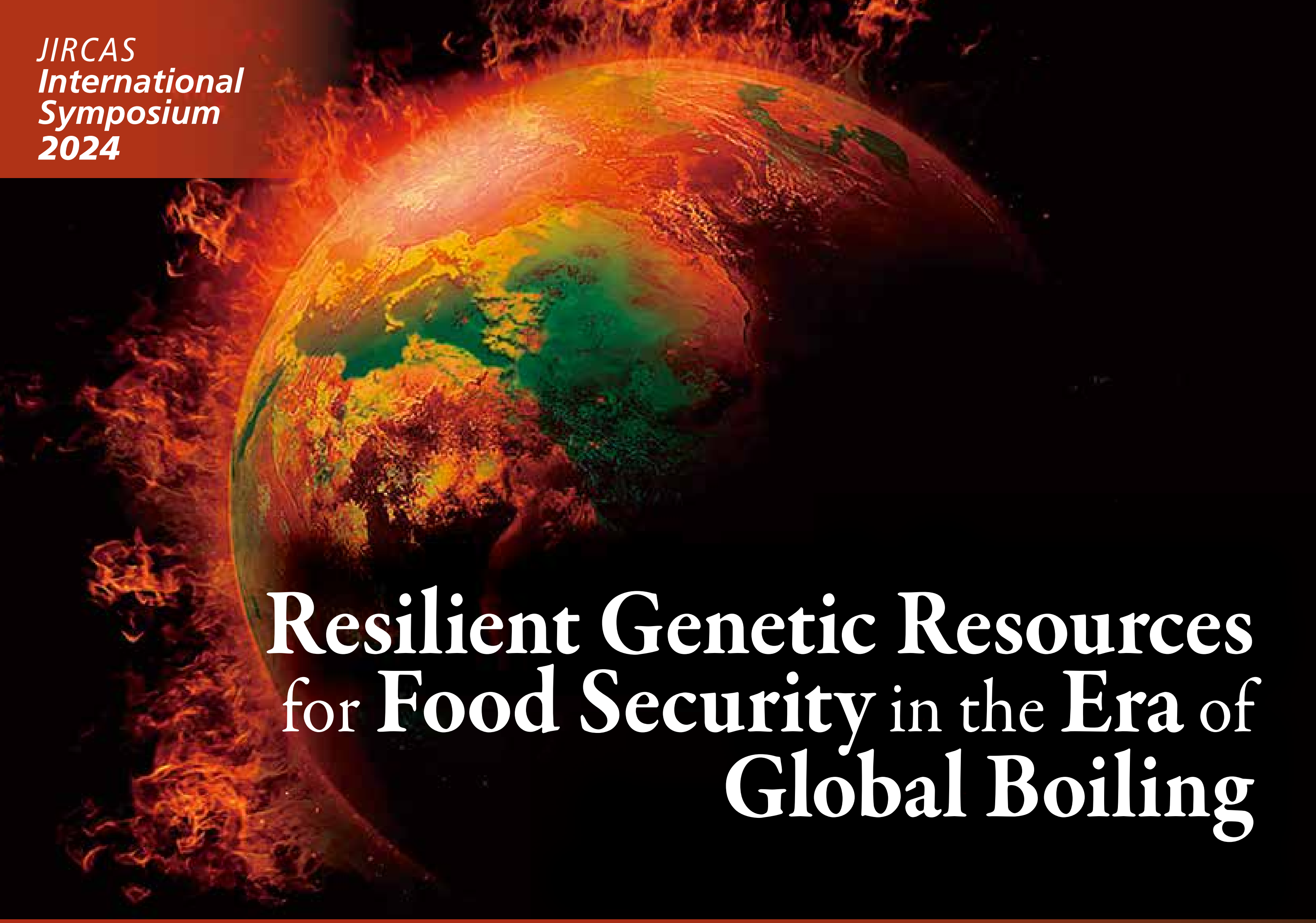

JIRCAS
International Symposium 2024

Resilient Genetic Resources for Food Security in the Era of Global Boiling

Proceedings

Date **November 22, 2024**

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JIRCAS International Symposium 2024
U Thant International Conference Hall
United Nations University
Tokyo, Japan,
November 22, 2024

Opening Remarks

KOYAMA Osamu

President, JIRCAS

Good afternoon, everyone. I would like to express my sincere gratitude to SAKAIDA Teruya, Director-General of the Agriculture, Forestry and Fisheries Research Council Secretariat, Ministry of Agriculture, Forestry and Fisheries (MAFF), the two distinguished keynote speakers, Dr. Sarada Krishnan of Crop Trust and Dr. HASEGAWA Toshihiro of the National Agriculture and Food Research Organization (NARO), as well as the speakers for the two sessions, for their cooperation in the JIRCAS International Symposium 2024. I would also like to thank all of the participants who have joined us, both in person and online, for taking the time out of your busy schedules.

In July 2023, UN Secretary-General said that we are now entering the era of global boiling. And recently, the media has reported that 2024 could almost certainly be the hottest year on record, and the first year that average temperatures rise to 1.5°C above the pre-industrial period.

Indeed, we have witnessed extreme weather events such as droughts and heavy rains affecting agricultural productivity. Countries in the Global South are facing protracted food security crises due to climate change. Also, as we recall, in Japan, the quality of rice declined last year due to heat stress.

Amid concerns that climate change will adversely affect crop productivity and grain quality, the need to develop crops that are resilient to the negative impacts of climate change is greater than ever to maintain global food and nutrition security. To this end, it is essential to conserve the diversity of crop genetic resources with resilient traits, such as those exhibiting stress tolerance to droughts, floods, poor environments, pests, and diseases, as well as traits that enable efficient use of water and external inputs.

JIRCAS has been working diligently to develop the technologies necessary to produce resilient crops, and to strengthen cooperation in the sharing of information on genetic resources and technologies to promote the sustainable production of tropical crops. In addition, this symposium brings together experts on various genetic resources to consider the diversity and potential of genetic resources, as well as the opportunities and challenges for institutional development to utilize diversity, in order to build resilient and nutritious food systems in the era of global boiling.

I sincerely hope that this International Symposium will serve as a platform for useful information exchange and lively discussions. Thank you very much.

　農林水産省技術会議事務局堺田輝也局長、基調講演者であるCrop Trustサラダクリシュナン博士・農研機構長谷川利拡様、また､セッションにご登壇いただく講演者の皆様､本日はJIRCAS国際シンポジウム2024へのご協力を賜り、厚く御礼を申し上げます。そして会場またはオンラインでご出席の皆様、貴重なお時間を割いて本日のシンポジウムにご参加くださり、心より御礼申し上げます。

2023年7月、国連事務総長は、地球温暖化 (global warming) の時代はおわり、地球沸騰化 (global boiling) 時代の到来の兆候であると表現しました。そして先日の報道によると、2024年はほぼ確実に史上最高に暑い年であり、産業革命期と比較して気温上昇が 1.5℃ を超える最初の年になることが確実視されています。

実際に、私たちは、干ばつ、集中豪雨などの異常気象が、農業の生産性に影響を与えているのを目撃しています。グローバルサウス諸国は、干ばつや洪水により長引く食料安全保障の危機にさらされています。また、記憶に新しいように、昨年日本でも猛暑の影響でコメの品質低下が起こりました。

気候変動が作物の生産性と品質に悪影響を及ぼすことが懸念される中、世界の食料と栄養の安全保障を維持する上で、レジリエントな作物開発の必要性がこれまで以上に高まっています。そのためには、気温変動・干ばつや洪水・不良環境・病害虫などのストレス耐性、同時に、効率的な水・肥料利用を可能にする形質など、気候にスマートな作物遺伝資源の保全・利用が喫緊の課題です。

国際農研では、レジリエントな作物を作出または生産するために必要な技術の開発や、熱帯性作物の持続的生産に向けた遺伝資源の情報整備と利用促進技術の開発の連携強化に取り組んできました。本シンポジウムは、作物遺伝資源に関する専門家をお招きし、地球沸騰化時代に強靭で栄養に富んだ食料システム構築を実現するにあたり、遺伝資源の多様性と可能性、多様性を利用していくための制度整備の機会と課題を考えます。

国際シンポジウムが有益な情報交換と活発な議論の場となりますことを祈念し、開催のあいさつに代えさせていただきます。

Welcome Remarks

SAKAIDA Teruya

Director-General, Agriculture, Forestry and Fisheries Research
Council Secretariat, Ministry of Agriculture, Forestry and Fisheries
(MAFF)

皆様、こんにちは。
ただいまご紹介を賜りました、農林水産省 農林水産技術会議事務局長の堺田 輝也でございます。

このたびは、「JIRCAS 国際シンポジウム 2024」が無事に開催されますことを、心よりお慶び申し上げます。

さて、世界では、気候変動などの影響により、食料需要の増加、食料生産・供給の不安定化がますます顕著になりつつあります。
今夏は、観測史上最も高い平均気温を記録するなど、日本各地で高温による農産物の生育不良や病害虫の発生など、農業現場に大きな影響を及ぼしているところであります。
また、海外でも異常気象の発生により大きな被害がもたらされていると聞いております。
このように、我が国を含め世界的な課題である気候変動に対応した強じんで持続可能な農業生産を実現し、食料安全保障の確保を進めていくことは、非常に重要な課題であります。

このような中、日本においては、2021年5月に決定した「みどりの食料システム戦略」に基づき、2050年を目標年としたKPIを掲げ、調達、生産、流通、消費のフードチェーン全体で、生産力向上と持続性を両立する取組を進めております。

また、本年5月、食料・農業・農村基本法を四半世紀ぶりに改正し、「食料安全保障の強化」や「環境と調和のとれた食料システムの確立」等を新たな柱に位置付け様々な施策を展開することとしています。

本日のシンポジウムでは、強靭な食料システムの構築に向けて、遺伝資源の多様性保全と活用、国際的な連携強化について、当分野で大変活躍されておられる方をお招きしての講演ならびに議論が行われる予定と伺っております。強じんで持続可能な農業生産の実現に向け、様々な視点から議論を深められる大変良い機会になることを期待しております。

最後になりましたが、本日のこのシンポジウムが実りあるものとなりますとともに、ご出席の皆様の益々のご活躍、ご健勝をお祈り申し上げ、私のあいさつを結ばせていただきます。本日はまことにおめでとうございます。

Keynote Speeches

Historical Perspectives on the Role of Crop Diversity in Achieving Food and Nutrition Security

Sarada Krishnan

Director of Programs, Global Crop Diversity Trust, Bonn, Germany

Dr. Sarada Krishnan is the Director of Programs at the Global Crop Diversity Trust based in Bonn, Germany. In this role, she supervises a team of scientists and project managers, overseeing the implementation of strategic projects and programs designed to support the organizational mandate of securing the world's crop diversity. She oversees the planning, development, and implementation of the overall programmatic technical framework of the organization. She currently serves on the United States Department of Agriculture (USDA) National Genetic Resources Advisory Council and is the chair of USDA's Coffee and Cacao Crop Germplasm Committee. She also serves on Colorado State University (CSU) College of Agricultural Sciences' AgIndustry Leadership Council, on the advisory board of 4C Services and is faculty affiliate in the CSU Department of Horticulture and Landscape Architecture. Her broad interests include biodiversity conservation - both ex situ and in situ, conservation and sustainable use of plant genetic resources with a research focus on coffee genetic resources, food and nutrition security, and economic empowerment of women and girls.

Abstracts

Diversity within and among domesticated species has been the cornerstone of agricultural development. Since the advent of agriculture, farmers around the world have served as custodians of this diversity, safeguarding it for future generations. Through thousands of years of cultivation, farmers have selected for plants that are adapted to local climatic conditions, which are called landraces. But the globalization of agriculture and plant breeding has led to the loss of genetic diversity in farmers' fields, causing genetic erosion. Conservation of plant diversity in genebanks safeguards it for use by current and future generations, both directly by farmers and as the raw materials for research and plant breeding. Genebanks therefore ultimately contribute to sustainable crop production systems, and hence food and nutrition security.

The most important person in the history of crop diversity conservation was Nikolai Vavilov. His work on the biogeography of crop plants provided a theoretical basis for the relationship between a crop's center of origin and the amount of genetic variation it displayed. He conducted numerous collecting trips around the world and identified main and secondary centers of diversity for numerous crops.

Another important historical figure in advancing the conservation of crop diversity was Otto H. Frankel. He developed the concepts of the genetic conservation of crop plants and was central to the efforts to organize genetic conservation from the 1960s onwards. He is credited with bringing together the International Biological Programme (IBP) and the United Nations Food and Agriculture Organization (FAO) in the common cause of halting genetic erosion and conserving crop diversity by advocating for the establishment of a network of regional genebanks. This led to the formation of the Consultative Group on International Agricultural Research, which we now know as CGIAR, and the subsequent formation of the International Board for Plant Genetic Resources, which is now under CGIAR as the Alliance of Bioversity International and CIAT.

Hundreds of genebanks now conserve the diversity of many crops from all over the world, representing variation at the genetic level, both within and among crop populations. Conservation in genebanks means that landraces threatened with genetic erosion in farmers' fields can be preserved and made available to users. The international genebanks of CGIAR centers conserve the global diversity of some of the major global crops, whereas national genebanks focus on the agricultural heritage of their country, which includes crops more specifically important to the country's culture and its agricultural development. The ultimate security of seed collections is the safety back up in the permafrost at the Svalbard Global Seed Vault. The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) provides a policy framework for the world's genebanks. The Global Crop Diversity Trust is an essential element of the funding strategy of the ITPGRFA and is raising an endowment to support the essential operations of key genebanks around the world, starting with international collections.

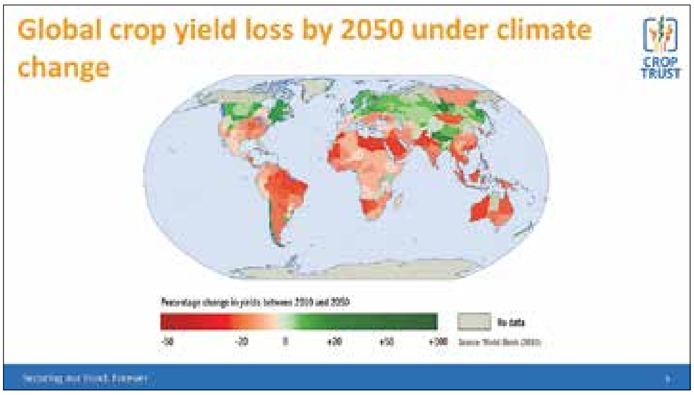
Role of Crop Diversity in Achieving Food and Nutrition Security: Historical Perspectives

Sarada Krishnan
22 November 2024

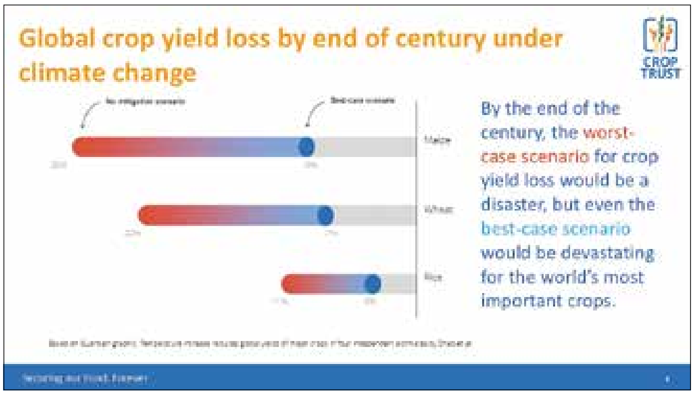
Transforming our food systems

Global Challenges:

- Climate change
- Biodiversity loss
- Increasing population
- Deforestation
- Increased incidence of pests and diseases
- Unsustainable agricultural practices
- Food loss and food waste



Global crop yield loss by 2050 under climate change

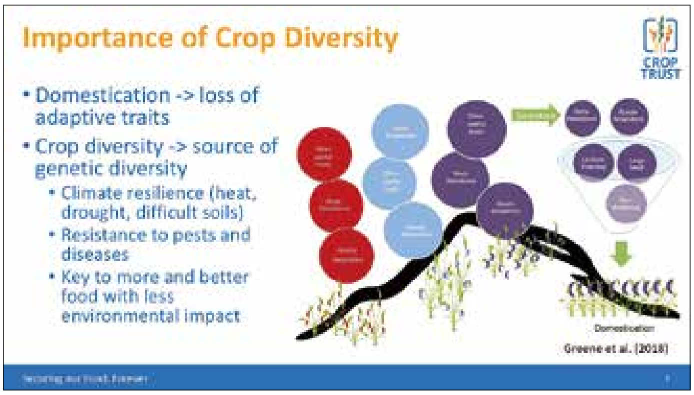


Global crop yield loss by end of century under climate change

By the end of the century, the worst-case scenario for crop yield loss would be a disaster, but even the best-case scenario would be devastating for the world's most important crops.

To deal with these global challenges we need crop diversity

Why crop diversity is crucial for a resilient food supply



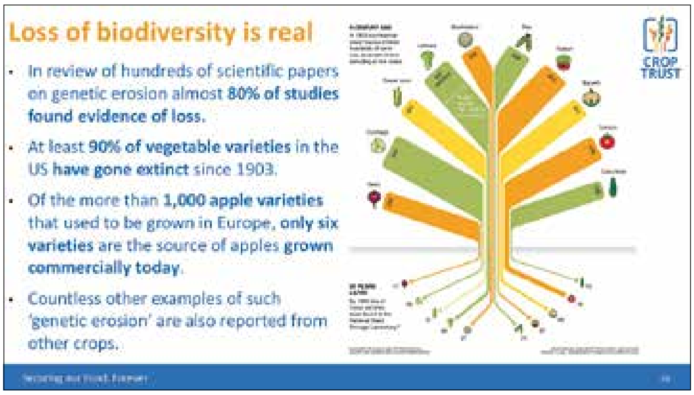
Importance of Crop Diversity

- Domestication -> loss of adaptive traits
- Crop diversity -> source of genetic diversity
  - Climate resilience (heat, drought, difficult soils)
  - Resistance to pests and diseases
  - Key to more and better food with less environmental impact

Greene et al. (2018)

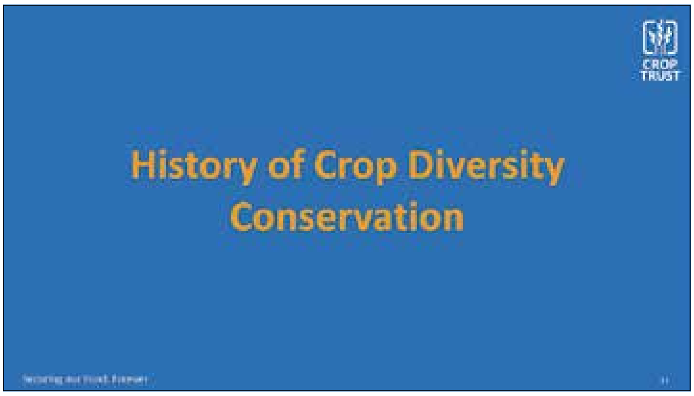
Diversity exists between different crop species

Diversity exists within individual crop species



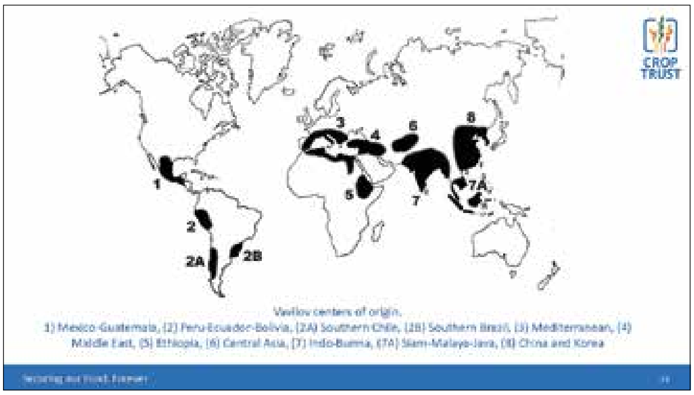
Loss of biodiversity is real

- In review of hundreds of scientific papers on genetic erosion almost **80% of studies found evidence of loss.**
- At least **90% of vegetable varieties** in the US **have gone extinct** since 1903.
- Of the more than **1,000 apple varieties** that used to be grown in Europe, **only six varieties** are the source of apples **grown commercially today**.
- Countless other examples of such 'genetic erosion' are also reported from other crops.



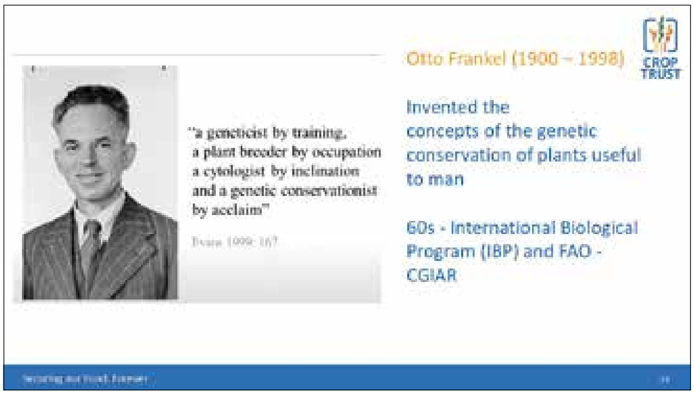
History of Crop Diversity Conservation

Nikolai Ivanovich Vavilov, 1887 - 1943



Vavilov centers of origin.
1) Mexico-Guatemala, (2) Peru-Ecuador-Bolivia, (2A) Southern Chile, (2B) Southern Brazil, (3) Mediterranean, (4) Middle East, (5) Ethiopia, (6) Central Asia, (7) Indo-Burma, (7A) Siam-Malaya-Java, (8) China and Korea

Securing our food, forever.



Otto Frankel (1900 – 1998)

"a geneticist by training,
a plant breeder by occupation
a cytologist by inclination
and a genetic conservationist
by acclaim"

Evans 1999: 167

Invented the concepts of the genetic conservation of plants useful to man

60s - International Biological Program (IBP) and FAO - CGIAR

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Important Milestones

1971 – CGIAR established
1974 – IBPGR established by the CGIAR (FAO administrative host)
1975 to 1995 – collection of >200,000 samples of landraces, CWRs and other materials in 136 countries
1991 - 1993 – Convention on Biological Diversity (CBD) negotiations and enters into force
1994 – "In-trust" agreement of CGIAR genebanks with FAO
2001 – Adoption of ITPGRFA
2004 – ITPGRFA enters into force (Multilateral System of Access and Benefit Sharing, Annex 1 crops – 64 majors crops and forages)
2004 – Crop Trust established by FAO and CGIAR to provide sustainable, long-term funding for *ex situ* conservation
2010/2014 – Nagoya Protocol adopted/entered into force

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In situ

Ex situ

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Role of Genebanks

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What is a genebank?

Genebanks are repositories where genetic materials are safely conserved and available for use

Some plants have seeds that cannot be dried and cooled for storage. These plants are often conserved as small plantlets, growing very slowly under specialized conditions in test tubes in an *in vitro* genebank, or cryopreserved. Others, like fruit trees, can be conserved as adult living specimens in a field.

Plant breeders and farmers can draw on genebanks in their search for particular traits that they need.

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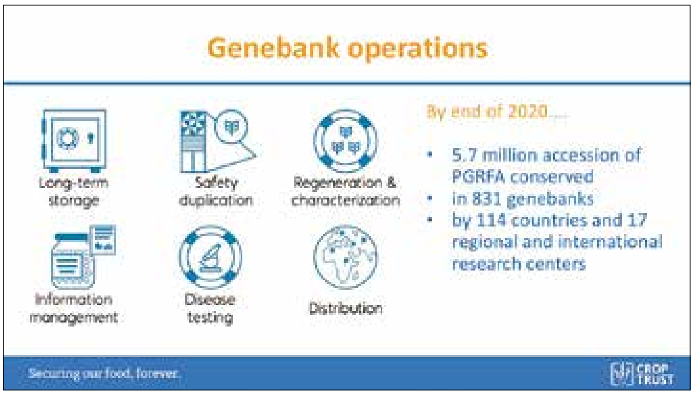

Genebank operations

- Long-term storage
- Safety duplication
- Regeneration & characterization
- Information management
- Disease testing
- Distribution

By end of 2020…..

- 5.7 million accession of PGRFA conserved
- in 831 genebanks
- by 114 countries and 17 regional and international research centers

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International Policy Agenda

The global community has specifically recognized the importance of safeguarding crop diversity for a sustainable future:

- United Nations **Sustainable Development Goals** (SDGs)
- **Paris Agreement** at UNFCCC COP21
- **Convention on Biological Diversity** (CBD): Strategic Plan 2011-2020, including the Aichi Biodiversity Targets and Post-2020 Global Biodiversity Framework

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RECOGNIZED IN THE UN SDGS

GOAL 2: End hunger, achieve food security and improved nutrition, and promote sustainable agriculture

TARGET 2.5: By 2020 maintain genetic diversity of seeds, cultivated plants, farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks at national, regional and international levels, and ensure access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge as internationally agreed

Indicator 2.5.1

Number of plant and animal genetic resources for food and agriculture secured in either medium or long-term conservation facilities

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We work closely with the International Treaty

- Funding and implementation mechanism
- Article 15 collections
- Policy training and guidance
- Policy advising and support
- Emergency reserve for genebanks
- Global information system on PGRFA
- Global crop conservation strategies

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Global system of *ex situ* conservation

1. Svalbard Global Seed Vault
2. International collections
3. National collections
4. Community collections, conservation in-situ, on farm

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Safety duplication at Svalbard Global Seed Vault

- Opened in February 2008
- > 1.2 million seed samples from 80 countries
- October 2024, more than 30,000 new seed samples deposited from 21 countries

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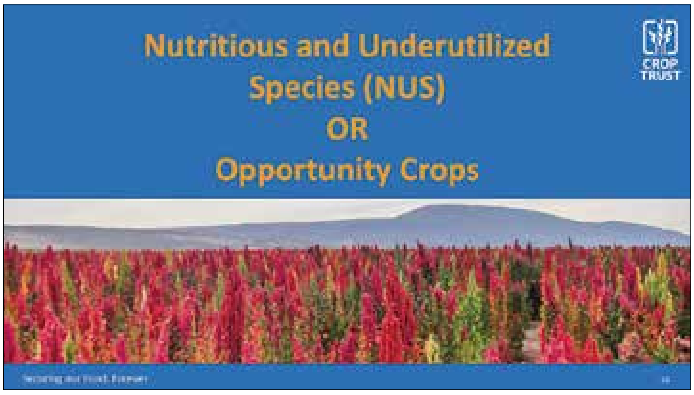
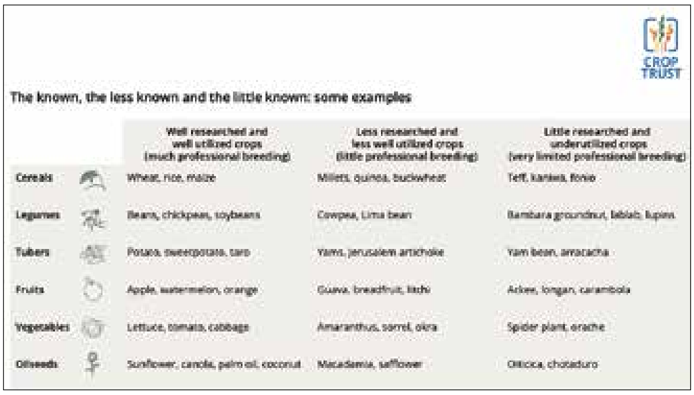
Future Actions for Food System Transformation



Nutritious and Underutilized Species (NUS) OR Opportunity Crops



The known, the less known and the little known: some examples

	Well researched and well utilized crops (much professional breeding)	Less researched and less well utilized crops (little professional breeding)	Little researched and underutilized crops (very limited professional breeding)
Cereals	Wheat, rice, maize	Millets, quinoa, buckwheat	Teff, kaniwa, fonio
Legumes	Beans, chickpeas, soybeans	Cowpea, Lima bean	Bambara groundnut, lablab, lupins
Tubers	Potato, sweetpotato, taro	Yams, jerusalem artichoke	Yam bean, arracacha
Fruits	Apple, watermelon, orange	Guava, breadfruit, litchi	Ackee, longan, carambola
Vegetables	Lettuce, tomato, cabbage	Amaranthus, sorrel, okra	Spider plant, orache
Oilseeds	Sunflower, canola, palm oil, coconut	Macadamia, safflower	Oiticica, chotaduro

We need collective action to deliver food systems:

- that embrace opportunity crops, and
- in which farmers are the agents of change and partners of innovation.

