85 and NDCMP49) and one susceptible variety (HCS). Rice leaves were injected with a *Xoc* isolate and collected at 0 hours post inoculation (hpi) and 9 hpi for RNA extraction and sequencing. The raw sequencing reads were aligned to a gap-free indica reference genome MH63KL1. RNA-seq analysis revealed that more DEGs were expressed at 9 hpi in HCS and more upregulated DEGs were observed at 9 hpi in all varieties. At 9 hpi, genes related to defense and resistance, such as receptor-like kinases, WRKY transcription factors, NAC transcription factors, heat shock proteins, chitinase, etc., are differentially expressed, indicating that genes related to pathogen recognition and signal transduction are functional at the early stage of infection. Our study has also shown that genes related to signal transduction are partly responsible for the susceptibility or resistance of HCS and DV85, while genes related to catalytic activity and translation may be good sources for the resistance of NDCMP49. Our results provide valuable information for future studies on the molecular mechanism of BLS resistance in rice.

Keywords: *Xoc* inoculation, RNA-seq, Transcriptome, DEGs, BLS.

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