Four mutually reinforcing pillars:

1. Securing crop diversity
2. Research and breeding
3. Value chains and seed systems
4. Policy support

1

Securing crop diversity

- Expanding conservation efforts on opportunity crops, enhancing their availability.

2

Research and breeding

- Making the diversity of opportunity crops available for use by researchers, plant breeders and farmers, by characterizing the collections for specific traits related to climate change resilience and nutrition.
- Integrating this diversity in breeding programs, including the development of public-private partnerships

3

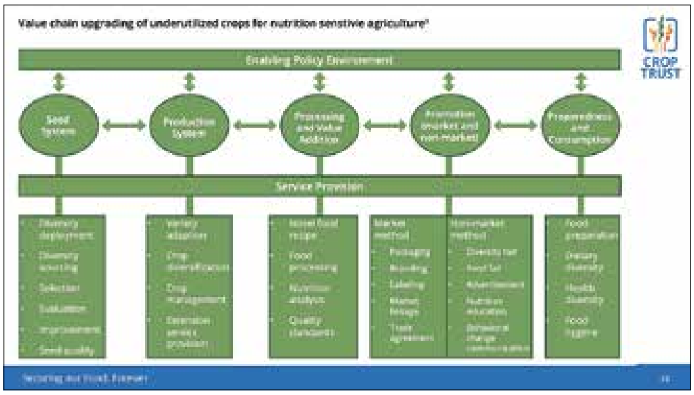
Value chains and seed systems

- Identifying socio-economic obstacles that prevent large-scale adoption of opportunity crops in current food systems
- Supporting integrated seed system development
- Strengthening extension services for opportunity crops

4

Policy support

- Working with international policy frameworks (first and foremost the Plant Treaty) and national governments on enabling environment of policies and regulations that are supportive of diverse food systems
- Raising awareness among broad stakeholder groups



Value chain upgrading of underutilized crops for nutrition sensitvie agriculture

→ A shift from intensive production of major staples to embracing a **much wider diversity of crops**, their products, and systems of cultivation is no small task.

→ Such an ambitious task is only possible with the support of a **wide range of actors**, including national governments, multilateral institutions, civil society organizations, the private sector, foundations, think tanks, farmers and others.

→ **Genebanks** can be at the forefront of this challenge, serving as engine and catalyst.

→ The **Crop Trust** is an important partner to help advance these ideas together with a wide range of actors.

Dr. Sarada Krishnan
Director of Programs
sarada.krishnan@croptrust.org

Securing our Food. Forever.

Toshihiro Hasegawa

Executive Scientist, Institute for Agro-Environmental Sciences, National Agriculture and Food Research Organization (NARO), Japan

Dr. Toshihiro Hasegawa is an executive researcher at the Institute for Agro-Environmental Sciences, National Agriculture and Food Research Organization (NARO), Tsukuba, Japan. After graduating from Kyoto University, he worked as an assistant professor at Kyushu Tokai University and an associate professor at Hokkaido University before joining NARO in 2016. He is a crop physiologist and specializes in environmental crop responses. He recently served as a Coordinating Lead Author of The Working Group II contribution to the IPCC Sixth Assessment Report.

Abstracts

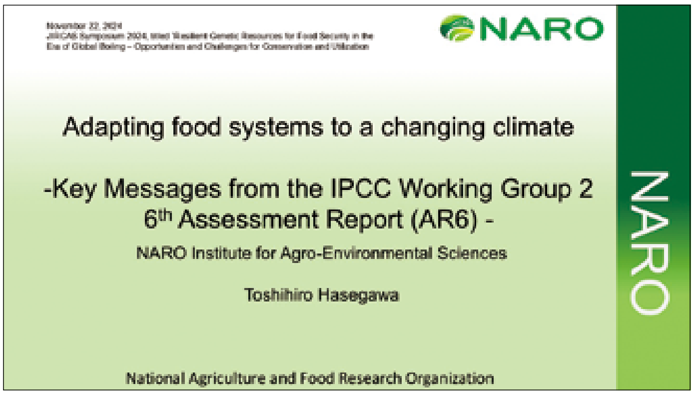
Climate change, including the increasing frequency and magnitude of climate extremes, has already negatively impacted food systems, undermining food security and nutrition. In 2022, the Intergovernmental Panel on Climate Change (IPCC) released the 6th Assessment Report (AR6) on climate change impacts, adaptation, and vulnerability to provide science-based and policy-relevant information. The report chapter comprehensively covers food, fibre, and other ecosystem service climate change impacts, projected risks, and adaptation solutions, leading to more resilient food systems[1].

The assessment in the chapter highlights the significant impacts that human-induced climate change, including extreme weather events, is having on food systems. These impacts include reduced productivity, declining food quality, and changes in species distributions, increasing the risks of malnutrition and resource competition, especially for vulnerable populations. Since the mid-20th century, the growing frequency of extreme events has resulted in sudden losses in food production, decreased availability, and rising food prices, leading to acute food insecurity and worsened livelihoods in many regions. While autonomous adaptation measures have been adopted in agriculture and aquatic food production, they often remain incremental and limited to specific sectors.

Ecosystem-based approaches, such as diversification, land restoration, agroecology, and agroforestry, can enhance food production while offering multiple benefits, including improved yield stability and ecosystem health. Sustainable management of resources in response to shifts in species distribution—both terrestrial and aquatic—due to climate change is an effective adaptation measure to mitigate risks to food security and nutrition. Increasing global warming levels will constrain these options, putting food security at even greater risk in vulnerable areas.

Overall, substantial mitigation efforts are required to minimize the impacts on food systems and the ecosystems that support them. Food systems contribute around 30% of total human-caused emissions, and adaptation and mitigation actions that overlook ecosystem functions and equity could worsen the negative impacts of climate change, increasing vulnerability in certain regions and groups. In contrast, some adaptation strategies can enhance the sustainability of food production, reduce vulnerabilities, and improve ecosystem health in the context of climate change. Societal changes, such as shifts in dietary patterns, are also explored, as well as the risks of maladaptation and approaches to avoid it, with the goal of ensuring fair food distribution. This presentation summarizes key messages from the IPCC AR6 and discusses strategies for using genetic resources to enhance the resilience of food systems in the face of climate change.

[1] Bezner Kerr, R. et al. Food, Fibre, and Other Ecosystem Products, in: Pörtner, H.O. et al. (Eds.), Climate Change 2022: Impact, Adaptation, And Vulnerability. Contribution of Working Group II to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge University Press (CUP), Cambridge, UK and New York, NY, USA, pp. 713–906 (2022) https://doi.org/10.1017/9781009325844.007



November 22, 2024
JIRCAS Symposium 2024, titled 'Resilient Genetic Resources for Food Security in the Era of Global Boiling – Opportunities and Challenges for Conservation and Utilization

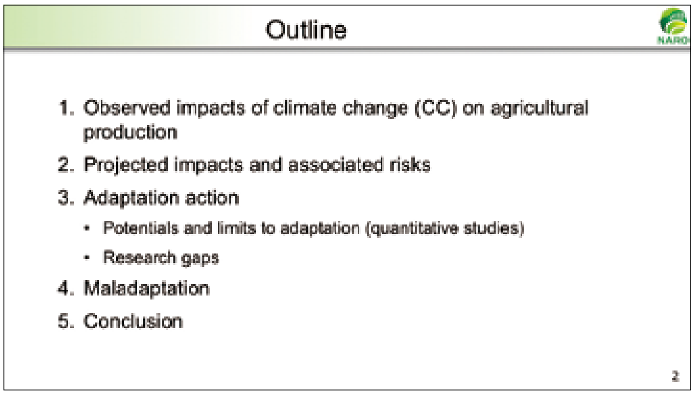
Adapting food systems to a changing climate

-Key Messages from the IPCC Working Group 2 6th Assessment Report (AR6) -

NARO Institute for Agro-Environmental Sciences

Toshihiro Hasegawa

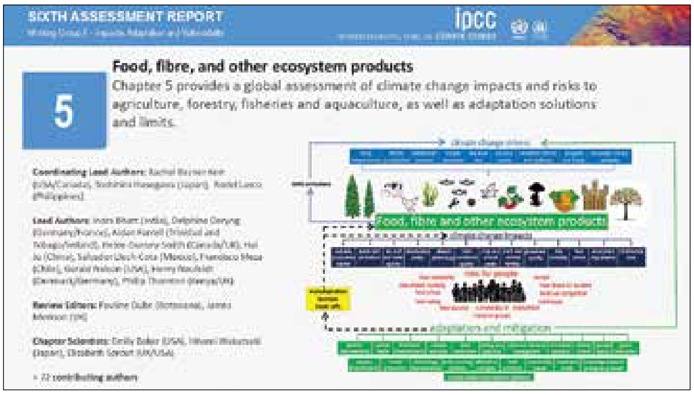
National Agriculture and Food Research Organization



Outline

1. Observed impacts of climate change (CC) on agricultural production
2. Projected impacts and associated risks
3. Adaptation action
   - Potentials and limits to adaptation (quantitative studies)
   - Research gaps
4. Maladaptation
5. Conclusion

2



SIXTH ASSESSMENT REPORT
Working Group II – Impacts, Adaptation and Vulnerability

Food, fibre, and other ecosystem products

Chapter 5 provides a global assessment of climate change impacts and risks to agriculture, forestry, fisheries and aquaculture, as well as adaptation solutions and limits.

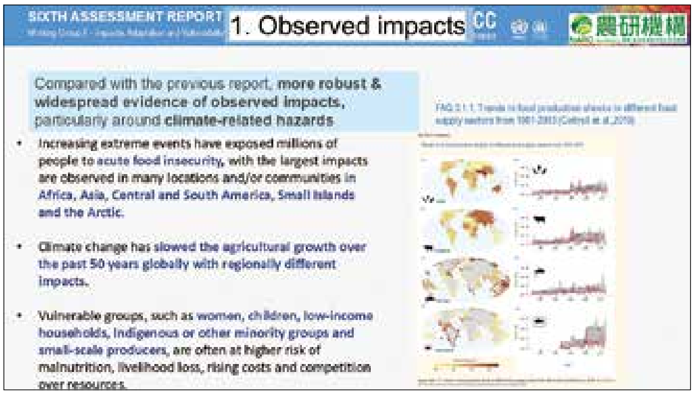
Coordinating Lead Authors: Rachel Bezner Kerr (USA/Canada), Toshihiro Hasegawa (Japan), Rodel Lasco (Philippines)

Lead Authors: Indra Bhatt (India), Delphine Deryng (Germany/France), Aidan Farrell (Trinidad and Tobago/Ireland), Helen Gurney-Smith (Canada/UK), Hui Ju (China), Salvador Lluch-Cota (Mexico), Francisco Meza (Chile), Gerald Nelson (USA), Henry Neufeldt (Denmark/Germany), Philip Thornton (Kenya/UK)

Review Editors: Pauline Dube (Botswana), James Morison (UK)

Chapter Scientists: Emily Baker (USA), Hitomi Wakatsuki (Japan), Elizabeth Sparks (UK/USA)

+ 72 contributing authors



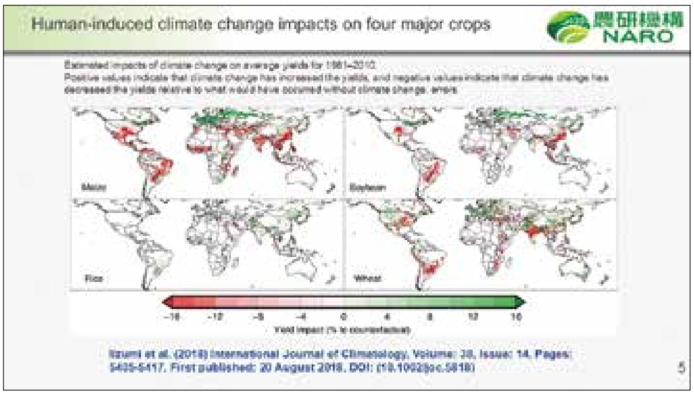
SIXTH ASSESSMENT REPORT
Working Group II – Impacts, Adaptation and Vulnerability

1. Observed impacts

Compared with the previous report, **more robust & widespread evidence of observed impacts,** particularly around **climate-related hazards**

- Increasing extreme events have exposed millions of people to acute food insecurity, with the largest impacts are observed in many locations and/or communities in Africa, Asia, Central and South America, Small Islands and the Arctic.
- Climate change has slowed the agricultural growth over the past 50 years globally with regionally different impacts.
- Vulnerable groups, such as women, children, low-income households, Indigenous or other minority groups and small-scale producers, are often at higher risk of malnutrition, livelihood loss, rising costs and competition over resources.

FAQ 5.1.1: Trends in food production shocks in different food supply sectors from 1961-2013 (Cottrell et al.,2019)



Human-induced climate change impacts on four major crops

Estimated impacts of climate change on average yields for 1981–2010.
Positive values indicate that climate change has increased the yields, and negative values indicate that climate change has decreased the yields relative to what would have occurred without climate change. errors

Iizumi et al. (2018) International Journal of Climatology, Volume: 38, Issue: 14, Pages: 5405-5417. First published: 20 August 2018. DOI: (10.1002/joc.5818)

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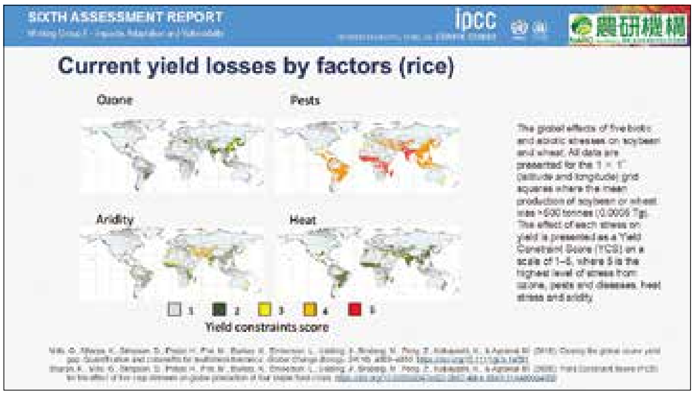
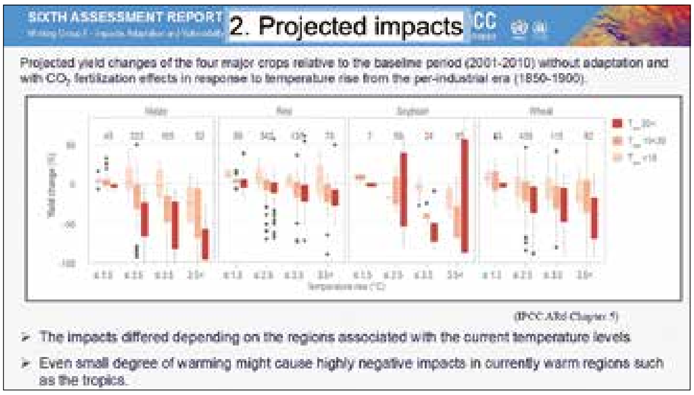


SIXTH ASSESSMENT REPORT
Working Group II – Impacts, Adaptation and Vulnerability

Current yield losses by factors (rice)

The global effects of five biotic and abiotic stresses on soybean and wheat. All data are presented for the 1° × 1° (latitude and longitude) grid squares where the mean production of soybean or wheat was >500 tonnes (0.0005 Tg). The effect of each stress on yield is presented as a Yield Constraint Score (YCS) on a scale of 1–5, where 5 is the highest level of stress from ozone, pests and diseases, heat stress and aridity.

Mills, G., Sharps, K., Simpson, D., Pleijel, H., Frei, M., Burkey, K., Emberson, L., Uddling, J., Broberg, M., Feng, Z., Kobayashi, K., & Agrawal, M. (2018). Closing the global ozone yield gap: Quantification and cobenefits for multistress tolerance. Global Change Biology, 24(10), 4869–4893. [illegible]
Sharps, K., Mills, G., Simpson, D., Pleijel, H., Frei, M., Burkey, K., Emberson, L., Uddling, J., Broberg, M., Feng, Z., Kobayashi, K., & Agrawal, M. (2020). Yield Constraint Score (YCS) for the effect of five crop stresses on global production of four staple food crops. [illegible]

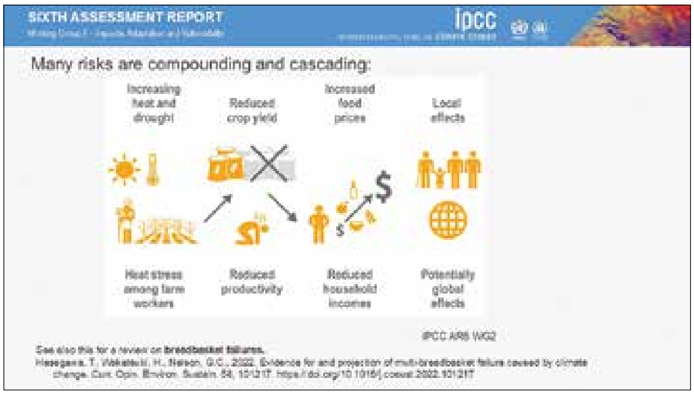


2. Projected impacts

Projected yield changes of the four major crops relative to the baseline period (2001-2010) without adaptation and with CO_2 fertilization effects in response to temperature rise from the per-industrial era (1850-1900).

(IPCC AR6 Chapter 5)

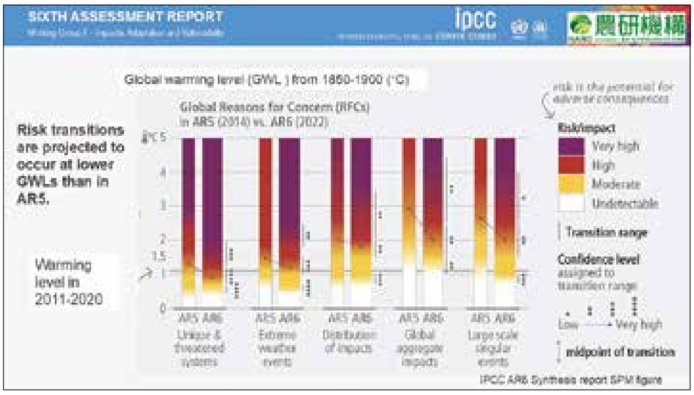
- ➢ The impacts differed depending on the regions associated with the current temperature levels
- ➢ Even small degree of warming might cause highly negative impacts in currently warm regions such as the tropics.



Many risks are compounding and cascading:

IPCC AR6 WG2

See also this for a review on **breadbasket failures.**
Hasegawa, T., Wakatsuki, H., Nelson, G.C., 2022. Evidence for and projection of multi-breadbasket failure caused by climate change. Curr. Opin. Environ. Sustain. 58, 101217. https://doi.org/10.1016/j.cosust.2022.101217



Global warming level (GWL) from 1850-1900 (°C)

Risk transitions are projected to occur at lower GWLs than in AR5.

Warming level in 2011-2020

IPCC AR6 Synthesis report SPM figure

3. Adaptation action

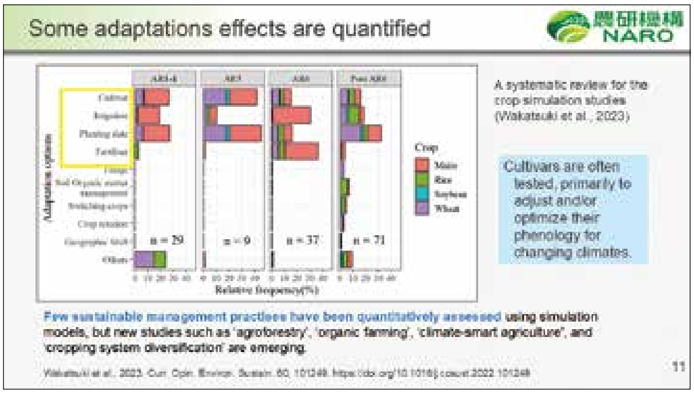
Ongoing adaptation action

Effective options:

- Cultivar improvements
- Agroforestry
- Farm and landscape diversification
- Community-based adaptation
- Strengthening biodiversity

Wider benefits:

- Food security and nutrition
- Health and well-being
- Livelihoods



Some adaptations effects are quantified

A systematic review for the crop simulation studies (Wakatsuki et al., 2023)

Cultivars are often tested, primarily to adjust and/or optimize their phenology for changing climates.

Few sustainable management practices have been quantitatively assessed using simulation models, but new studies such as 'agroforestry', 'organic farming', 'climate-smart agriculture', and 'cropping system diversification' are emerging.

Wakatsuki et al., 2023. Curr. Opin. Environ. Sustain. 60, 101249. https://doi.org/10.1016/j.cosust.2022.101249

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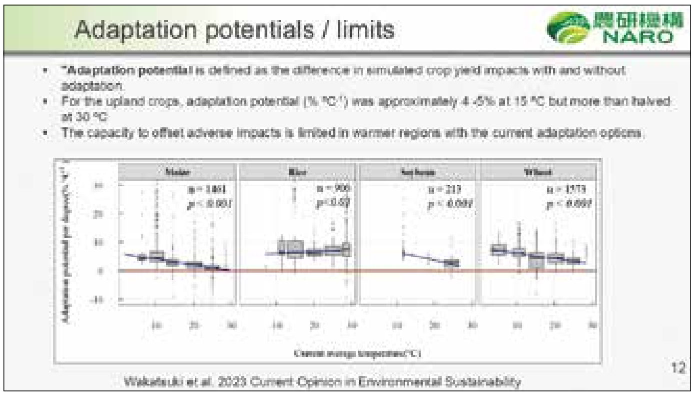

Adaptation potentials / limits

- "**Adaptation potential** is defined as the difference in simulated crop yield impacts with and without adaptation.
- For the upland crops, adaptation potential (% °C⁻¹) was approximately 4 -5% at 15 °C but more than halved at 30 °C
- The capacity to offset adverse impacts is limited in warmer regions with the current adaptation options.

Wakatsuki et al. 2023 Current Opinion in Environmental Sustainability

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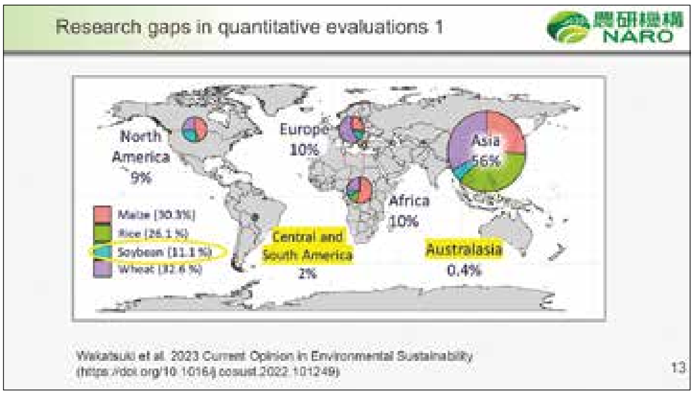

Research gaps in quantitative evaluations 1

Wakatsuki et al. 2023 Current Opinion in Environmental Sustainability
(https://doi.org/10.1016/j.cosust.2022.101249)

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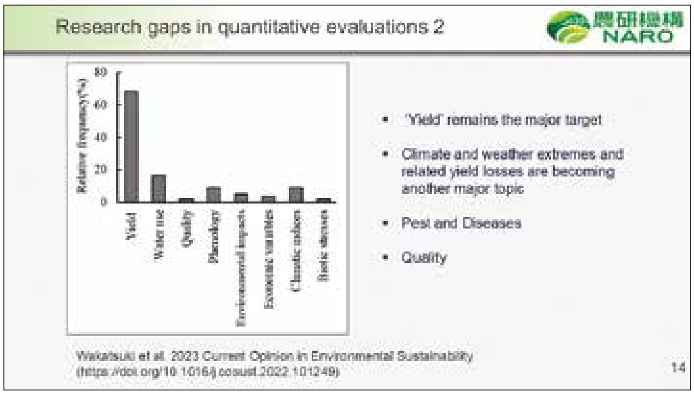


Research gaps in quantitative evaluations 2

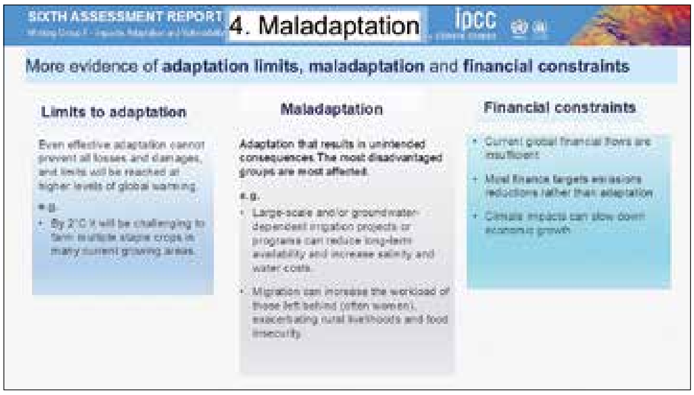
- 'Yield' remains the major target
- Climate and weather extremes and related yield losses are becoming another major topic
- Pest and Diseases
- Quality

Wakatsuki et al. 2023 Current Opinion in Environmental Sustainability
(https://doi.org/10.1016/j.cosust.2022.101249)

14

Systematic review provides evidence of synergies of adaptation with SDGs.

IPCC WG2 AR6 Chp. 5



4. Maladaptation

More evidence of **adaptation limits, maladaptation** and **financial constraints**

Limits to adaptation

Even effective adaptation cannot prevent all losses and damages, and limits will be reached at higher levels of global warming.

e.g.

- By 2°C it will be challenging to farm multiple staple crops in many current growing areas.

Maladaptation

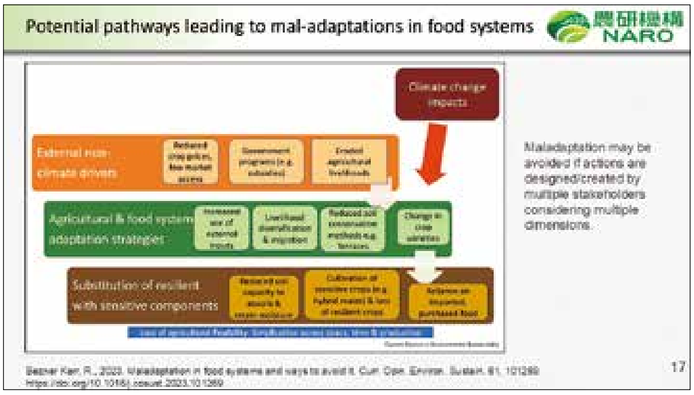
Adaptation that results in unintended consequences. The most disadvantaged groups are most affected.

e.g.

- Large-scale and/or groundwater-dependent irrigation projects or programs can reduce long-term availability and increase salinity and water costs.
- Migration can increase the workload of those left behind (often women), exacerbating rural livelihoods and food insecurity.

Financial constraints

- Current global financial flows are insufficient
- Most finance targets emissions reductions rather than adaptation
- Climate impacts can slow down economic growth



Potential pathways leading to mal-adaptations in food systems

Maladaptation may be avoided if actions are designed/created by multiple stakeholders considering multiple dimensions.

Bezner Kerr, R., 2023. Maladaptation in food systems and ways to avoid it. Curr. Opin. Environ. Sustain. 61, 101269
https://doi.org/10.1016/j.cosust.2023.101269

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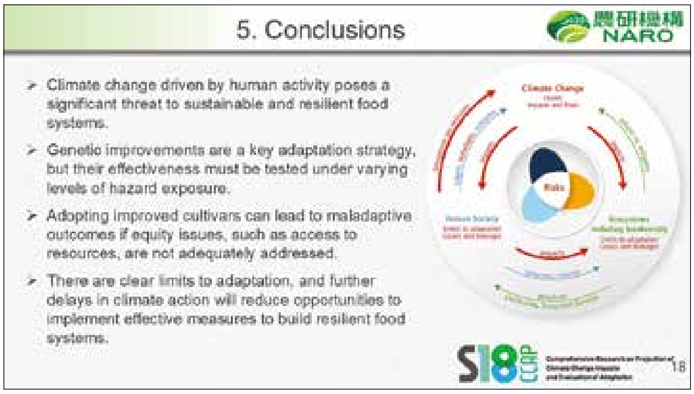

5. Conclusions

- Climate change driven by human activity poses a significant threat to sustainable and resilient food systems.
- Genetic improvements are a key adaptation strategy, but their effectiveness must be tested under varying levels of hazard exposure.
- Adopting improved cultivars can lead to maladaptive outcomes if equity issues, such as access to resources, are not adequately addressed.
- There are clear limits to adaptation, and further delays in climate action will reduce opportunities to implement effective measures to build resilient food systems.

18

Session 1

Potentials of Genetic Resource Diversity for Resilient and Nutritious Food Systems

Chairperson: **Miyuki Iiyama**

Program Director/Information, JIRCAS

Potential of Quinoa for Food and Nutritious Security Under Climate Change in the Era of Global Boiling

Yukari Nagatoshi

Project Leader, Biological Resources and Post-harvest Division,
Japan International Research Center for Agricultural Sciences (JIRCAS), Japan

Dr. Yukari Nagatoshi is the Project Leader of the "Resilient crops: Development of resilient crops and production technologies" project at JIRCAS, assuming the role in 2024. She completed her doctoral program at Yokohama National University in 2009. Following her graduation, she began her career as a postdoctoral fellow at the National Institute of Advanced Industrial Science and Technology (AIST) in the same year. In 2013, she transitioned to a postdoctoral position at JIRCAS. The following year, in 2014, she secured a tenure-track researcher position at JIRCAS. Her career continued to progress, and in 2019, she was promoted to the role of senior researcher at JIRCAS.

Abstracts

Climate change has entered a new phase, often referred to as the era of global boiling, even as we rethink the conventional crop production system that is extremely dependent on a few crops from a food and nutrition security point of view. For a resilient food system, it is necessary not only to improve current major crops, but also to create new major crop candidates. It is from this perspective that we focus on quinoa (*Chenopodium quinoa*).

Quinoa, an annual pseudocereal, was first domesticated at least 7,500 years ago in the Andean region of South America. Quinoa seeds are extremely nutritious, containing a good balance of the five macronutrients (carbohydrates, proteins, fats, minerals, and vitamins) and dietary fiber. In addition, quinoa can be grown at low and high latitudes, from lowlands such as coastal areas to highlands as high as 4,000 meters, and in areas with temperatures ranging from below freezing to as high as 40˚C. With its high nutritional value and diverse traits that allow it to adapt to different agroecosystems, quinoa is a promising candidate for a major crop for the next generation.

Quinoa was the staple food of the indigenous peoples of the Andes before Columbus, but its production and consumption were historically banned by the Spanish conquistadors in the 16th century because it was revered as a sacred "mother grain" used in indigenous ceremonies. As a result, quinoa was neglected for almost 500 years until the latter half of the 20th century, and the development of varieties and cultivation techniques lagged far behind. To expand the cultivation of quinoa as a major crop candidate worldwide, we are conducting research and development to accelerate quinoa breeding through cutting-edge plant science research. First, we created a representative quinoa inbred line and sequenced its genome for efficient genome breeding[1]. We have since developed almost 200 genotyped quinoa inbred lines, covering almost all quinoa-growing areas in South America, and performed their Genotyped-by-Sequencing (GBS) and phenotypic analyses to clarify the overall relationship between genotypes and phenotypes for salt tolerance and key growth traits[2]. In addition, we have developed a technology to elucidate quinoa gene function using a viral vector method that allows the analysis of endogenous gene function in quinoa[3]. We have recently sequenced the genomes of quinoa at the chromosomal level and are currently providing the most accurate reference genome information in the world[4]. Based on these findings, we are developing breeding materials and elucidating quinoa’s stress tolerance mechanisms through breeding populations and genome-wide genotyping using next-generation sequencers[5].

By recovering the lost 500 years of quinoa breeding in a short period of time through cutting-edge plant science research, we expect to contribute to the development of new crops that take full advantage of quinoa’s diversity and potential. We hope that the genetic diversity of quinoa will contribute to future food and nutrition security as an important component of a robust food system under climate change in the era of global boiling.

[1] Yasui Y. *et. al.*, ***DNA Res.***, 23, 535-546 (2016).

[2] Mizuno N. *et. al.*, ***DNA Res.***, 27, dsaa022 (2020).

[3] Ogata T. *et. al.*, ***Front. Plant Sci.***, 12, 643499 (2021).

[4] Kobayashi Y. *et. al.*, ***Front. Plant Sci.***, 15, 1434388 (2024).

[5] Kobayashi Y. & Fujita Y., ***Plant Biotech.***, *in press* (2024).

Further Potential of Sago Palm and Sago Starch in Shaping the Future of the Asia-Pacific Region

Hiroshi Ehara

Director, International Center for Research and Education in Agriculture,
Nagoya University, Japan
Professor, Graduate School of Bioagricultural Sciences, Nagoya University, Japan

Dr. Hiroshi Ehara is the Director of the International Center for Research and Education in Agriculture at Nagoya University. He studied as a visiting scientist in the Palm Room, Herbarium, at the Royal Botanic Gardens, Kew, under the Royal Society – Japan Society for the Promotion of Science (JSPS) fellowship from 1999 to 2000. From 2011 to 2015, he contributed to Mie University as the Vice President for International Affairs. In 2008, he received the Academic Award from the Japanese Society for Tropical Agriculture (JSTA) for his ecophysiological and phylogenetic studies on the sago palm. He was elected President of the Society of Sago Palm Studies in 2016 and Vice President of the JSTA in 2020.

Abstracts

The sago palm (*Metroxylon sagu*), a starch-producing plant found across Southeast Asia and Melanesia that thrives in challenging environments, is not only a food source but is also gaining attention as a raw material for allergen-free foods, biofuels, and other industrial applications. Recently, the demand for sago palm has been increasing, driven by the new societal norms emerging after the COVID-19 pandemic and by Sustainable Development Goals (SDGs). This growing demand for sago palm and sago starch is set against a backdrop of environmental degradation due to climate change, unexpected social issues, and an urgent need to bolster food security and the resilience of food systems. Another contributing factor is the increasing global desire to promote a healthy life.

Metroxylon palms, including the sago palm and related species, grow in swamps, as well as on alluvial and peat soils, where few other major crops can thrive without drainage and soil improvement. These palms are essential biological resources for promoting sustainable agriculture and rural development in tropical wetlands. The potential habitat range for *Metroxylon* palms is likely to expand over the next 45 years as a result of climate change[1]. *Metroxylon* palms, such as the sago palm, are considered underutilized, as they are mainly harvested from natural forests and semi-cultivated with minimal care. Given the social context of the past two decades, characterized by rising competition between biofuel and food production as well as diversifying food demands, there is increasing interest in the efficient utilization of carbohydrates from sago palm and related species, which could drive further land development and greater use of wetland areas. Against this background, the FAO Technical Cooperation Program, "Enhancing Food Security and Combating Climate Change through Scaling Up Sago Palm Production," was conducted in Papua New Guinea from 2022 to 2024[2].

This presentation will showcase recent activities and initiatives based on interdisciplinary thinking and multidisciplinary approaches aimed at advancing the SDGs through collaboration between sago palm-producing countries and Japan, one of the world's largest consumers of sago starch. Highlights include developments in tolerance to various environmental stresses, such as submergence, salt stress, and acidic soils; innovative approaches to using beneficial microorganisms for sustainable plant nutrition management; and emerging trends in utilizing sago starch to promote health and well-being. The goal is to inspire consideration of the further potential of sago palm and sago starch in shaping the future of the Asia-Pacific region.

[1] Itaya, A., M. Masamitsu, H. Ehara, H. Naito, I. Rounds, A. Naikatini and M. Tuiwawa. *Tropical Ecology* 63, 596-603 (2022).

[2] Toyoda, Y., H. Ehara, H. Naito, T. Mishima and K. Galgal. *Proceedings of the 14th International Sago Symposium*, The Society of Sago Palm Studies (Tokyo), 33-36 (2023).

Further Potential of Sago Palm and Sago Starch in Shaping the Future of Asia-Pacific Region

Hiroshi Ehara

Director, International Center for Research and Education in Agriculture, Nagoya Univ
Professor, Graduate School of Bioagricultural Sciences, Nagoya Univ

President, The Society of Sago Palm Studies (SSPS)
Vice President, Japanese Society of Tropical Agriculture (JSTA)
Executive Secretary, Japan Intellectual Support Network in Agricultural Sciences (JISNAS)

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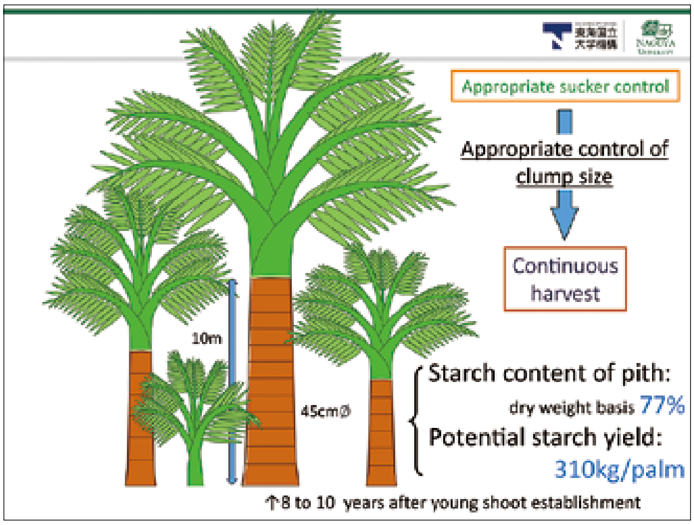


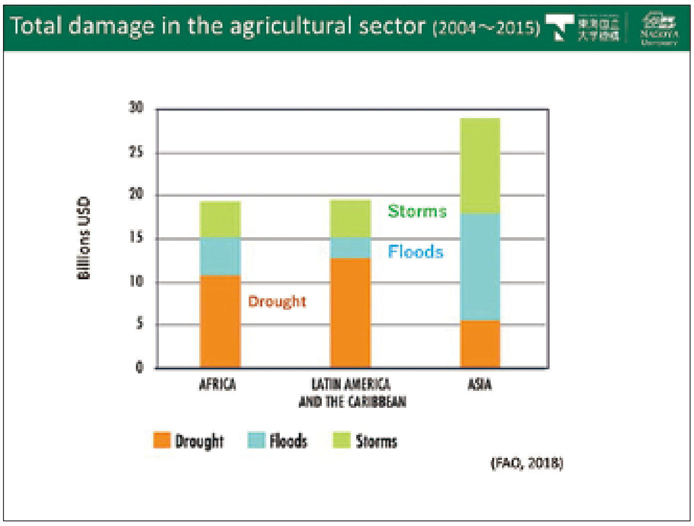
Appropriate sucker control

Appropriate control of clump size

Continuous harvest

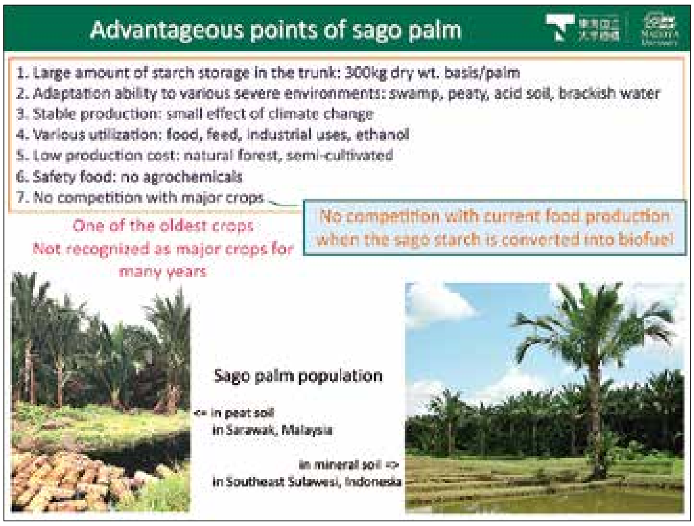
Starch content of pith: dry weight basis 77%
Potential starch yield: 310kg/palm

↑8 to 10 years after young shoot establishment



Total damage in the agricultural sector (2004～2015)

(FAO, 2018)



Advantageous points of sago palm

1. Large amount of starch storage in the trunk: 300kg dry wt. basis/palm
2. Adaptation ability to various severe environments: swamp, peaty, acid soil, brackish water
3. Stable production: small effect of climate change
4. Various utilization: food, feed, industrial uses, ethanol
5. Low production cost: natural forest, semi-cultivated
6. Safety food: no agrochemicals
7. No competition with major crops

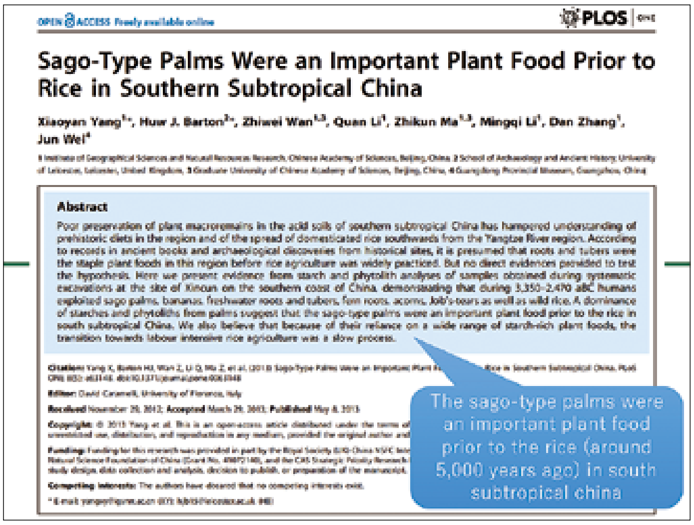
No competition with current food production when the sago starch is converted into biofuel

One of the oldest crops
Not recognized as major crops for many years

Sago palm population

<= in peat soil
in Sarawak, Malaysia

in mineral soil =>
in Southeast Sulawesi, Indonesia



OPEN ACCESS Freely available online PLOS | ONE

Sago-Type Palms Were an Important Plant Food Prior to Rice in Southern Subtropical China

Xiaoyan Yang[1*], Huw J. Barton[2*], Zhiwei Wan[1,3], Quan Li[1], Zhikun Ma[1,3], Mingqi Li[1], Dan Zhang[1], Jun Wei[4]

1 Institute of Geographical Sciences and Natural Resources Research, Chinese Academy of Sciences, Beijing, China, 2 School of Archaeology and Ancient History, University of Leicester, Leicester, United Kingdom, 3 Graduate University of Chinese Academy of Sciences, Beijing, China, 4 Guangdong Provincial Museum, Guangzhou, China

Abstract

Poor preservation of plant macroremains in the acid soils of southern subtropical China has hampered understanding of prehistoric diets in the region and of the spread of domesticated rice southwards from the Yangtze River region. According to records in ancient books and archaeological discoveries from historical sites, it is presumed that roots and tubers were the staple plant foods in this region before rice agriculture was widely practiced. But no direct evidences provided to test the hypothesis. Here we present evidence from starch and phytolith analyses of samples obtained during systematic excavations at the site of Xincun on the southern coast of China, demonstrating that during 3,350–2,470 aBC humans exploited sago palms, bananas, freshwater roots and tubers, fern roots, acorns, Job's-tears as well as wild rice. A dominance of starches and phytoliths from palms suggest that the sago-type palms were an important plant food prior to the rice in south subtropical China. We also believe that because of their reliance on a wide range of starch-rich plant foods, the transition towards labour intensive rice agriculture was a slow process.

Citation: Yang X, Barton HJ, Wan Z, Li Q, Ma Z, et al. (2013) Sago-Type Palms Were an Important Plant F… Rice in Southern Subtropical China. PLoS ONE 8(5): e63148. doi:10.1371/journal.pone.0063148

Editor: David Caramelli, University of Florence, Italy

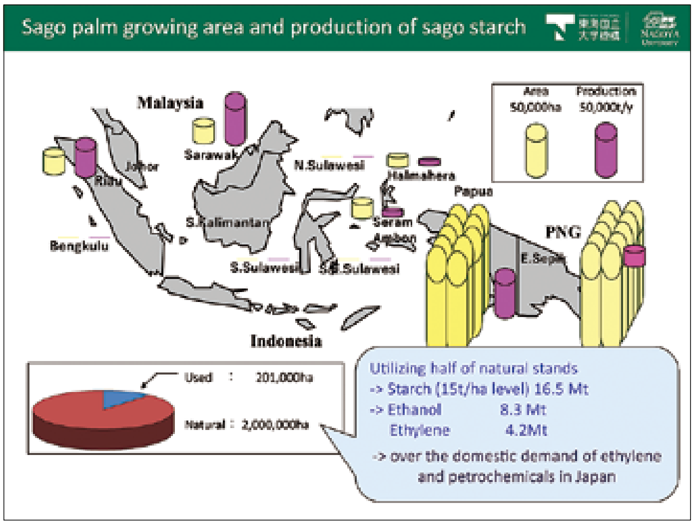
Received November 29, 2012; Accepted March 29, 2013; Published May 8, 2013

Funding: Funding for this research was provided in part by the Royal Society (UK)-China NSFC Inte… Natural Science Foundation of China (Grant No. 40872140), and the CAS Strategic Priority Research… study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: yangxy@igsnrr.ac.cn (XY); hjb3@leicester.ac.uk (HB)

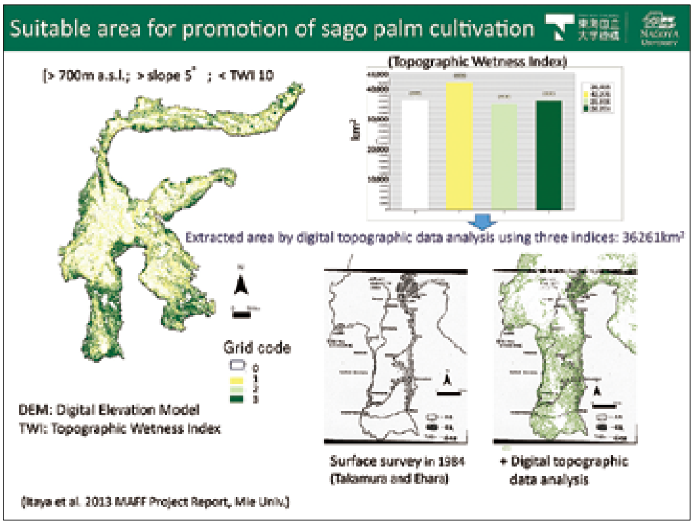
The sago-type palms were an important plant food prior to the rice (around 5,000 years ago) in south subtropical china



Sago palm growing area and production of sago starch

Used : 201,000ha
Natural : 2,000,000ha

Utilizing half of natural stands
-> Starch (15t/ha level) 16.5 Mt
-> Ethanol 8.3 Mt
Ethylene 4.2Mt
-> over the domestic demand of ethylene and petrochemicals in Japan



Suitable area for promotion of sago palm cultivation

[> 700m a.s.l.; > slope 5˚ ; < TWI 10

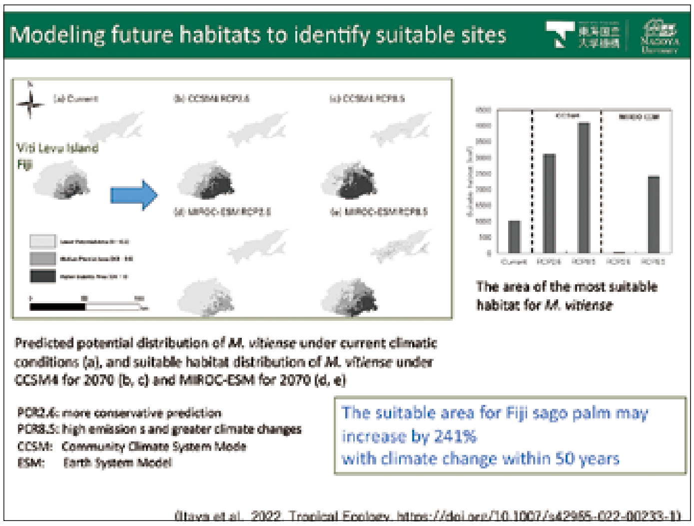
Extracted area by digital topographic data analysis using three indices: 36261km²

DEM: Digital Elevation Model
TWI: Topographic Wetness Index

Surface survey in 1984 (Takamura and Ehara)

+ Digital topographic data analysis

(Itaya et al. 2013 MAFF Project Report, Mie Univ.)



Modeling future habitats to identify suitable sites

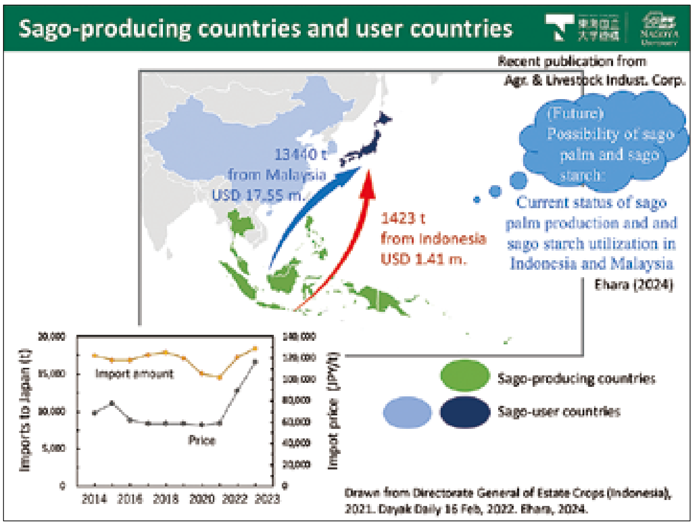
The area of the most suitable habitat for *M. vitiense*

Predicted potential distribution of *M. vitiense* under current climatic conditions (a), and suitable habitat distribution of *M. vitiense* under CCSM4 for 2070 (b, c) and MIROC-ESM for 2070 (d, e)

PCR2.6: more conservative prediction
PCR8.5: high emission s and greater climate changes
CCSM: Community Climate System Mode
ESM: Earth System Model

The suitable area for Fiji sago palm may increase by 241% with climate change within 50 years

(Itaya et al. 2022. Tropical Ecology. https://doi.org/10.1007/s42965-022-00233-1)



Sago-producing countries and user countries

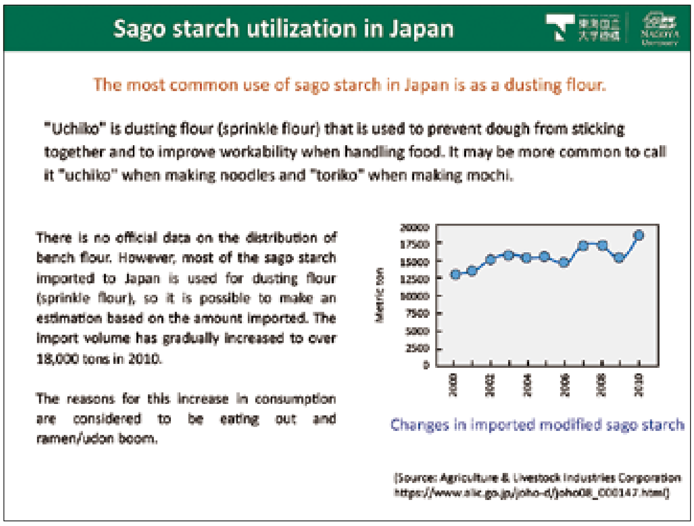
Recent publication from Agr. & Livestock Indust. Corp.

(Future) Possibility of sago palm and sago starch:

Current status of sago palm production and and sago starch utilization in Indonesia and Malaysia

Ehara (2024)

Drawn from Directorate General of Estate Crops (Indonesia), 2021. Dayak Daily 16 Feb, 2022. Ehara, 2024.



Sago starch utilization in Japan

The most common use of sago starch in Japan is as a dusting flour.

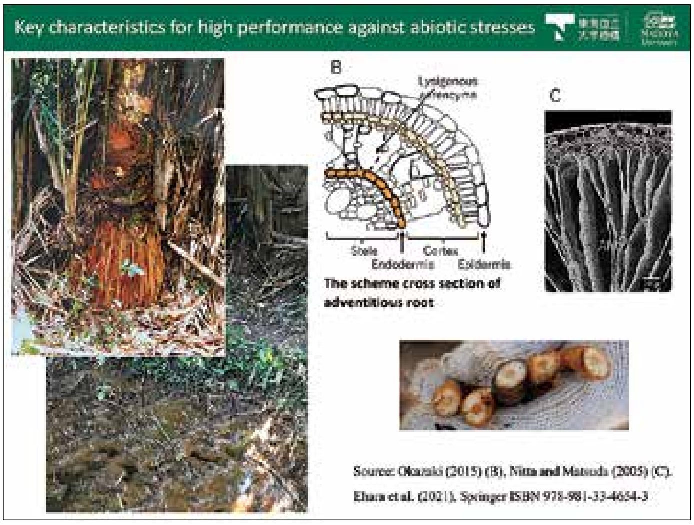
"Uchiko" is dusting flour (sprinkle flour) that is used to prevent dough from sticking together and to improve workability when handling food. It may be more common to call it "uchiko" when making noodles and "toriko" when making mochi.

There is no official data on the distribution of bench flour. However, most of the sago starch imported to Japan is used for dusting flour (sprinkle flour), so it is possible to make an estimation based on the amount imported. The import volume has gradually increased to over 18,000 tons in 2010.

The reasons for this increase in consumption are considered to be eating out and ramen/udon boom.

Changes in imported modified sago starch

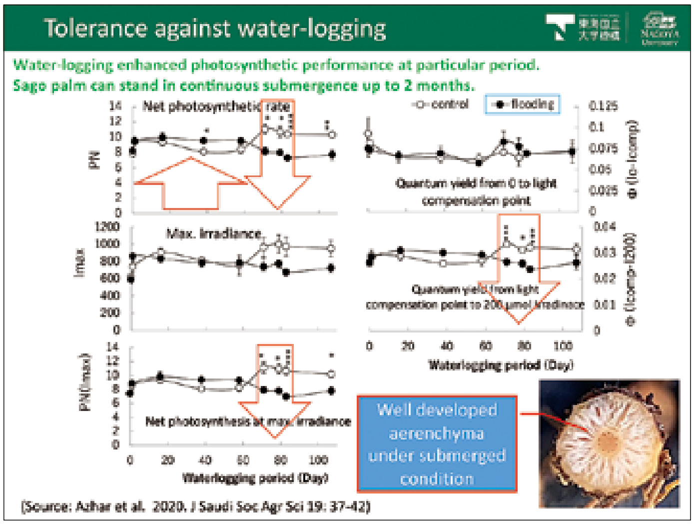
(Source: Agriculture & Livestock Industries Corporation https://www.alic.go.jp/joho-d/joho08_000147.html)



Key characteristics for high performance against abiotic stresses

The scheme cross section of adventitious root

Source: Okazaki (2015) (B), Nitta and Matsuda (2005) (C).
Ehara et al. (2021), Springer ISBN 978-981-33-4654-3

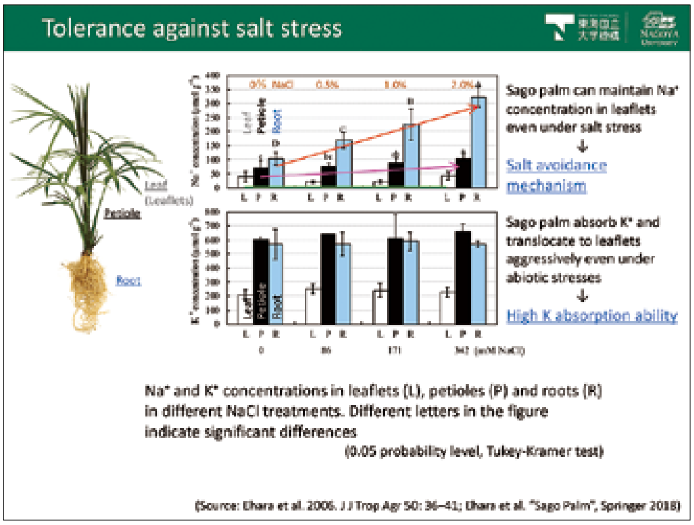


Tolerance against water-logging

Water-logging enhanced photosynthetic performance at particular period.
Sago palm can stand in continuous submergence up to 2 months.

Well developed aerenchyma under submerged condition

(Source: Azhar et al. 2020. J Saudi Soc Agr Sci 19: 37-42)



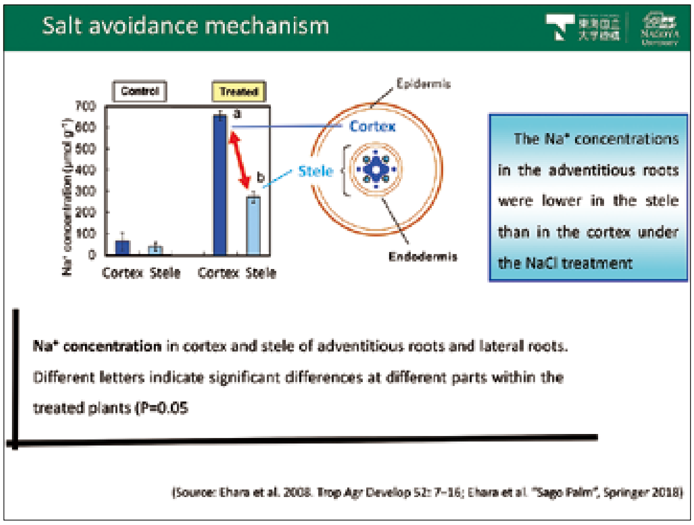
Tolerance against salt stress

Sago palm can maintain Na^+ concentration in leaflets even under salt stress
↓
Salt avoidance mechanism

Sago palm absorb K^+ and translocate to leaflets aggressively even under abiotic stresses
↓
High K absorption ability

Na^+ and K^+ concentrations in leaflets (L), petioles (P) and roots (R) in different NaCl treatments. Different letters in the figure indicate significant differences
(0.05 probability level, Tukey-Kramer test)

(Source: Ehara et al. 2006. J J Trop Agr 50: 36–41; Ehara et al. "Sago Palm", Springer 2018)

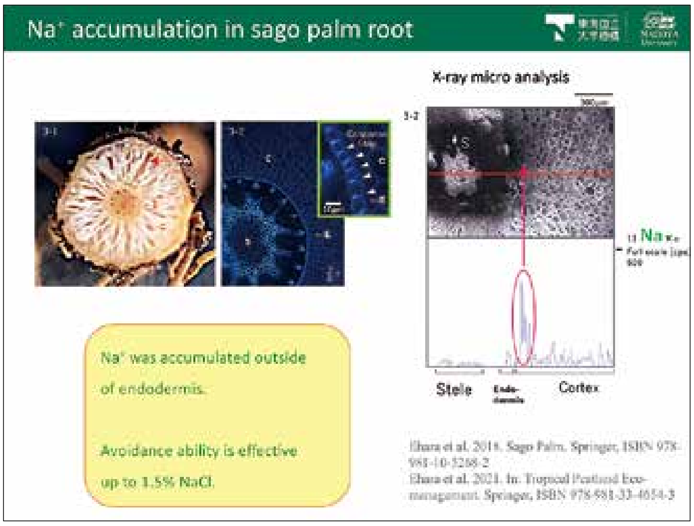


Salt avoidance mechanism

The Na^+ concentrations in the adventitious roots were lower in the stele than in the cortex under the NaCl treatment

Na^+ concentration in cortex and stele of adventitious roots and lateral roots. Different letters indicate significant differences at different parts within the treated plants (P=0.05

(Source: Ehara et al. 2008. Trop Agr Develop 52: 7–16; Ehara et al. "Sago Palm", Springer 2018)



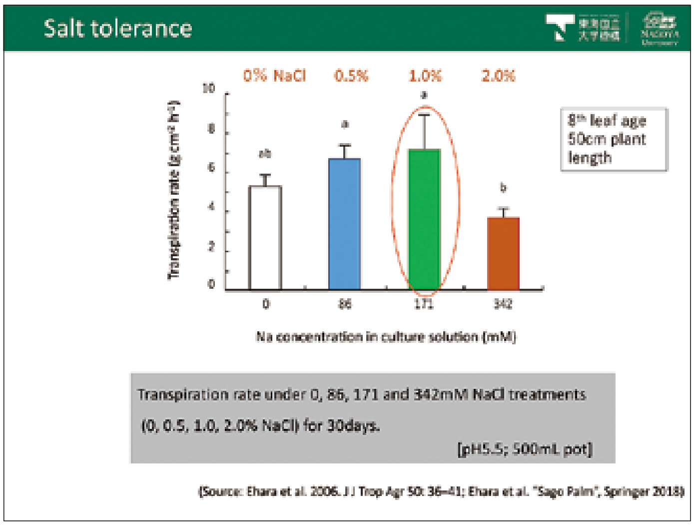
Na^+ accumulation in sago palm root

X-ray micro analysis

Na^+ was accumulated outside of endodermis.

Avoidance ability is effective up to 1.5% NaCl.

Ehara et al. 2018. Sago Palm. Springer, ISBN 978-981-10-5268-2
Ehara et al. 2021. In: Tropical Peatland Eco-management. Springer, ISBN 978-981-33-4654-3

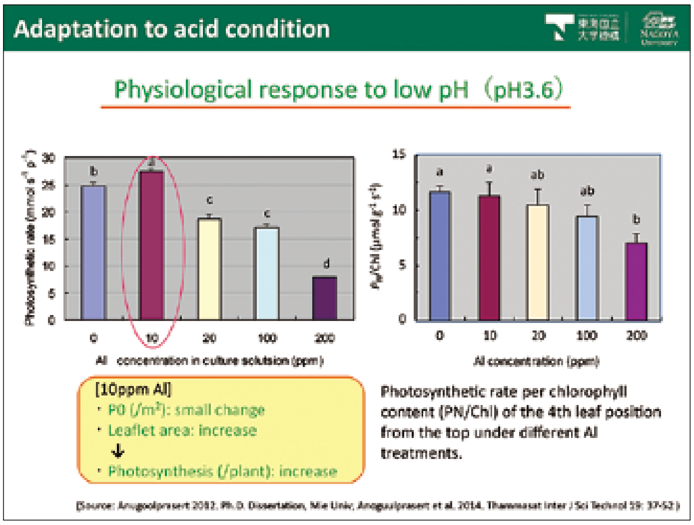


Salt tolerance

8th leaf age
50cm plant length

Transpiration rate under 0, 86, 171 and 342mM NaCl treatments
(0, 0.5, 1.0, 2.0% NaCl) for 30days.
[pH5.5; 500mL pot]

(Source: Ehara et al. 2006. J J Trop Agr 50: 36–41; Ehara et al. "Sago Palm", Springer 2018)



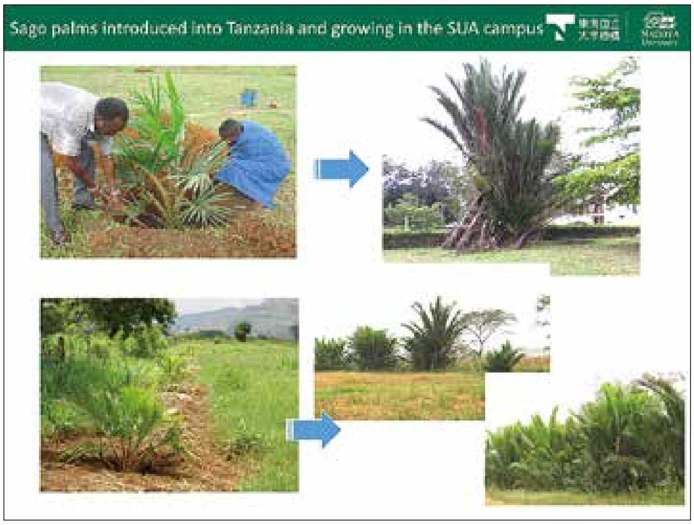
Adaptation to acid condition

Physiological response to low pH（pH3.6）

[10ppm Al]
- P0 (/m^2): small change
- Leaflet area: increase
↓
- Photosynthesis (/plant): increase

Photosynthetic rate per chlorophyll content (PN/Chl) of the 4th leaf position from the top under different Al treatments.

(Source: Anugoolprasert 2012. Ph.D. Dissertation, Mie Univ; Anugoolprasert et al. 2014. Thammasat Inter J Sci Technol 19: 37-52)



Sago palms introduced into Tanzania and growing in the SUA campus

Traditional use of sago starch

Flour dumpling soup

Noodle (fried noodle)

Sago mochi (sago cake): sweets

Sago pearl

Sago mochi (sago cake): less taste

Recent FAO programs and project on sago palm

"Promoting Sago Starch Utilization in Indonesia – Phase I " in Indonesia
TCP/INS/3503 (Phase I)
Nov. 2015 – Dec. 2017

"Promoting Sago Starch Utilization in Indonesia - Phase II " in Indonesia
TCP/INS/3701 (Phase II)
July 2018 – March 2019

The project was expected to contribute to food diversification and food security in Sulawesi island of Indonesia, through capacity building designed to improve the production, utilization and marketing of sago starch and its downstream processed products as alternative carbohydrates sources.

"Enhancing food security and combating climate change through scaling up sago palm production" in Papua New Guinea
TCP/PNG/3901 (Feb. 2022 – Feb. 2024)

"Capacity building of smallholders on improved sago processing and value chains in Jayapura, Papua Province" in Indonesia (Feb. 2024 -)

Function of sago starch

Intestinal retention :

Resistant starch:
Preferable for diet control

"Chrononutrition study of sago pancakes"
Furutani, A. 2022 Sago Palm 29 (2): 75.
The dominant inhibitory effect of sago starch on elevated blood glucose levels was confirmed. This may be due too the size of the starch particles.

Allergen free :

JAL In-flight Minimal Allergen Meal:
(https://www.jal.co.jp/en/inter/service/meal/special/menu/common/pdf/en_pyy_flight_to_japan.pdf)

ANA In-flight Allergen-Free Meal
(https://www.ana.co.jp/www2/pdf/travel-informtion/meals/atml_en_2209.pdf)

Prevention of accidental ingestion :

Adhesion: Does not stick to the inside of the throat
Condensation: Ease of mixing
→ Swallowing support
(http://tender-hearts.jp/kaigoshoku.html)

New arrival (1)

Gluten free noodle & Gluten free pasta (IDN)

Improvement of gluten free pasta (Prof. T. Kondo, JPN)

Instant Linut Segera (MYS)

New arrival (2)

Sago cup noodles and sweets (IDN)

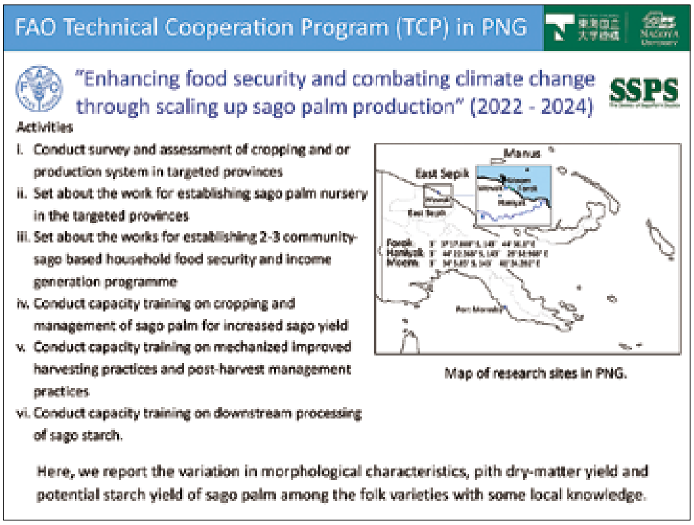
Gluten free Cookies

Thanks to CRAUN (MYS)

at Intern'l Airport (IDN)

New arrival (3)

How to prepare sago cup rice to eat (IDN)



FAO Technical Cooperation Program (TCP) in PNG

"Enhancing food security and combating climate change through scaling up sago palm production" (2022 - 2024)

Activities

- i. Conduct survey and assessment of cropping and or production system in targeted provinces
- ii. Set about the work for establishing sago palm nursery in the targeted provinces
- iii. Set about the works for establishing 2-3 community-sago based household food security and income generation programme
- iv. Conduct capacity training on cropping and management of sago palm for increased sago yield
- v. Conduct capacity training on mechanized improved harvesting practices and post-harvest management practices
- vi. Conduct capacity training on downstream processing of sago starch.

Map of research sites in PNG.

Here, we report the variation in morphological characteristics, pith dry-matter yield and potential starch yield of sago palm among the folk varieties with some local knowledge.

TCP PNG Interim results report event (May 2023)

FAO TCP Workshop in PNG (Oct 2022)

First transplanting utilizing seedlings germinated from seeds in PNG

Transplanted seedling at the new opened field in Moem.

A stick was placed next to the seedling as a marker

Technology Catalog Contributing to Production Potential and Sustainability in the Asia-Monsoon Region

Ver. 3.0 is available.

https://www.jircas.go.jp/en/greenasia/techcatalog

Sago Palm Studies

Sago Seed Germination

URL:
https://icrea95.wixsite.com/labo/sago-palm-studies

Published Sago Palm books

Ehara, H., Toyoda, H. and Johnson, D. V. (eds.) (2018). Sago Palm: Multiple Contributions to Food Security and Sustainable Livelihoods. Springer, pp330. ISBN 978-981-10-5268-2 ISBN 978-981-10-5268-2 (eBook).

Bintoro, H. M. H., Ehara, H., Azhar, A., Dewi, R. K., Nurulhaq, M. I., Ahyuni, D. (2021). Ekofisiologi Sagu. IPB Press, pp167. ISBN 978-623-256-832-7

Ehara, H. et al. (2021). Sago palm in peatland. In: Osaki, M. et al. eds., Tropical Peatland Eco-management. Springer, p477-507. ISBN 978-981-33-4654-3 (ISBN 978-981-33-4653-6)

The Society of Sago Palm Studies; Yamamoto, Y., Ehara, H. et al. eds. (2015). The Sago Palm. The Food and Environmental Challenges of the 21st Century. Kyoto University Press (Kyoto) and Trans Pacific Press (Melbourne), pp450. ISBN 978-4-876988-35-3

Discovery of Genes for Stress Resistance in Mungbean (*Vigna radiata*)

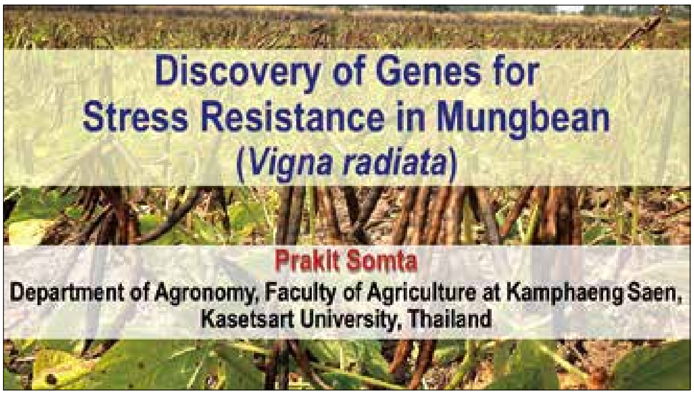
Prakit Somta

Associate Professor, Department of Agronomy, Faculty of Agriculture at Kamphaeng Saen,
Kasetsart University, Nakhon Pathom, Thailand

Dr. Prakit Somta is an Associate Professor in the Department of Agronomy, Faculty of Agriculture, at Kasetsart University's Kamphaeng Saen Campus, Thailand. He received his Ph.D. in Agronomy from Kasetsart University in 2005. From 2009 to 2013, he worked as a senior lecturer at the Kamphaeng Saen Campus. He was appointed assistant professor in 2013 and associate professor in 2018. Since earning his Ph.D., he has been working on genetic resources and breeding of legume crops, especially mungbean.

Abstracts

Mungbean is a socio-economically important legume crop in Asia. It is generally grown in rotation with cereal crops such as rice, maize, and wheat. However, the average seed yield of mungbean is low, being only about 900 kg per hectare, due to biotic and abiotic stresses including bruchid (*Callosobruchus analis, Callosobruchus chinensis* and *Callosobruchus maculatus*) infestation, powdery mildew (PM) disease caused by *Erysiphe polygoni*, Cercospora leaf spot (CLS) disease caused by *Cercospora canescens*, yellow mosaic disease (YMD) caused by *Mungbean Yellow Mosaic Virus* (*MYMV*) and *Mungbean Yellow Mosaic Indian Virus* (*MYMIV*), calcareous soil (iron deficiency chlorosis), and soil salinity. These stresses are believed to be exacerbated by climate change, threatening food security. Marker-assisted breeding (MAB) and genomics-assisted breeding (GAB) are promising approaches to efficiently and rapidly develop new crop cultivars with improved yield, quality, and resistance to biotic and abiotic stresses. Although mungbean was among the first legume crops subjected to genomics studies three decades ago, progress in genomics research for this crop has been very slow due to a lack of genomic resources. Additionally, there are only a few laboratories/institutes that consistently and continuously work on genomics and molecular breeding of mungbean. However, in recent years, quantitative trait loci (QTL) controlling bruchid resistance, PM resistance, CLS resistance, YMD resistance, calcareous soil tolerance, and salt tolerance have been identified by high-resolution mapping and/or genome-wide association studies. In addition, candidate genes controlling these stresses have been identified: *VrPGIP1* and *VrPGIP2* encoding polygalactorunase inhibitors for bruchid resistance, *VrMLO12* encoding Mildew Locus O 12 protein and *VrRPP13L* encoding Peronospora parasitica 13-like protein for PM resistance, *VrTAF5* encoding TATA-binding-protein-associated factor 5 and *VrRLP12* encoding receptor-like protein 12 for CLS resistance, *VrYSL3* encoding yellow stripe-like3 protein for calcareous soil tolerance, and *VrCYBDOMG1* encoding a cytochrome b561 domain-containing protein. Tightly linked and/or functional markers have been developed for these genes for MAB of mungbean and are being used in the development of stress-resistant mungbean cultivars.



Discovery of Genes for Stress Resistance in Mungbean (*Vigna radiata*)

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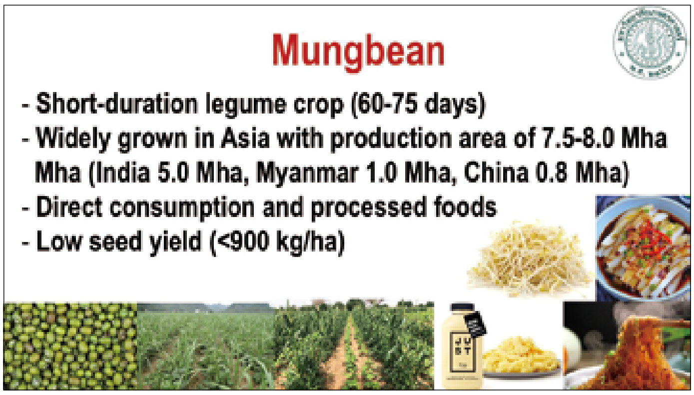
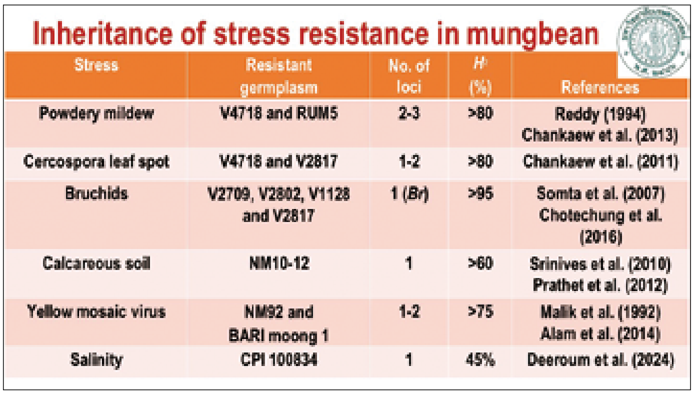
Kasetsart University, Thailand



Mungbean

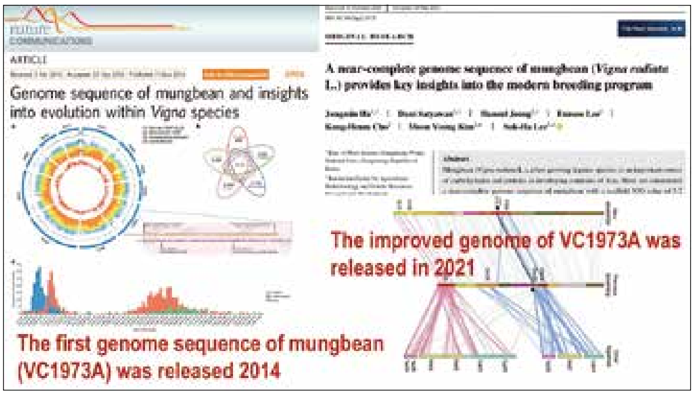
- Short-duration legume crop (60-75 days)
- Widely grown in Asia with production area of 7.5-8.0 Mha Mha (India 5.0 Mha, Myanmar 1.0 Mha, China 0.8 Mha)
- Direct consumption and processed foods
- Low seed yield (<900 kg/ha)

Important stresses cuasing low mungbean yield



Inheritance of stress resistance in mungbean

Stress	Resistant germplasm	No. of loci	H^2 (%)	References
Powdery mildew	V4718 and RUM5	2-3	>80	Reddy (1994) Chankaew et al. (2013)
Cercospora leaf spot	V4718 and V2817	1-2	>80	Chankaew et al. (2011)
Bruchids	V2709, V2802, V1128 and V2817	1 (*Br*)	>95	Somta et al. (2007) Chotechung et al. (2016)
Calcareous soil	NM10-12	1	>60	Srinives et al. (2010) Prathet et al. (2012)
Yellow mosaic virus	NM92 and BARI moong 1	1-2	>75	Malik et al. (1992) Alam et al. (2014)
Salinity	CPI 100834	1	45%	Deeroum et al. (2024)



nature COMMUNICATIONS

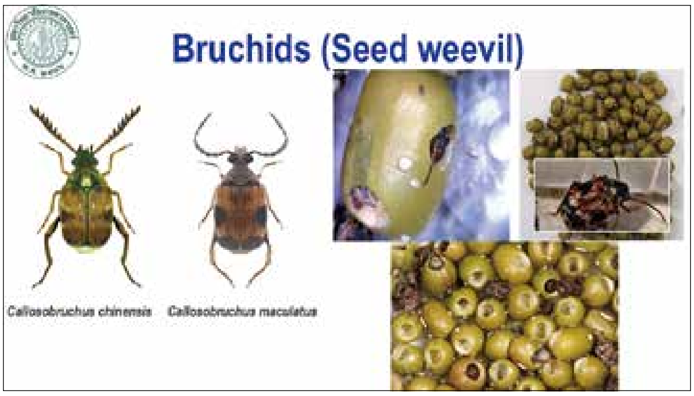
ARTICLE

Genome sequence of mungbean and insights into evolution within *Vigna* species

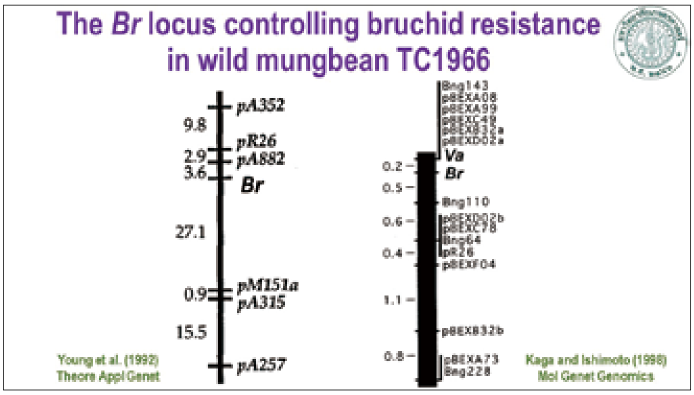
A near-complete genome sequence of mungbean (*Vigna radiata* L.) provides key insights into the modern breeding program

The improved genome of VC1973A was released in 2021

The first genome sequence of mungbean (VC1973A) was released 2014



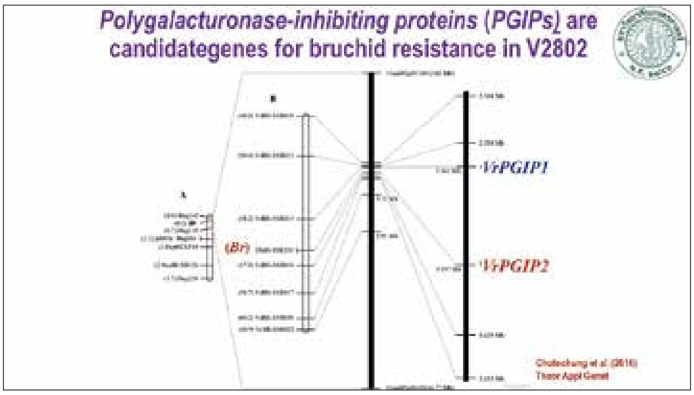
Bruchids (Seed weevil)



The *Br* locus controlling bruchid resistance in wild mungbean TC1966

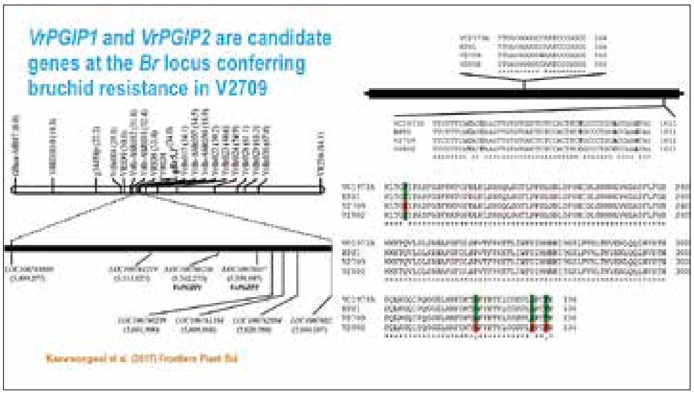
Young et al. (1992)
Theore Appl Genet

Kaga and Ishimoto (1998)
Mol Genet Genomics



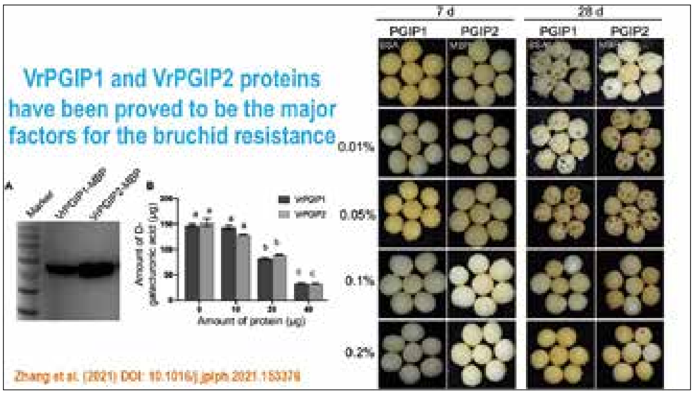
Polygalacturonase-inhibiting proteins (*PGIPs*) are candidategenes for bruchid resistance in V2802

Chotechung et al. (2016)
Theor Appl Genet



VrPGIP1 and *VrPGIP2* are candidate genes at the *Br* locus conferring bruchid resistance in V2709

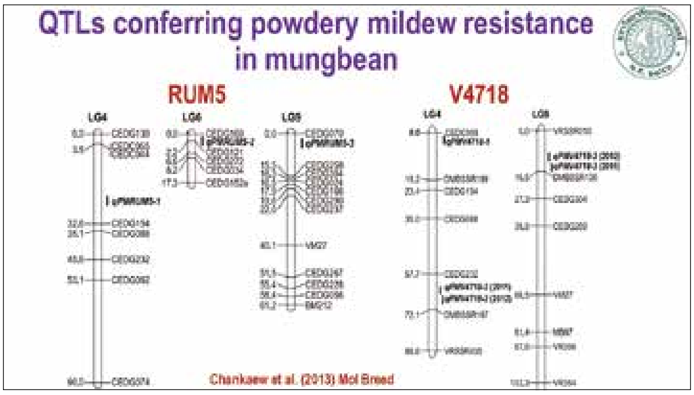
Kaewwongwal et al. (2017) Frontiers Plant Sci



VrPGIP1 and VrPGIP2 proteins have been proved to be the major factors for the bruchid resistance

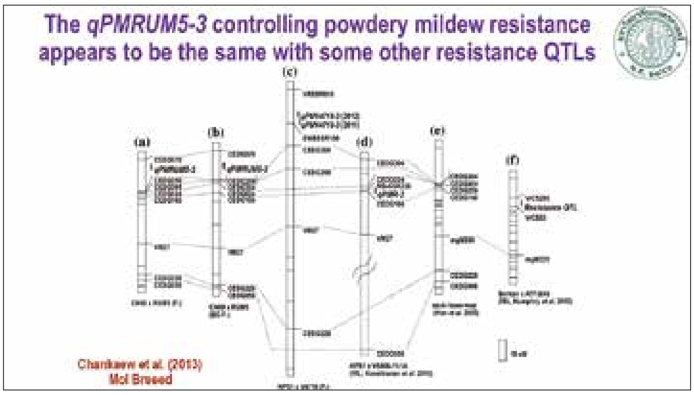
Zhang et al. (2021) DOI: 10.1016/j.jplph.2021.153376

Powdery mildew



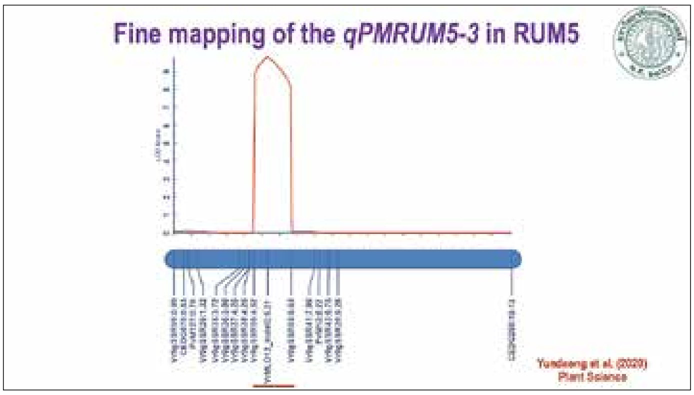
QTLs conferring powdery mildew resistance in mungbean

Chankaew et al. (2013) Mol Breed



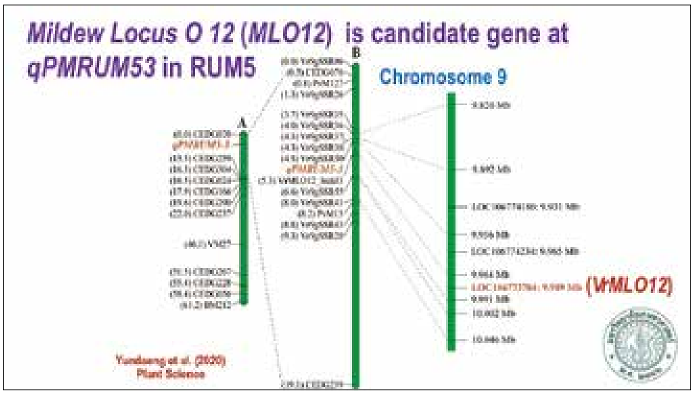
The *qPMRUM5-3* controlling powdery mildew resistance appears to be the same with some other resistance QTLs

Chankaew et al. (2013)
Mol Breed



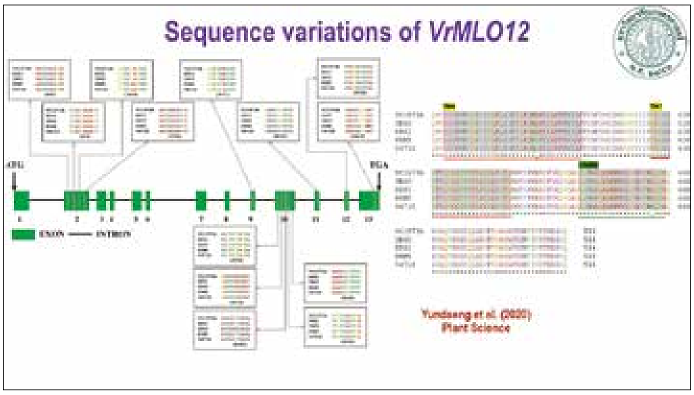
Fine mapping of the *qPMRUM5-3* in RUM5

Yundaeng et al. (2020)
Plant Science



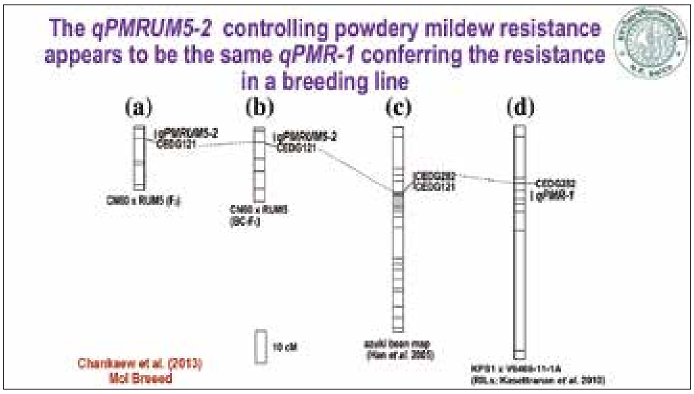
Mildew Locus O 12 (*MLO12*) is candidate gene at *qPMRUM53* in RUM5

Yundaeng et al. (2020)
Plant Science



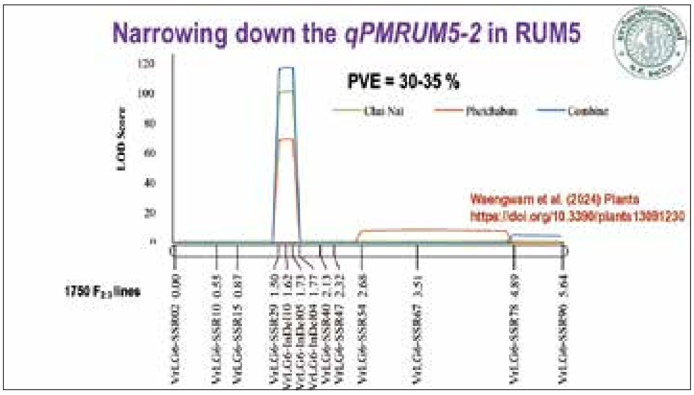
Sequence variations of *VrMLO12*

Yundaeng et al. (2020)
Plant Science



The *qPMRUM5-2* controlling powdery mildew resistance appears to be the same *qPMR-1* conferring the resistance in a breeding line

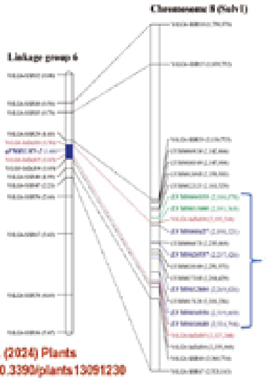
Chankaew et al. (2013)
Mol Breed



Narrowing down the *qPMRUM5-2* in RUM5

Waengwam et al. (2024) Plants
https://doi.org/10.3390/plants13091230

A comparative genome map illustrating location of *qPMRUM5-2* (left) and candidate genes for the *qPMRUM5-2* on chromosome 8 of the mungbean reference genome (Sulv1) (right). The candidate genes are bolded and highlighted in blue and green.



Recognition of Peronospora parasitica 13-like protein (RPP13L) are candidate genes at *qPMRUM5-2*

Waengwan et al. (2024) Plants
https://doi.org/10.3390/plants13091230

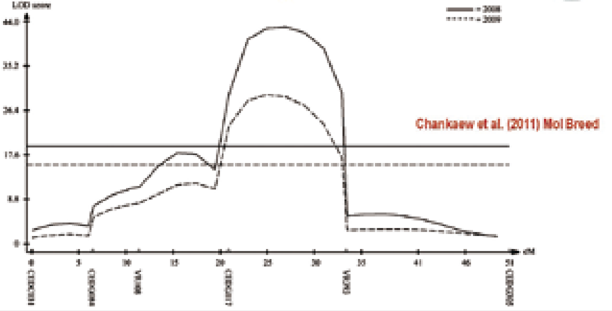
Single nucleotide polymorphisms (SNP) identified between Chai Nat 60 (CN60) and RUM5 in *RPP13L* genes locating in and nearby the *qPMRUM5-2* region

Gene	No. of SNPs	Types of SNPs
EVM0031008 (*VrRPP13L-2*)	151	nonsynonymous SNP (102), synonymous SNP (46), and splicing-relevant SNP (3)
EVM0008427 (*VrRPP13L-3*)	229 and 5	nonsynonymous SNP (158) and synonymous SNP (71)
EVM0028537 (*VrRPP13L-4*)	51 and 8	nonsynonymous SNP (31), synonymous SNP (18) and stop-gain SNP (2)
EVM0032804 (*VrRPP13L-5*)	77 and 1	nonsynonymous SNP (52), synonymous SNP (22), and stop-gain SNP (3)
EVM0016936 (*VrRPP13L-6*)	35 and 2	nonsynonymous SNP (21), synonymous SNP (11), and stop-gain SNP (3)
EVM0018688 (*VrRPP13L-7*)	25 and 10	nonsynonymous SNP (16) and synonymous SNP (9)

Waengwan et al. (2024) Plants. https://doi.org/10.3390/plants13091230

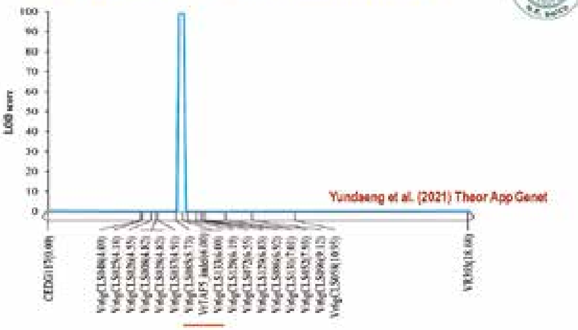
Cercospora leaf spot

qCLS conferring Cercospora leaf spot (CLS) resistance in mungbean V4718



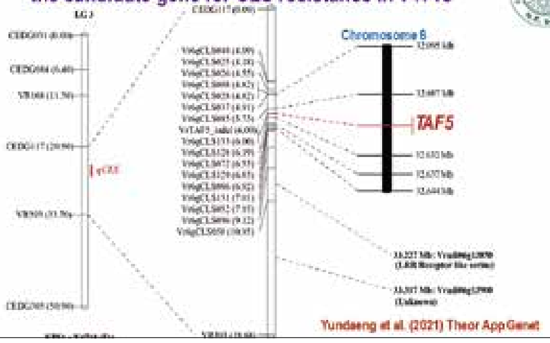
Chankaew et al. (2011) Mol Breed

Fine mapping of the *qCLS* in V4718

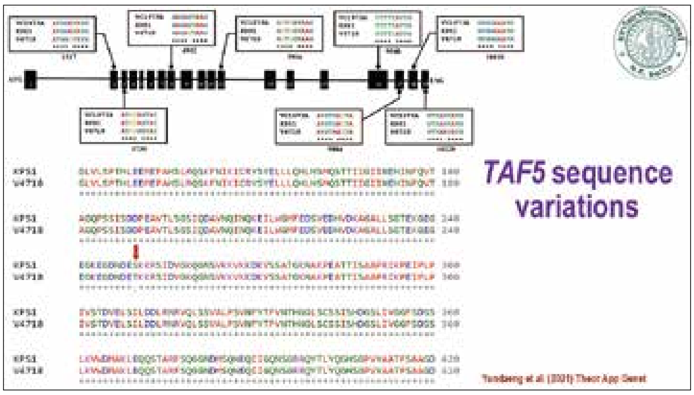


Yundaeng et al. (2021) Theor App Genet

TATA-binding-protein-associated factor 5 (*TAF5*) is the candidate gene for CLS resistance in V4718

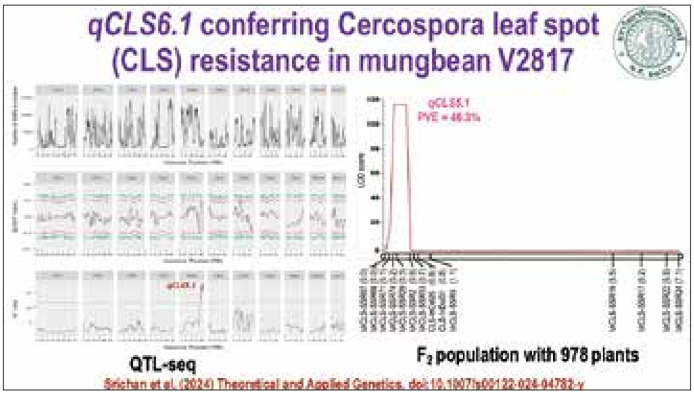


Yundaeng et al. (2021) Theor App Genet



***TAF5* sequence variations**

Yundaeng et al. (2021) Theor App Genet

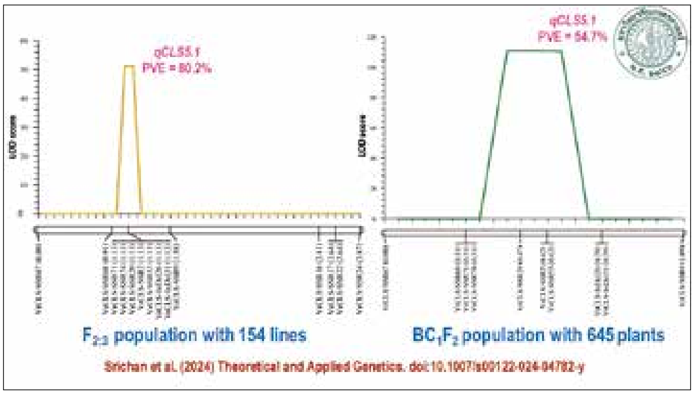


qCLS6.1 conferring Cercospora leaf spot (CLS) resistance in mungbean V2817

QTL-seq

F_2 population with 978 plants

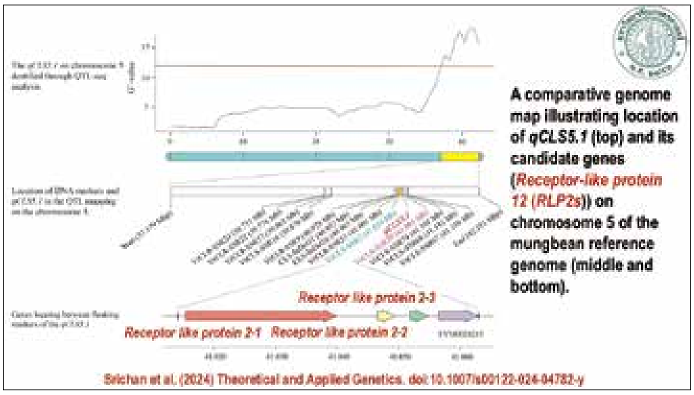
Srichan et al. (2024) Theoretical and Applied Genetics. doi:10.1007/s00122-024-04782-y



$F_{2:3}$ population with 154 lines

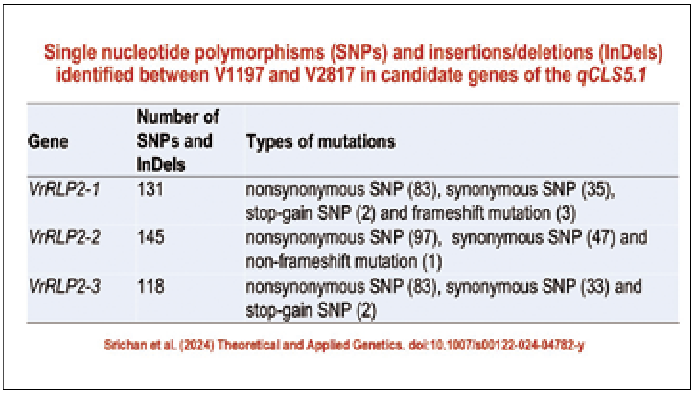
BC_1F_2 population with 645 plants

Srichan et al. (2024) Theoretical and Applied Genetics. doi:10.1007/s00122-024-04782-y



A comparative genome map illustrating location of ***qCLS5.1*** (top) and its candidate genes (***Receptor-like protein 12* (*RLP2s*)**) on chromosome 5 of the mungbean reference genome (middle and bottom).

Srichan et al. (2024) Theoretical and Applied Genetics. doi:10.1007/s00122-024-04782-y

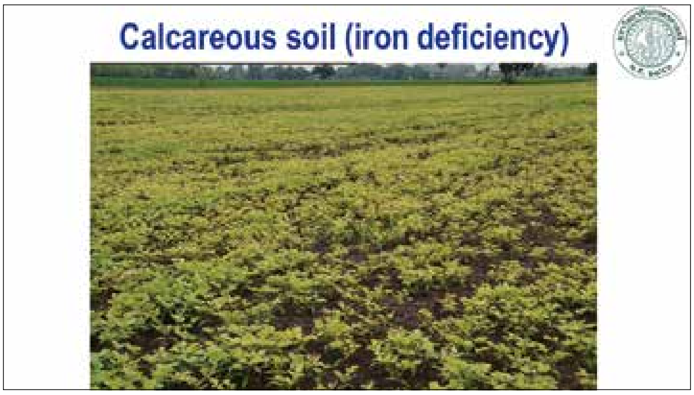


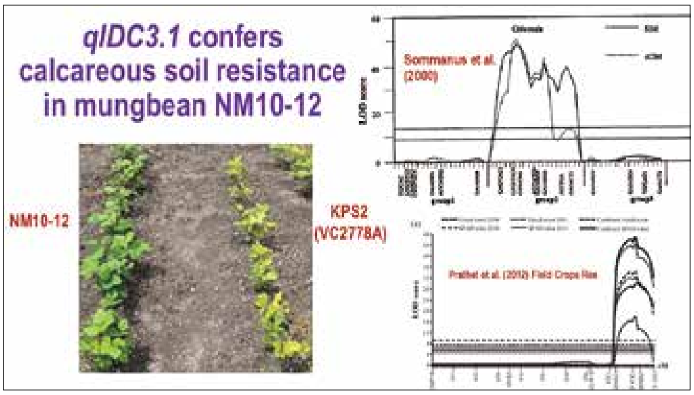
Single nucleotide polymorphisms (SNPs) and insertions/deletions (InDels) identified between V1197 and V2817 in candidate genes of the *qCLS5.1*

Gene	Number of SNPs and InDels	Types of mutations
VrRLP2-1	131	nonsynonymous SNP (83), synonymous SNP (35), stop-gain SNP (2) and frameshift mutation (3)
VrRLP2-2	145	nonsynonymous SNP (97), synonymous SNP (47) and non-frameshift mutation (1)
VrRLP2-3	118	nonsynonymous SNP (83), synonymous SNP (33) and stop-gain SNP (2)

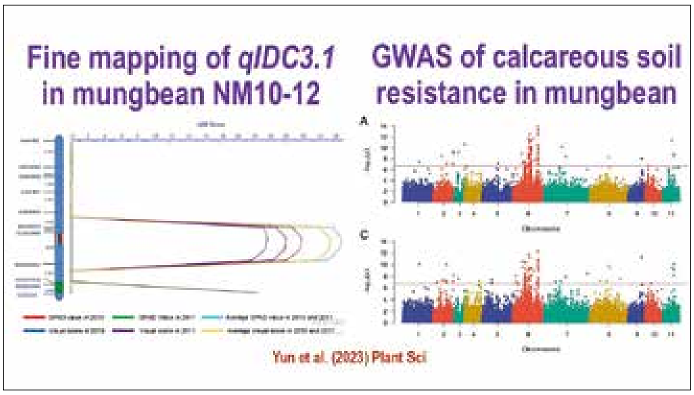
Srichan et al. (2024) Theoretical and Applied Genetics. doi:10.1007/s00122-024-04782-y

Calcareous soil (iron deficiency)





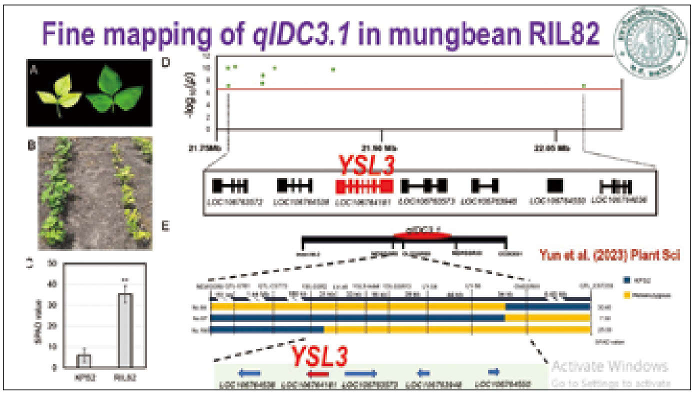
qIDC3.1 confers calcareous soil resistance in mungbean NM10-12



Fine mapping of *qIDC3.1* in mungbean NM10-12

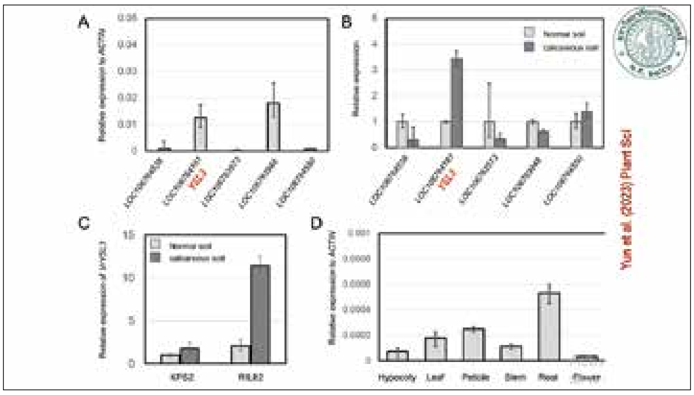
GWAS of calcareous soil resistance in mungbean

Yun et al. (2023) Plant Sci

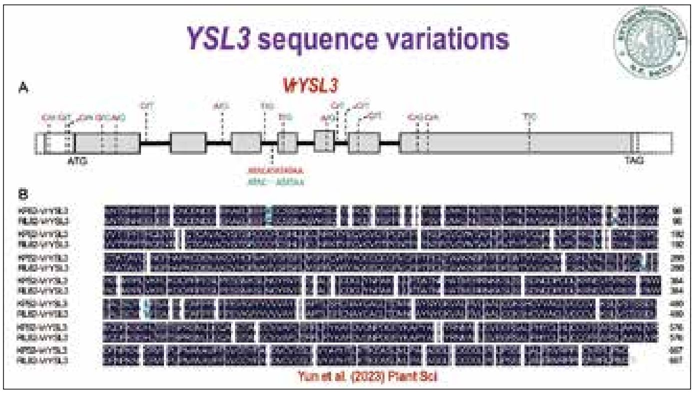


Fine mapping of *qIDC3.1* in mungbean RIL82

Yun et al. (2023) Plant Sci

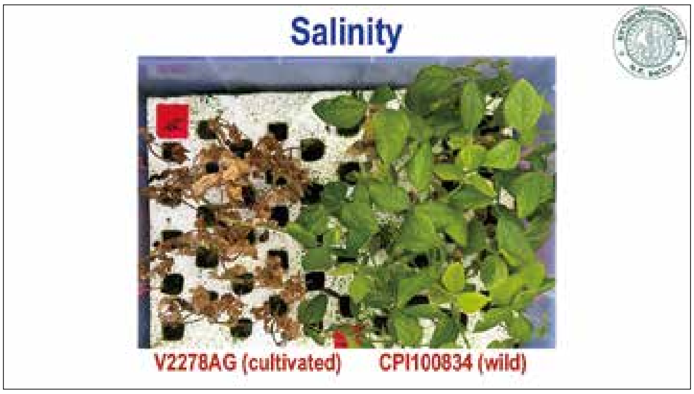


Yun et al. (2023) Plant Sci



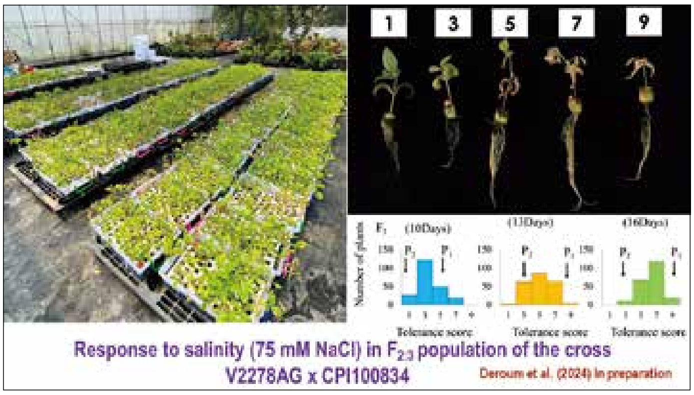
YSL3 sequence variations

Yun et al. (2023) Plant Sci



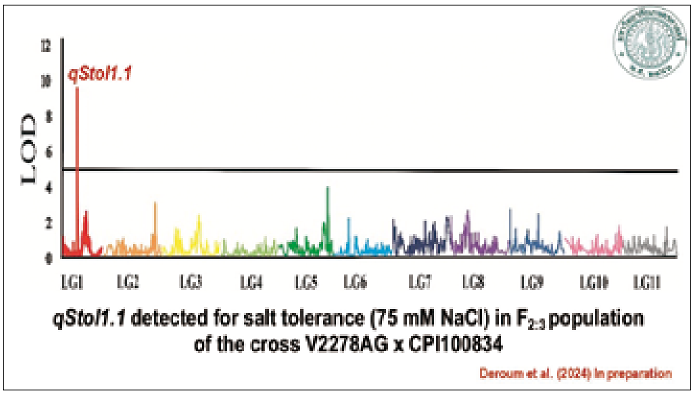
Salinity

V2278AG (cultivated) CPI100834 (wild)



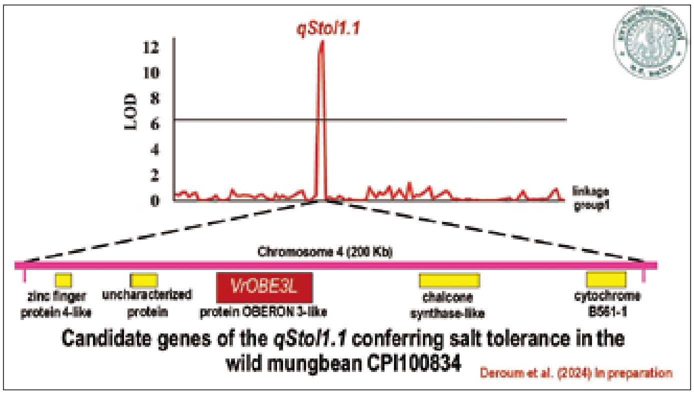
Response to salinity (75 mM NaCl) in $F_{2:3}$ population of the cross V2278AG x CPI100834

Deroum et al. (2024) In preparation



qStol1.1 detected for salt tolerance (75 mM NaCl) in $F_{2:3}$ population of the cross V2278AG x CPI100834

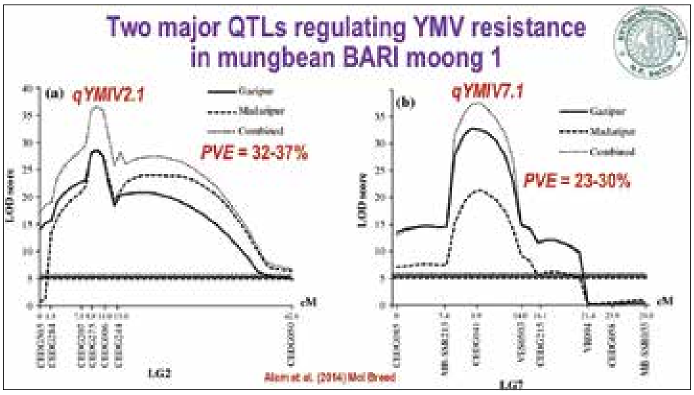
Deroum et al. (2024) In preparation



Candidate genes of the *qStol1.1* conferring salt tolerance in the wild mungbean CPI100834

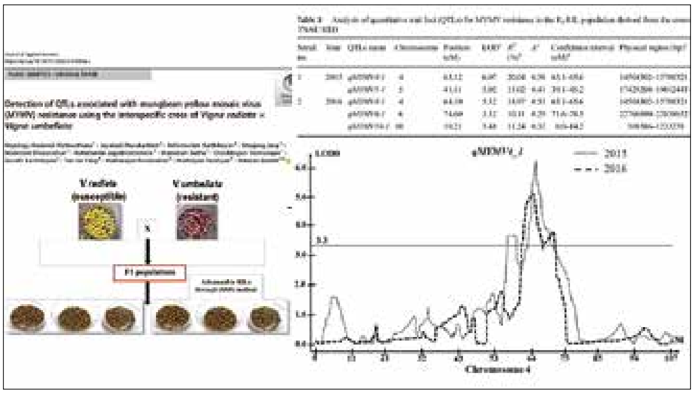
Deroum et al. (2024) In preparation

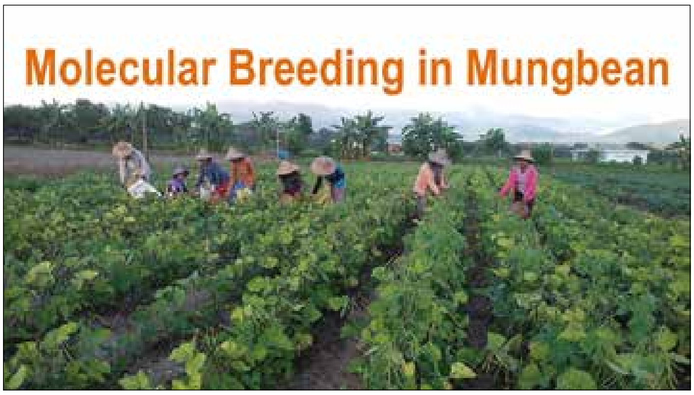
Yellow mosaic disease



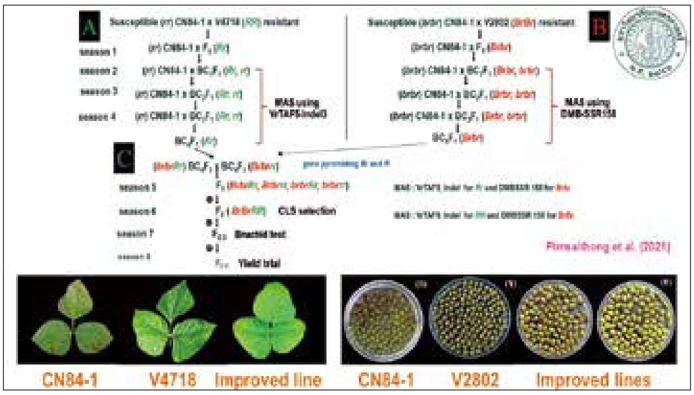
Two major QTLs regulating YMV resistance in mungbean BARI moong 1

Alam et al. (2014) Mol Breed

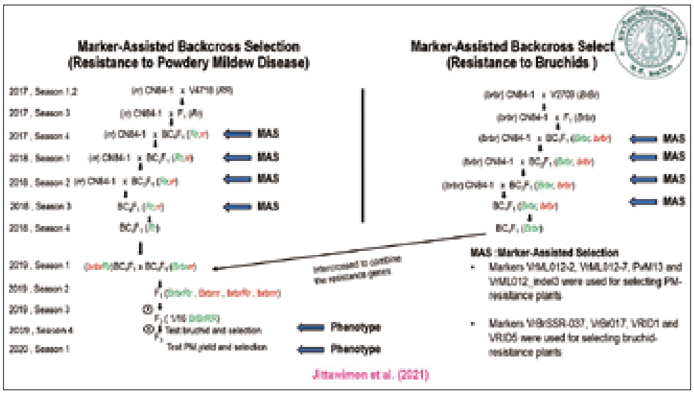




Molecular Breeding in Mungbean



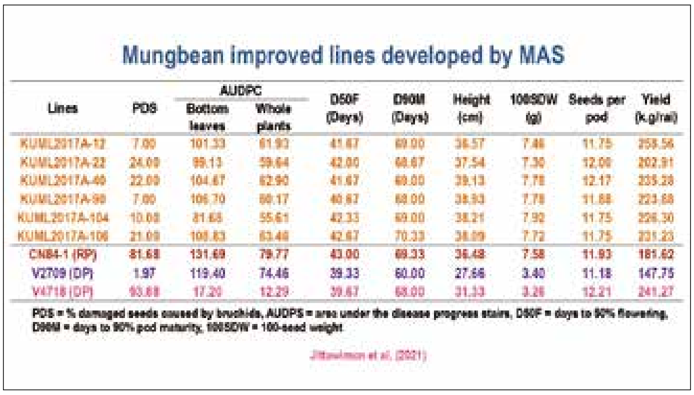
Pimsaithong et al. (2021)



MAS :Marker-Assisted Selection

- Markers VrMLO12-2, VrMLO12-7, PvM13 and VrMLO12_indel3 were used for selecting PM-resistance plants
- Markers VrBrSSR-037, VrBr017, VRID1 and VRID5 were used for selecting bruchid-resistance plants

Jittawimon et al. (2021)

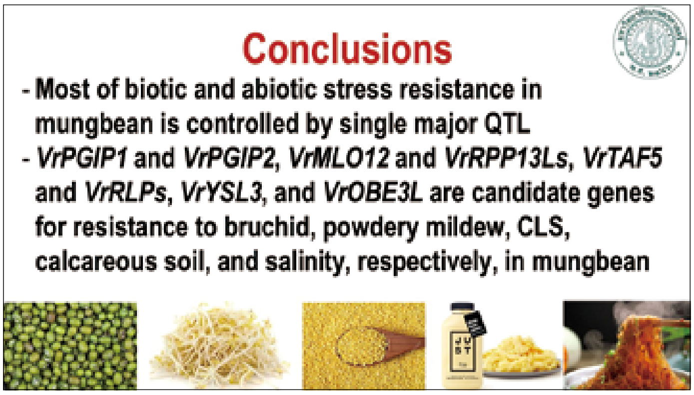


Mungbean improved lines developed by MAS

Lines	PDS	AUDPC		D50F (Days)	D90M (Days)	Height (cm)	100SDW (g)	Seeds per pod	Yield (k.g/rai)
		Bottom leaves	Whole plants						
KUML2017A-12	7.00	101.33	61.93	41.67	69.00	38.57	7.46	11.75	258.56
KUML2017A-22	24.00	99.13	59.64	42.00	68.67	37.54	7.30	12.00	202.91
KUML2017A-40	22.00	104.67	62.90	41.67	69.00	39.13	7.78	12.17	235.28
KUML2017A-90	7.00	106.70	60.17	40.67	68.00	38.93	7.78	11.88	223.68
KUML2017A-104	10.00	81.65	55.61	42.33	69.00	38.21	7.92	11.75	226.30
KUML2017A-106	21.00	108.83	63.48	42.67	70.33	38.09	7.72	11.75	231.23
CN84-1 (RP)	81.68	131.69	79.77	43.00	69.33	36.48	7.58	11.93	181.62
V2709 (DP)	1.97	119.40	74.46	39.33	60.00	27.66	3.40	11.18	147.75
V4718 (DP)	93.68	17.20	12.29	39.67	68.00	31.33	3.26	12.21	241.27

PDS = % damaged seeds caused by bruchids, AUDPS = area under the disease progress stairs, D50F = days to 50% flowering, D90M = days to 90% pod maturity, 100SDW = 100-seed weight

Jittawimon et al. (2021)



Conclusions

- Most of biotic and abiotic stress resistance in mungbean is controlled by single major QTL
- *VrPGIP1* and *VrPGIP2*, *VrMLO12* and *VrRPP13Ls*, *VrTAF5* and *VrRLPs*, *VrYSL3*, and *VrOBE3L* are candidate genes for resistance to bruchid, powdery mildew, CLS, calcareous soil, and salinity, respectively, in mungbean

PMU-B
The Program Management Unit for Human Resources & Institutional Development, Research and Innovation

JAAS
江苏省农业科学院

สวทช
NSTDA

서 울 대 학 교
SEOUL NATIONAL UNIVERSITY

สกว
T R F

NARO
National Agriculture and Food Research Organization

Thank you

Session 2

Opportunities of Utilizing Genetic Resources to Build Resilient Food Systems

Chairperson: **Keiichi Hayashi**

Program Director/ Environment, JIRCAS

IRRI’s Strategies to Utilize Genetic Resources for Breeding Resilient Rice

Venuprasad Ramaiah

Research Unit Leader, International Rice Research Institute (IRRI), Philippines

Dr. Venuprasad Ramaiah is an Indian plant geneticist and rice breeder who heads the Fit-for-Future Genetic Resources cluster at the International Rice Research Institute (IRRI) in the Philippines. Since joining IRRI in 2018, he has overseen the International Rice Genebank, the world’s largest rice genetic collection with over 132,000 accessions, leveraging rice biodiversity to develop climate-resilient varieties. Previously, Dr. Ramaiah served as Principal Scientist at the Africa Rice Center, where he released eight high-yielding, stress-tolerant rice varieties across West and Central Africa. His work supports sustainable agriculture and addresses climate challenges through improved rice varieties for global food security.

Abstracts

Plant genetic resources are essential for food security and environmental sustainability, and genebanks play a crucial role in their conservation. However, genebanks worldwide are often underutilized; for example, only 5% of the 132,000 rice samples conserved at IRRI's International Rice Genebank (IRG) have been actively used in breeding programs. Addressing climate change challenges requires accelerating the effective use of genebank resources. While genebanks primarily focus on conserving genetic diversity, they also play a vital role in enhancing germplasm utilization by generating critical trait information. Traditional germplasm evaluation, however, relies on manually assessing limited traits, which is time-intensive and costly.

This presentation will outline IRRI's strategic approaches to harness genetic resources for breeding resilient rice, focusing on three key areas:

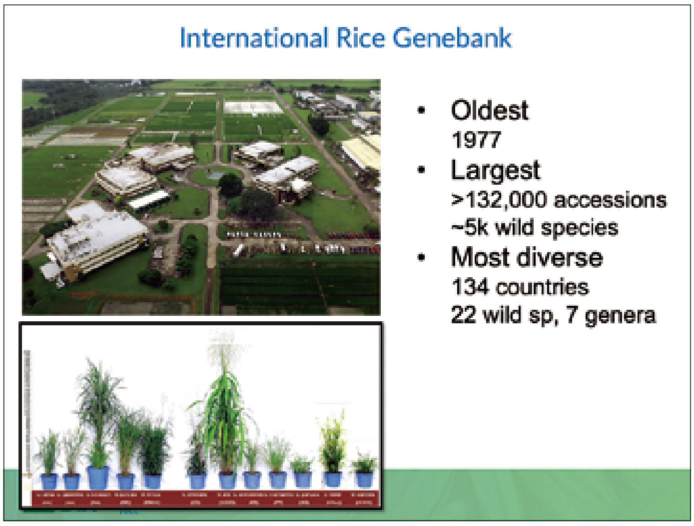
1. Unlocking Novel Variation: The IRG collection includes unique, yet-to-be-utilized traits. Efforts to identify and leverage these traits for breeding novel rice varieties will be discussed.

2. Exploiting Genotype by Environment (GxE) Interactions: Our recent work in Southeast Asia highlights the value of exotic genetic resources. We will cover strategies to rapidly deploy genetic variation that leverages GxE interactions, boosting breeding outcomes.

3. Applying AI/ML in Genebanking: Artificial intelligence (AI) and machine learning (ML) are transforming genebank operations. This section will discuss the progress of AI-driven genebank practices, including curation, characterization, and subset selection. At IRG, we are integrating AI-driven systems with high-throughput phenotyping to streamline the screening of rice samples for climate-resilient traits. As a pilot study, we showcase the application to screen for tolerance to flood, drought, and salinity stresses. In 2024 alone, about half of IRG's collection was screened for these traits.

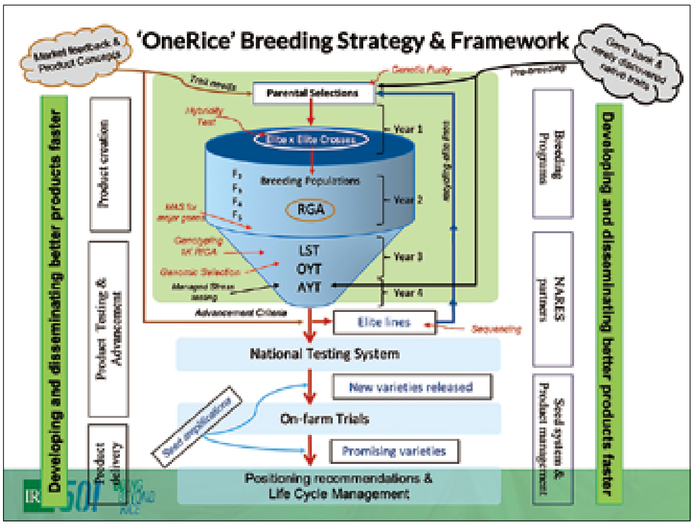
IRRI's Strategies to Utilize Genetic Resources for Breeding Resilient Rice

Venuprasad Ramaiah
FFGR Unit
IRRI, Philippines

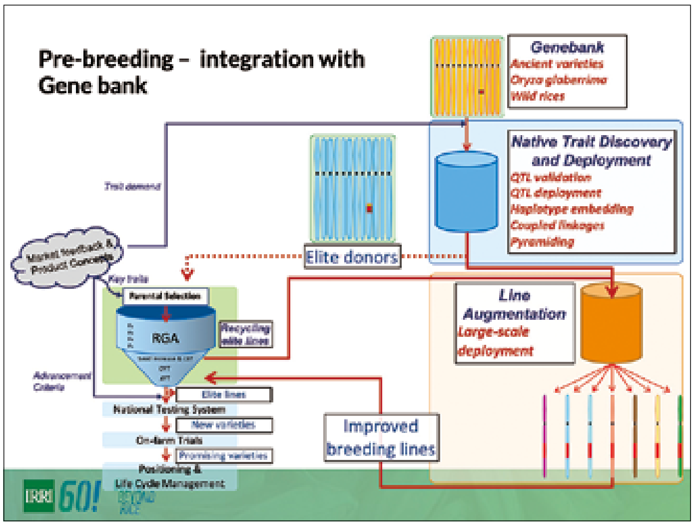


International Rice Genebank

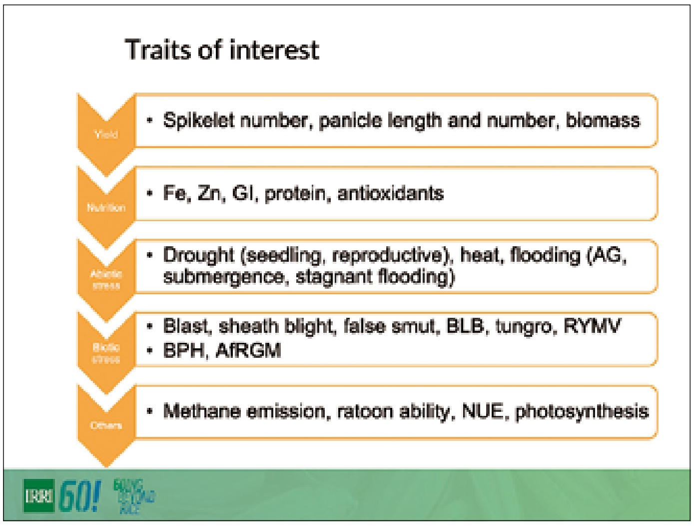
- Oldest
  1977
- Largest
  >132,000 accessions
  ~5k wild species
- Most diverse
  134 countries
  22 wild sp, 7 genera



'OneRice' Breeding Strategy & Framework

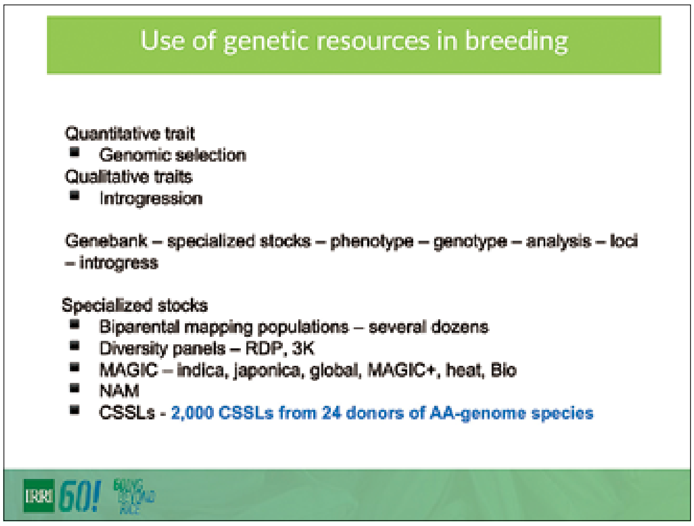


Pre-breeding – integration with Gene bank



Traits of interest

- Spikelet number, panicle length and number, biomass
- Fe, Zn, GI, protein, antioxidants
- Drought (seedling, reproductive), heat, flooding (AG, submergence, stagnant flooding)
- Blast, sheath blight, false smut, BLB, tungro, RYMV
- BPH, AfRGM
- Methane emission, ratoon ability, NUE, photosynthesis



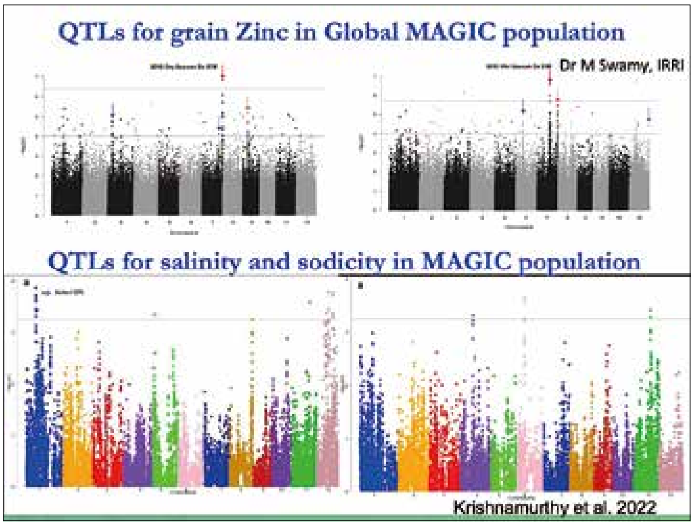
Use of genetic resources in breeding

Quantitative trait
- Genomic selection

Qualitative traits
- Introgression

Genebank – specialized stocks – phenotype – genotype – analysis – loci – introgress

Specialized stocks
- Biparental mapping populations – several dozens
- Diversity panels – RDP, 3K
- MAGIC – indica, japonica, global, MAGIC+, heat, Bio
- NAM
- CSSLs - 2,000 CSSLs from 24 donors of AA-genome species

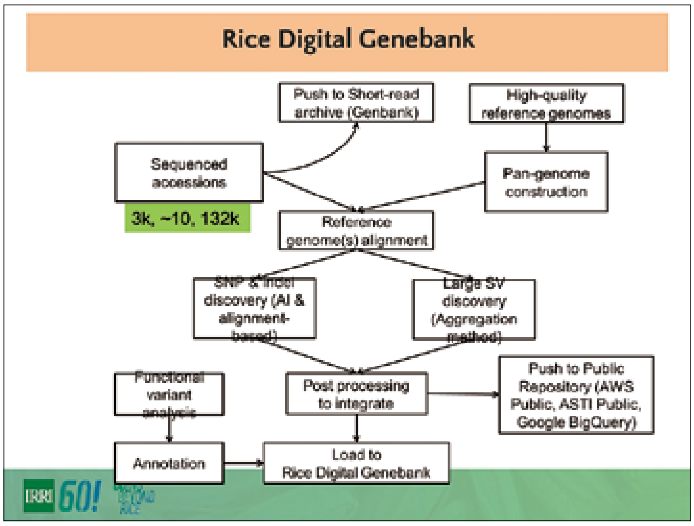


QTLs for grain Zinc in Global MAGIC population

Dr M Swamy, IRRI

QTLs for salinity and sodicity in MAGIC population

Krishnamurthy et al. 2022



Rice Digital Genebank

Sequenced accessions

3k, ~10, 132k

Push to Short-read archive (Genbank)

High-quality reference genomes

Pan-genome construction

Reference genome(s) alignment

SNP & Indel discovery (AI & alignment-based)

Large SV discovery (Aggregation method)

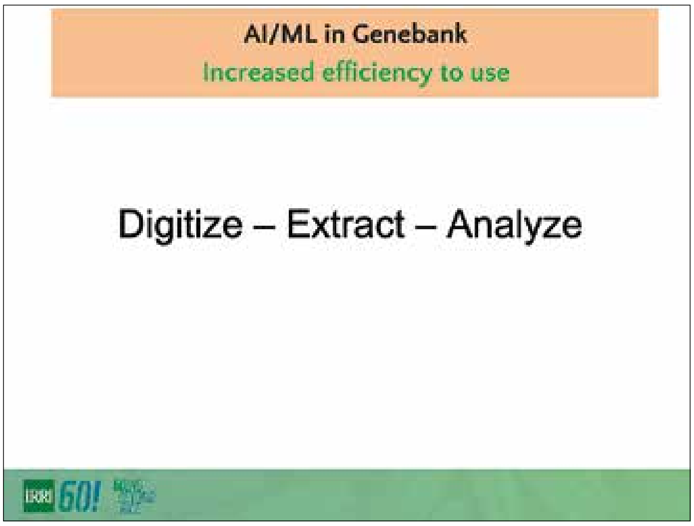
Functional variant analysis

Post processing to integrate

Push to Public Repository (AWS Public, ASTI Public, Google BigQuery)

Annotation

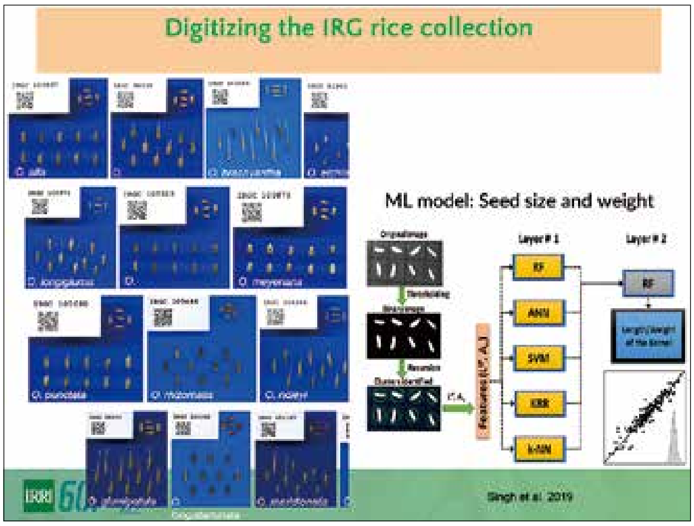
Load to Rice Digital Genebank



AI/ML in Genebank

Increased efficiency to use

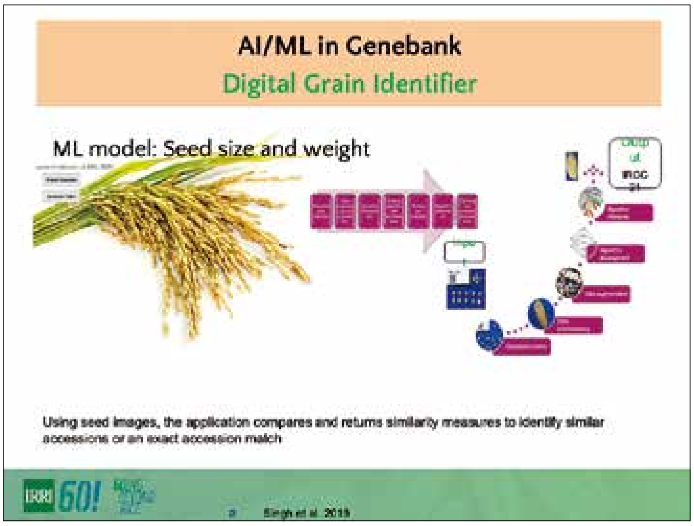
Digitize – Extract – Analyze



Digitizing the IRG rice collection

ML model: Seed size and weight

Singh et al. 2019



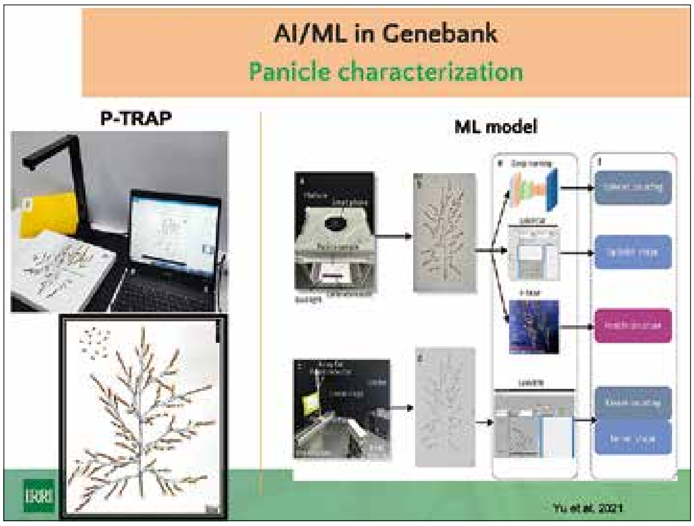
AI/ML in Genebank

Digital Grain Identifier

ML model: Seed size and weight

Using seed images, the application compares and returns similarity measures to identify similar accessions or an exact accession match

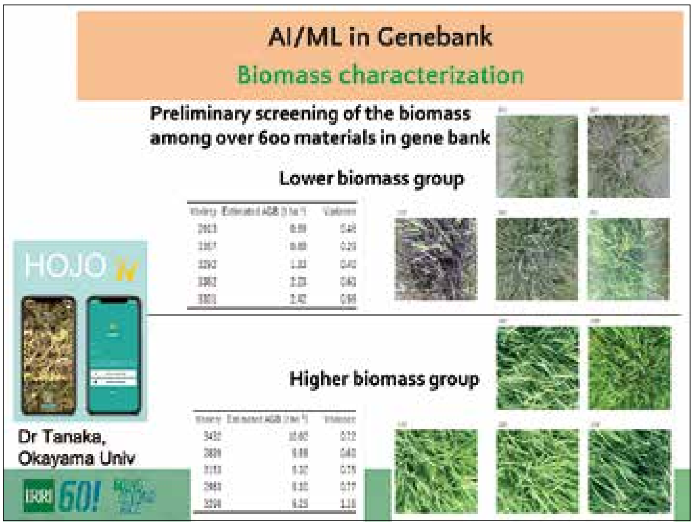
Singh et al. 2019



AI/ML in Genebank

Panicle characterization

Yu et al. 2021



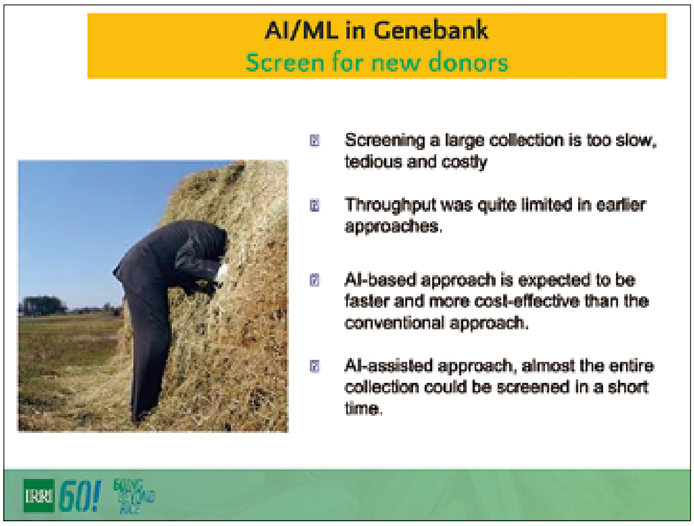
AI/ML in Genebank
Biomass characterization

Preliminary screening of the biomass among over 600 materials in gene bank

Lower biomass group

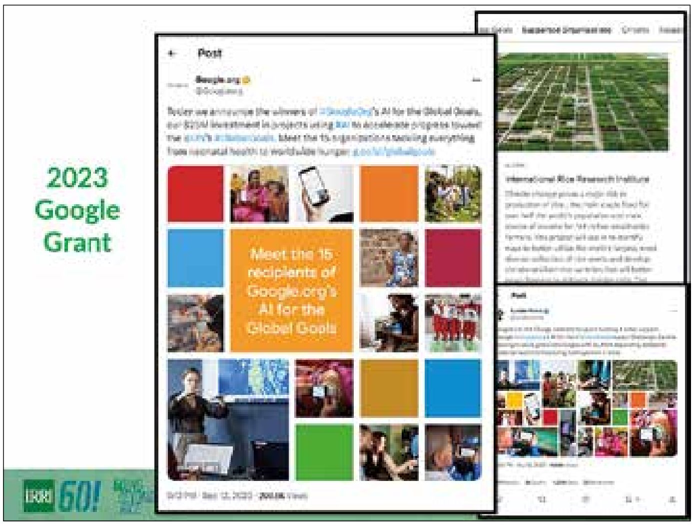
Higher biomass group

Dr Tanaka, Okayama Univ



AI/ML in Genebank
Screen for new donors

- Screening a large collection is too slow, tedious and costly
- Throughput was quite limited in earlier approaches.
- AI-based approach is expected to be faster and more cost-effective than the conventional approach.
- AI-assisted approach, almost the entire collection could be screened in a short time.



2023 Google Grant

Screening 60k accessions for tolerance to abiotic stresses

Flooding

Flooding

Flood tolerance screening-summary

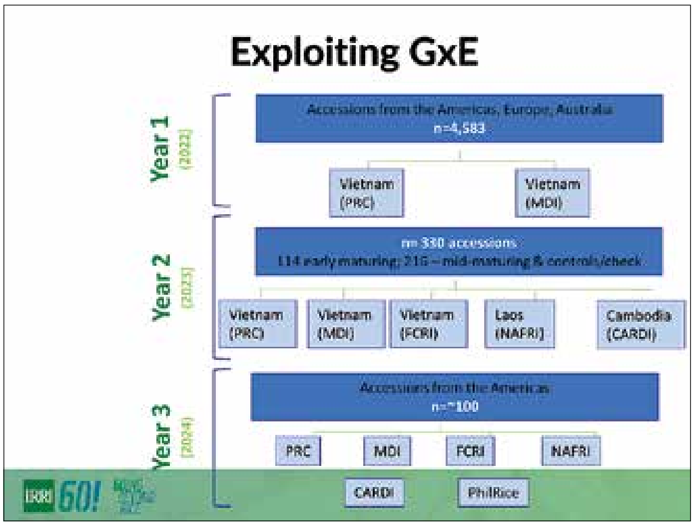
1977 – 2023
~20k IRG accessions have been screened for submergence

DS2024
– we screened 60k accessions
– selected 1207 tolerant accessions

Time: 1/10th
Cost: 1/16th

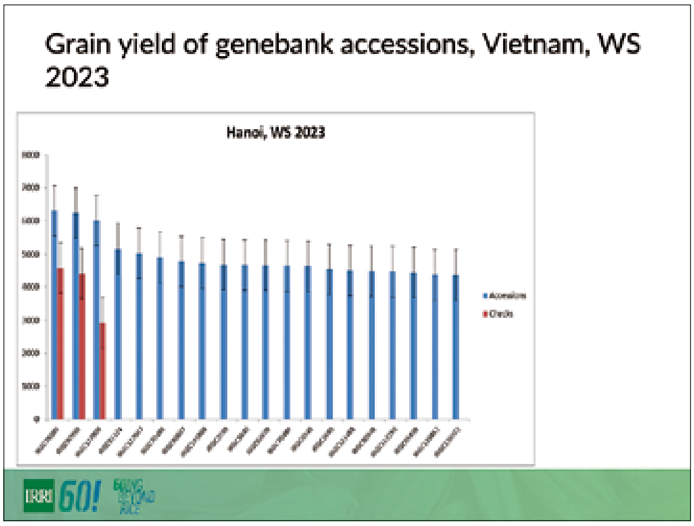
Drought

Salinity tolerance

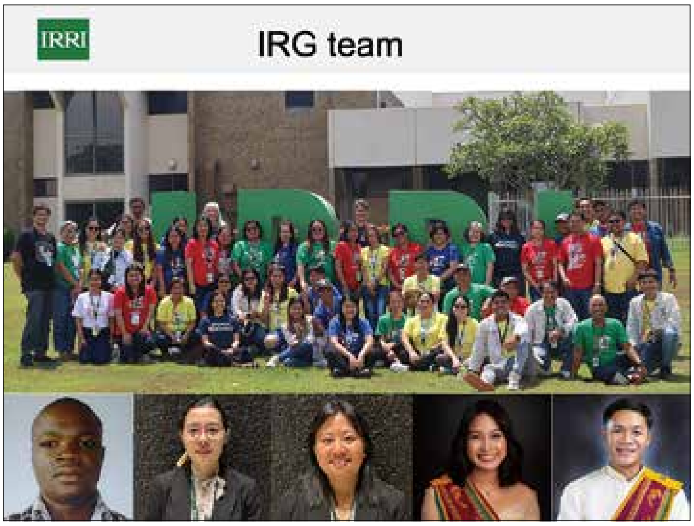


Exploiting GxE

Participatory accession selection



Grain yield of genebank accessions, Vietnam, WS 2023



IRG team

Collaborators/ contributors

Diving into Genetic Diversity in Wild Wheats: A Case Study on *Aegilops tauschii* Coss.

Yoshihiro Matsuoka
Professor, Graduate School of Agricultural Science, Kobe University, Japan

Dr. Yoshihiro Matsuoka is a Professor at the Graduate School of Agricultural Science at Kobe University, Japan. Dr. Matsuoka uses wheat and its relatives as a model system to study the mechanisms for polyploid species formation. His current research interests include understanding how wild wheat populations are structured, investigating the adaptive mechanisms in wild wheats, exploring the genetic and ecological nature of the origins of common wheat, and finding ways to better utilize wheat genetic resources in breeding. To address questions related to these interests, he conducts cross-experiments and applies evolutionary and quantitative genetic analyses.

Abstracts

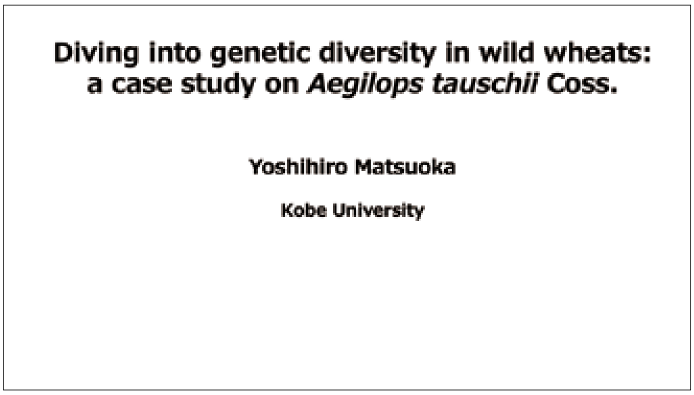
Climate change may have a significant impact on wheat production, which around one-third of the world's population relies on for subsistence. Wild wheats provide valuable genetic resources to help develop improved varieties that can adapt to harsh environments. *Aegilops tauschii* Coss. (formerly known as *Aegilops squarrosa* L.) is a wild diploid species native to the central part of Eurasia, from the Middle East and Caucasus to southwest and central Asia and central China. As the D genome progenitor of bread wheat, it serves as a valuable source of the "left-in-the-wild" alleles that can be used in breeding. Such alleles may have the potential to express useful phenotypes when transferred to bread wheat (*Triticum aestivum* L. subsp. *aestivum*). Within its vast geographic range, *Ae. tauschii* populations adapt to diverse local environments and exhibit high degrees of phenotypic variability. Understanding the species' natural trait variation patterns provides the basis for studies on the genetic mechanisms that underlie adaptation and, ultimately, is essential for enhancing the agronomic utilization of the species.

Ae. tauschii comprises two major lineages (TauL1 and TauL2) and one smaller (TauL3) lineage, which are defined by the similarity of accessions in nuclear and chloroplast molecular marker genotypes. Each lineage may correspond to an intraspecific group of accessions sharing a common ancestor that existed at some point in the past. These lineages differ in their patterns of geographic distribution: TauL1 exhibits a wide distribution across the species' range, whereas TauL2 is restricted to the western part of the range. TauL3 has been found in Georgia.

We examined the natural variation patterns in relation to these lineages for agronomic traits, including salt tolerance during gemination and seedling growth, crossability with durum wheat, using a set of approximately 200 accessions (130 accessions for TauL1, 65 for TauL2, and five for TauL3) representing the entire species' range. Our findings include: (1) relative to TauL1, TauL2 and TauL3 showed sensitivity to salt at the germination and seedling stages, (2) some TauL2 accessions from the southern Caspian region showed a high potential for hybridization with durum wheat in terms of anther size and crossability. Overall, we conclude that the lineages provide a useful viewpoint to explore the natural variation patterns in agronomic traits in *Ae. tauschii*.

To facilitate the search for *Ae. tauschii* genes responsible for the expression of agronomic trait phenotypes, we assembled an enlarged set of non-redundant accessions (> 500 accessions). A population structure analysis revealed a small number of previously unknown TauL3 accessions from Azerbaijan and northern Iran.

A downside of the lineages is that they are difficult to distinguish based on morphology; we need to genotype an *Ae. tauschii* accession to determine which lineage it belongs to. To address this issue, we adopted a machine learning approach, feeding thousands of spike photos into the model to enable it to classify the images according to the lineages used as labels. I will briefly report on the progress made with the approach.

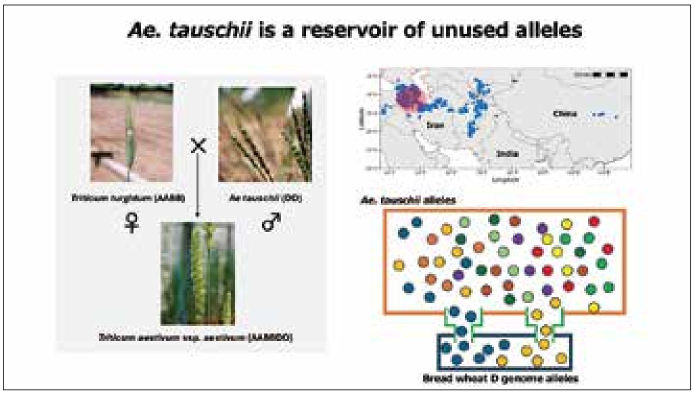


Diving into genetic diversity in wild wheats: a case study on *Aegilops tauschii* Coss.

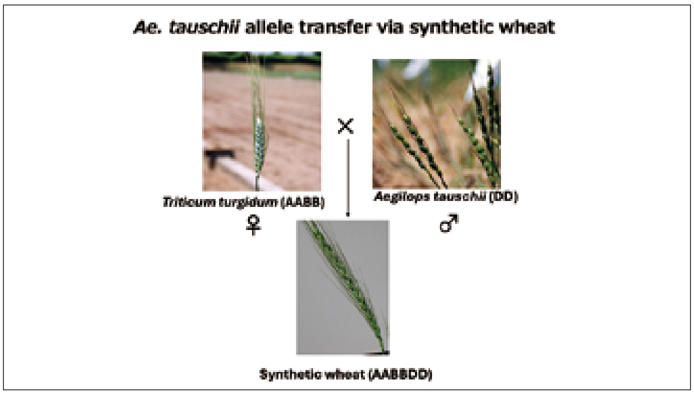
Yoshihiro Matsuoka

Kobe University

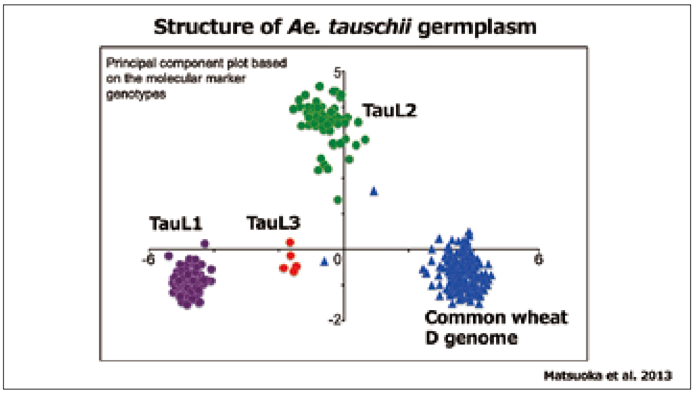
Aegilops tauschii Coss.



Ae. tauschii is a reservoir of unused alleles



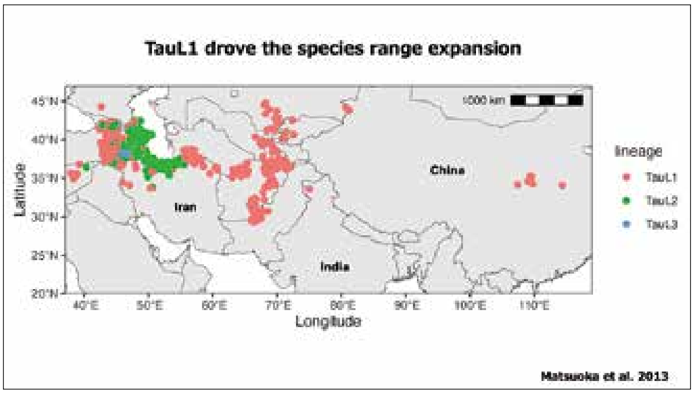
Ae. tauschii allele transfer via synthetic wheat



Structure of *Ae. tauschii* germplasm

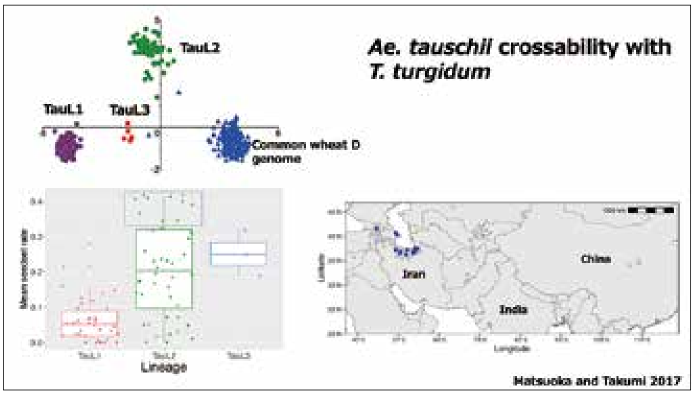
Principal component plot based on the molecular marker genotypes

Matsuoka et al. 2013



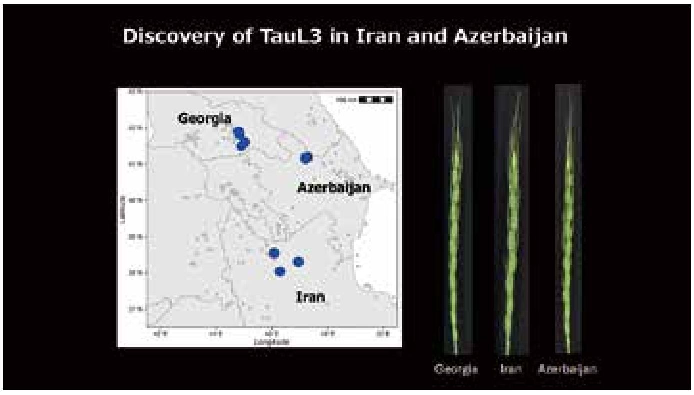
TauL1 drove the species range expansion

Matsuoka et al. 2013

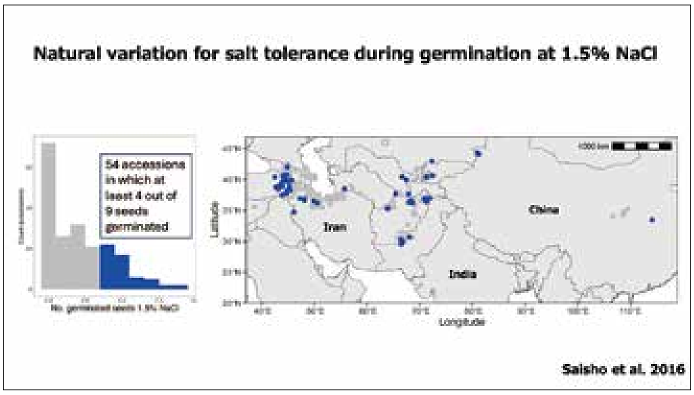


Ae. tauschii crossability with *T. turgidum*

Matsuoka and Takumi 2017

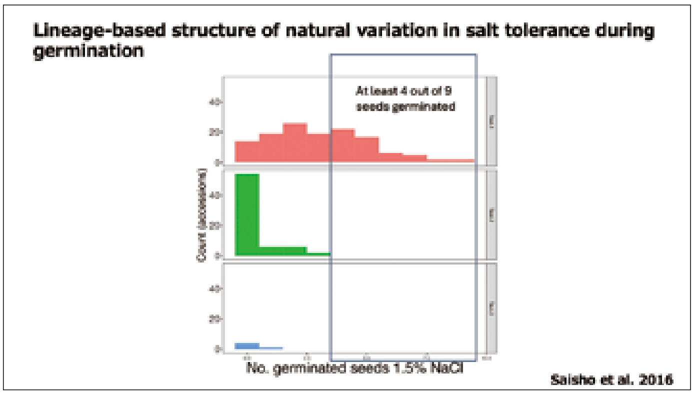


Discovery of TauL3 in Iran and Azerbaijan



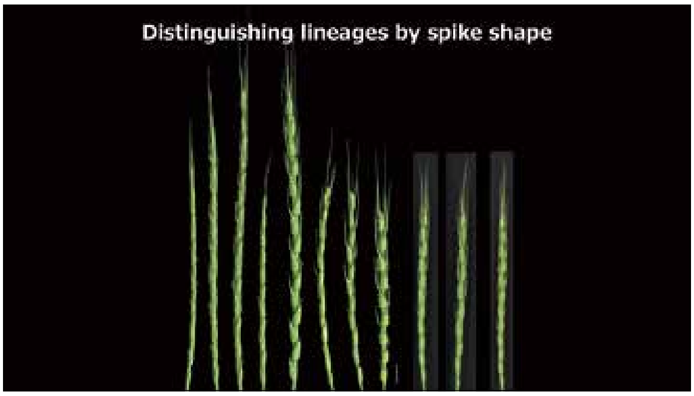
Natural variation for salt tolerance during germination at 1.5% NaCl

Saisho et al. 2016

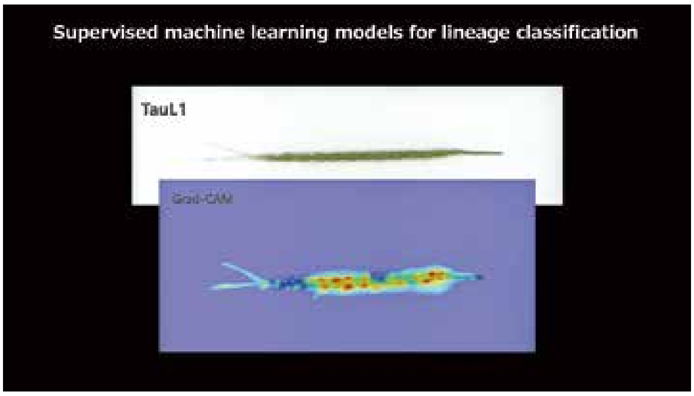


Lineage-based structure of natural variation in salt tolerance during germination

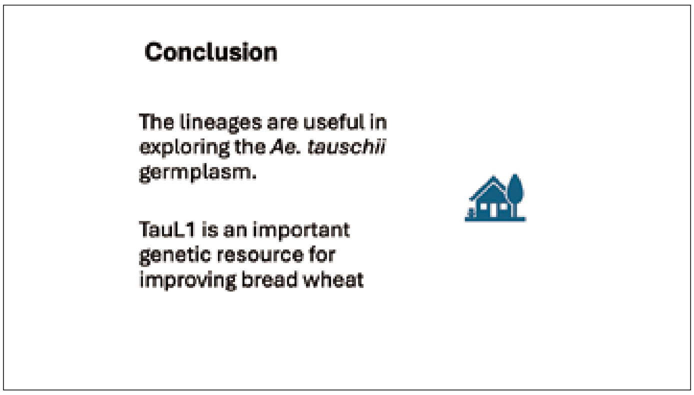
Saisho et al. 2016



Distinguishing lineages by spike shape



Supervised machine learning models for lineage classification



Conclusion

The lineages are useful in exploring the *Ae. tauschii* germplasm.

TauL1 is an important genetic resource for improving bread wheat

Acknowledgements

Takumi Shigeo (Kobe University)

Yoshihiro Koyama (Kobe University)

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Joint Research Program of Arid Land Research Center, Tottori University

Advancement of Tropical Crop Genetic Resources Utilization through the Development of Database, Technologies and Research Networking

Shinsuke Yamanaka

Director & Project Leader, Tropical Agriculture Research Front (TARF),
Japan International Research Center for Agricultural Sciences (JIRCAS), Japan

Dr. Shinsuke Yamanaka is the Director of Tropical Agriculture Research Front (TARF) and the Project Leader of the "Tropical crop genetic resources: Advancement of tropical crop genetic resources utilization through the development of database, technologies, and research networking" project at JIRCAS. He graduated from the Department of Applied Physics, Faculty of Science and Engineering, Waseda University. He changed research fields and graduated from the United Graduate School of Agricultural Science, Gifu University with a Ph.D. After working as a postdoctoral fellow at the University of Tsukuba and the National Institute of Agrobiological Sciences (NIAS) Genebank, he joined JIRCAS-TARF as a senior researcher in 2008. His area of expertise is plant genetic resources, an area he has been studying continuously since graduate school. He is currently conducting research on the diversity and utilization of tropical crop genetic resources, including tropical fruits.

Abstracts

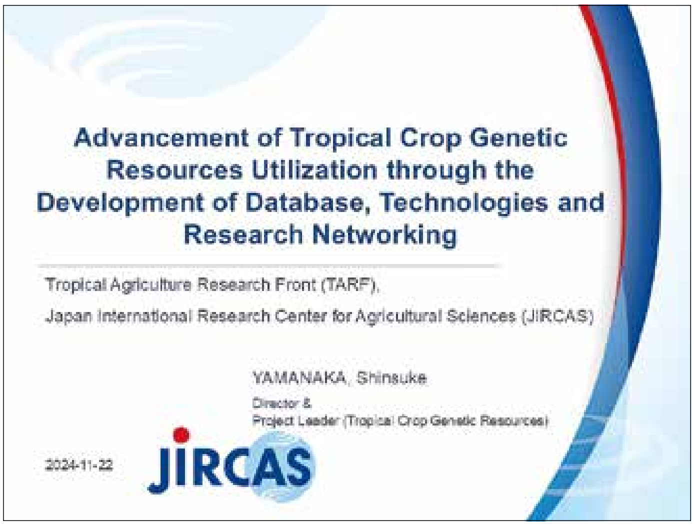
JIRCAS maintains diverse genetic resources of sugarcane, indica rice, tropical fruit trees, and *Urochloa* (tropical grass) at the Tropical Agriculture Research Front (TARF) in Ishigaki Island, Okinawa Prefecture. These tropical crops play an important role as sources of food, energy (biofuel), calories, nutrients, cash crops, and fodder in production areas. Amid concerns about global climate change, the sustainable and stable production of these crops is an urgent issue. The introduction of tropical crops and their cultivation and dissemination technologies is expected to be one of the measures to combat global warming in Japan, and will contribute to the expansion of production areas and diversification of food and nutrient sources.

TARF has climatic and geographical conditions similar to those of the experimental fields used in JIRCAS's overseas research. The research environment is suitable for conducting detailed basic experiments, along with demonstration research in tropical crop growing environments, which can contribute to close cooperative partnerships with developing regions and to agriculture in the Southwest (Nansei) Islands of Japan.

The ongoing JIRCAS project "Advancement of tropical crop genetic resources utilization through the development of database, technologies and research networking" (Tropical crop genetic resources project) based at TARF aims to create a shared resource of information, technology, and materials, and contribute to the promotion of sustainable production under unstable environmental conditions, as well as their production and utilization in Japan. This will be achieved through research networking on tropical crop genetic resources to address issues with overseas and domestic organizations, as well as through the development of varieties and technologies that take advantage of this diversity.

In this project, we have developed strategic genetic resource information[1-2], breeding technologies[3], varieties and materials, and cultivation and dissemination technologies[4], taking advantage of the diverse and abundant genetic resources maintained at TARF and the geographical location of the facility, based on international and domestic issues and needs that must be addressed. Through the sharing of information, materials, and technologies, we aim to strengthen collaborations with domestic and overseas research institutions for the advancement of tropical crop genetic resource utilization.

[1] JIRCAS Mango Genetic Resources Site:
https://www.jircas.go.jp/en/database/mango/mango-top
[2] JIRCAS-*Erianthus* Database:
https://www.jircas.go.jp/en/database/erianthus
[3] JIRCAS Research Highlights (2023):
https://www.jircas.go.jp/en/publication/research_results/2023_c02
[4] JIRCAS Research Highlights (2021):
https://www.jircas.go.jp/en/publication/research_results/2021_c02



Advancement of Tropical Crop Genetic Resources Utilization through the Development of Database, Technologies and Research Networking

Tropical Agriculture Research Front (TARF),
Japan International Research Center for Agricultural Sciences (JIRCAS)

YAMANAKA, Shinsuke
Director &
Project Leader (Tropical Crop Genetic Resources)

2024-11-22

Japan International Research Center for Agricultural Sciences

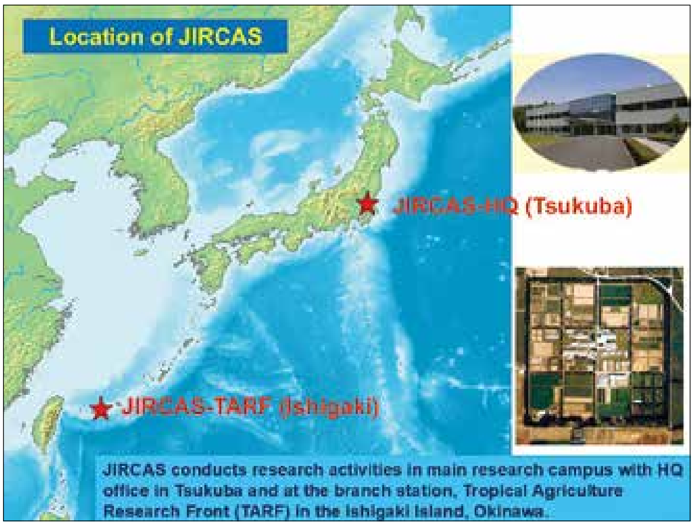
JIRCAS Headquarters (Tsukuba, Ibaraki)

TARF (Ishigaki, Okinawa)

- ● 1,952 km to Tokyo, 411 km to Naha
  277 km to Taipei
  1057 km to Manila
  1884 km to Hanoi
  2741 km to Bangkok
- ● Average Temperature: 24.3℃
- ● Annual Rainfall: 2107 mm

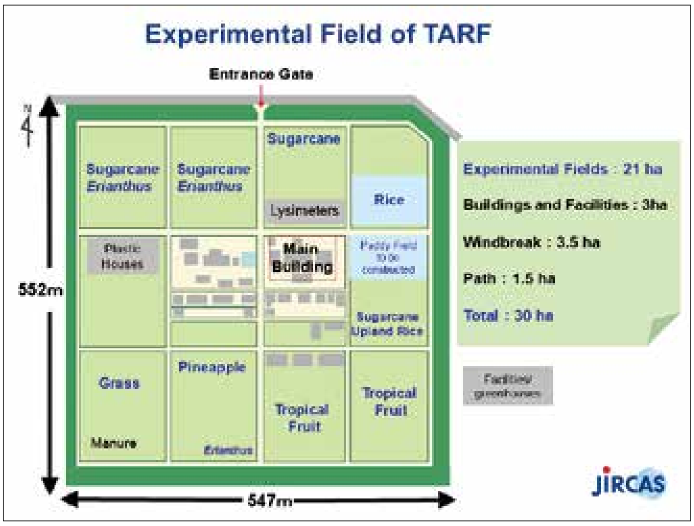
Main entrance

Main building



Location of JIRCAS

JIRCAS conducts research activities in main research campus with HQ office in Tsukuba and at the branch station, Tropical Agriculture Research Front (TARF) in the Ishigaki Island, Okinawa.



Experimental Field of TARF

Experimental Fields : 21 ha

Buildings and Facilities : 3ha

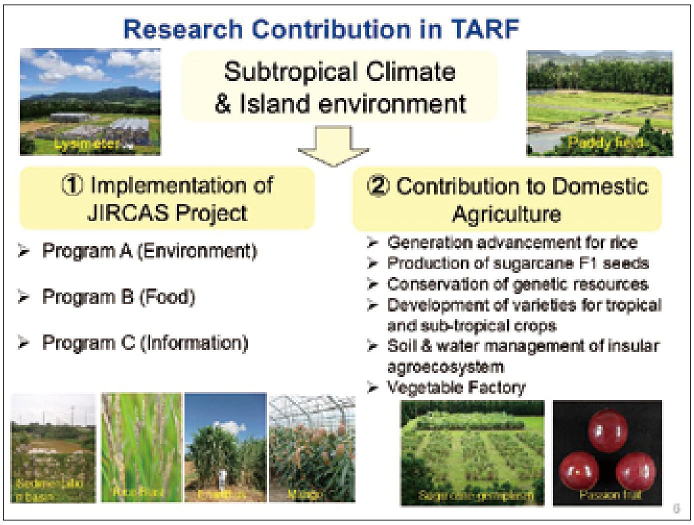
Windbreak : 3.5 ha

Path : 1.5 ha

Total : 30 ha

Facilities at TARF

- Greenhouses
- Experimental Fields
- Open Laboratory



Research Contribution in TARF

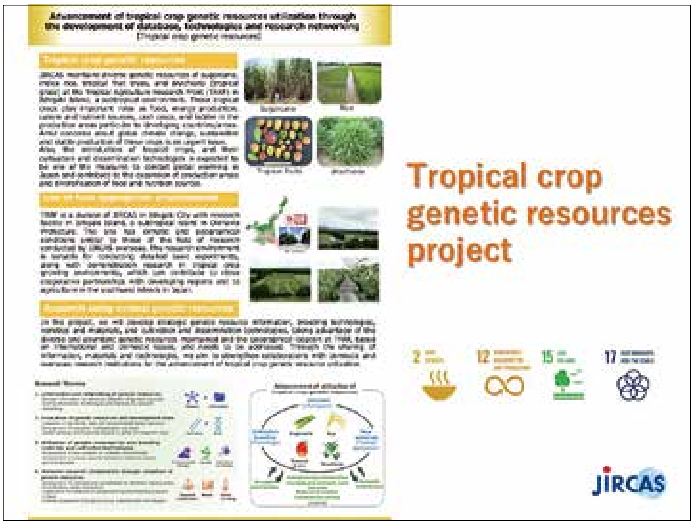
Subtropical Climate
& Island environment

① Implementation of JIRCAS Project

- Program A (Environment)
- Program B (Food)
- Program C (Information)

② Contribution to Domestic Agriculture

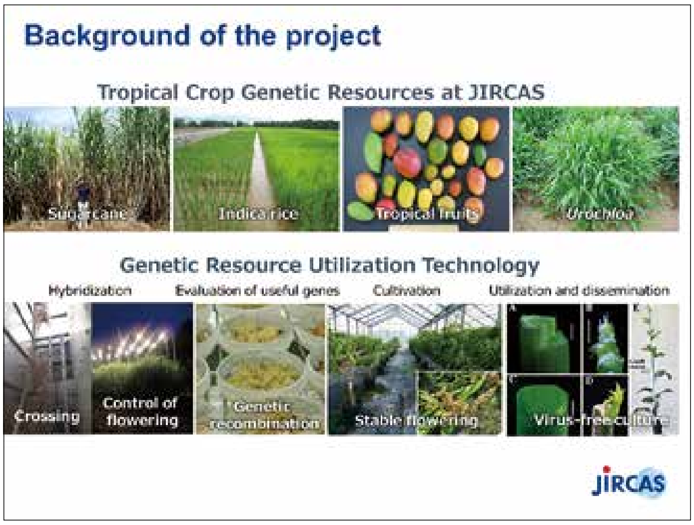
- Generation advancement for rice
- Production of sugarcane F1 seeds
- Conservation of genetic resources
- Development of varieties for tropical and sub-tropical crops
- Soil & water management of insular agroecosystem
- Vegetable Factory



Advancement of tropical crop genetic resources utilization through the development of database, technologies and research networking

[Tropical crop genetic resources]

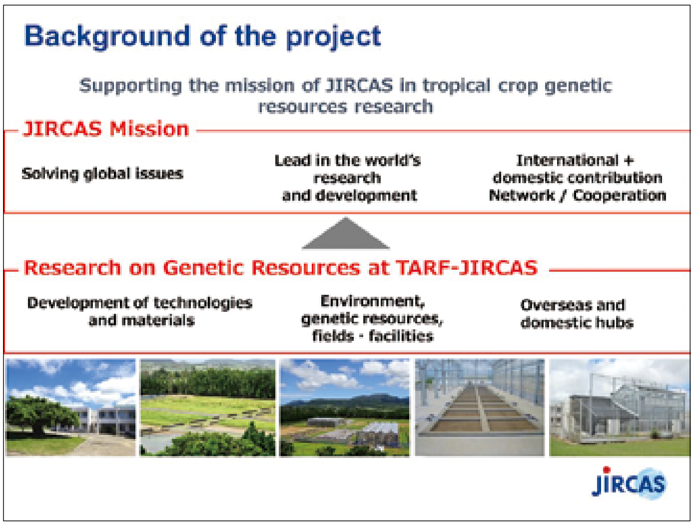
Tropical crop genetic resources project



Background of the project

Tropical Crop Genetic Resources at JIRCAS

Genetic Resource Utilization Technology



Background of the project

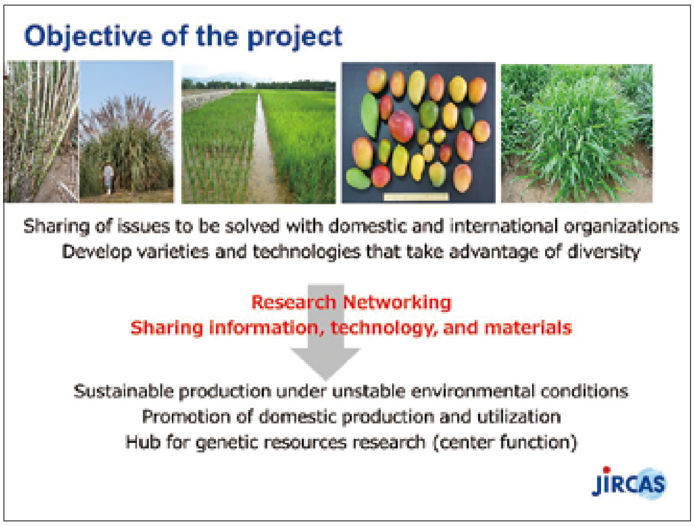
Supporting the mission of JIRCAS in tropical crop genetic resources research

JIRCAS Mission

Solving global issues	Lead in the world's research and development	International + domestic contribution Network / Cooperation

Research on Genetic Resources at TARF-JIRCAS

Development of technologies and materials	Environment, genetic resources, fields · facilities	Overseas and domestic hubs



Objective of the project

Sharing of issues to be solved with domestic and international organizations
Develop varieties and technologies that take advantage of diversity

Research Networking
Sharing information, technology, and materials

Sustainable production under unstable environmental conditions
Promotion of domestic production and utilization
Hub for genetic resources research (center function)

Research themes of the project

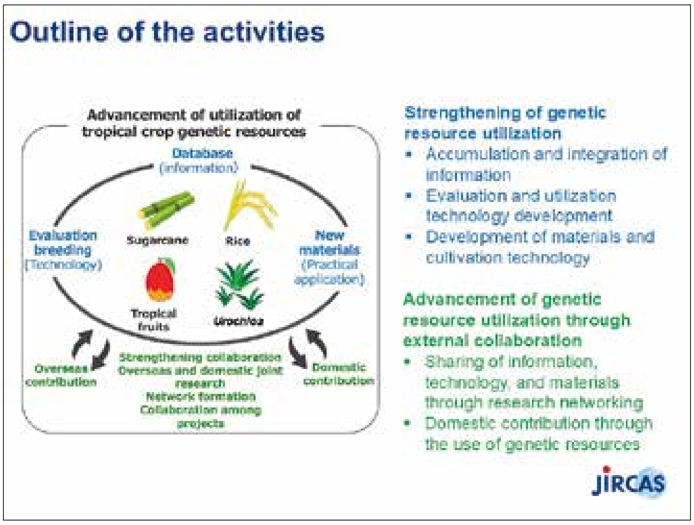
[Research Themes]

1. Information and networking of genetic resources
   Diversity information for advanced utilization of genetic resources
   Sharing information, technologies and materials by research networking

2. Evaluation of genetic resources and development tools
   Evaluation of agronomic traits and environmental stress tolerance
   Development of evaluation methodologies and tools
   Genetic analysis and functional analysis of genes for important traits

3. Utilization of genetic resources for new breeding materials and cultivation technologies
   Development of new varieties for unstable environments
   Development of cultural practice techniques based on variety and environment

4. Domestic research collaboration through utilization of genetic resources
   Development of materials and technologies for domestic needs (variety diversification, stable production)
   Cooperation for measures of global warming and breeding program in Japan
   External cooperation through providing materials and technologies



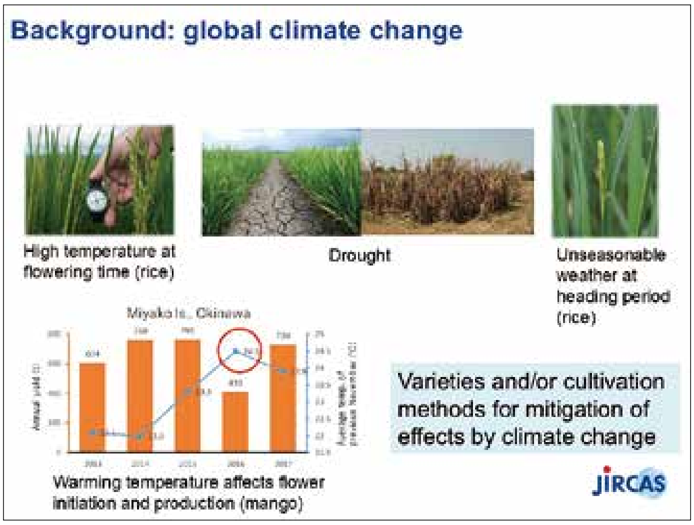
Outline of the activities

Strengthening of genetic resource utilization

- Accumulation and integration of information
- Evaluation and utilization technology development
- Development of materials and cultivation technology

Advancement of genetic resource utilization through external collaboration

- Sharing of information, technology, and materials through research networking
- Domestic contribution through the use of genetic resources



Background: global climate change

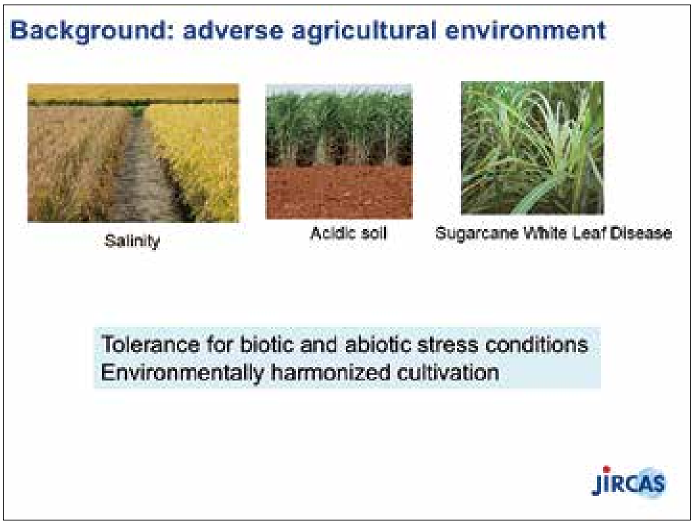
High temperature at flowering time (rice)

Drought

Unseasonable weather at heading period (rice)

Warming temperature affects flower initiation and production (mango)

Varieties and/or cultivation methods for mitigation of effects by climate change



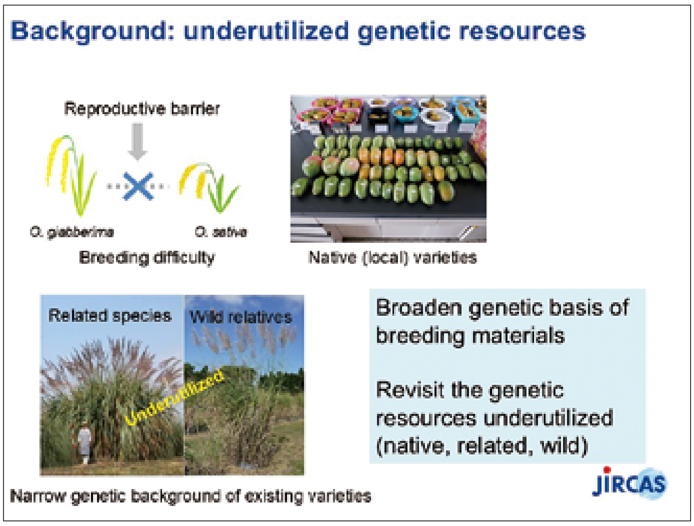
Background: adverse agricultural environment

Salinity

Acidic soil

Sugarcane White Leaf Disease

Tolerance for biotic and abiotic stress conditions
Environmentally harmonized cultivation



Background: underutilized genetic resources

Reproductive barrier

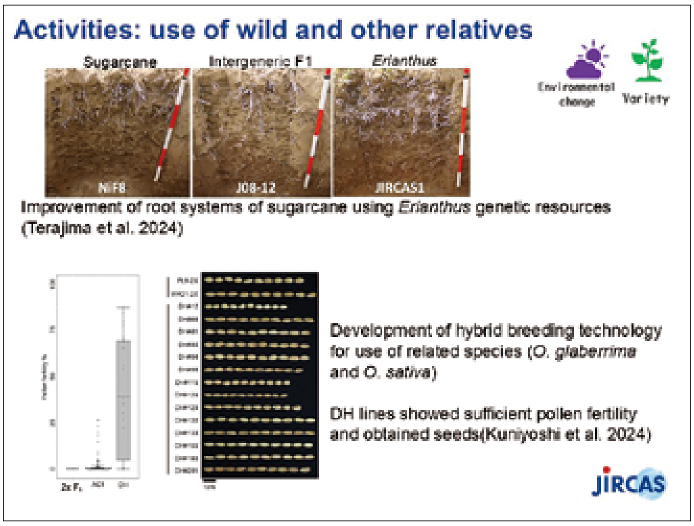
Breeding difficulty

Native (local) varieties

Narrow genetic background of existing varieties

Broaden genetic basis of breeding materials

Revisit the genetic resources underutilized (native, related, wild)

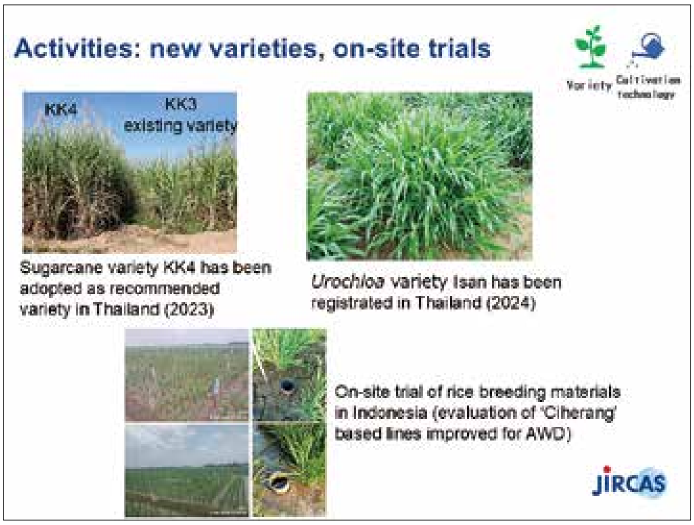


Activities: use of wild and other relatives

Improvement of root systems of sugarcane using *Erianthus* genetic resources (Terajima et al. 2024)

Development of hybrid breeding technology for use of related species (*O. glaberrima* and *O. sativa*)

DH lines showed sufficient pollen fertility and obtained seeds(Kuniyoshi et al. 2024)

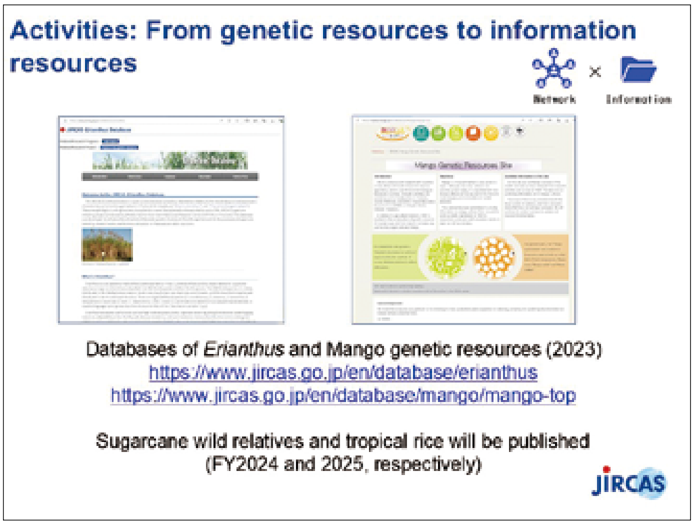


Activities: new varieties, on-site trials

Sugarcane variety KK4 has been adopted as recommended variety in Thailand (2023)

Urochloa variety Isan has been registrated in Thailand (2024)

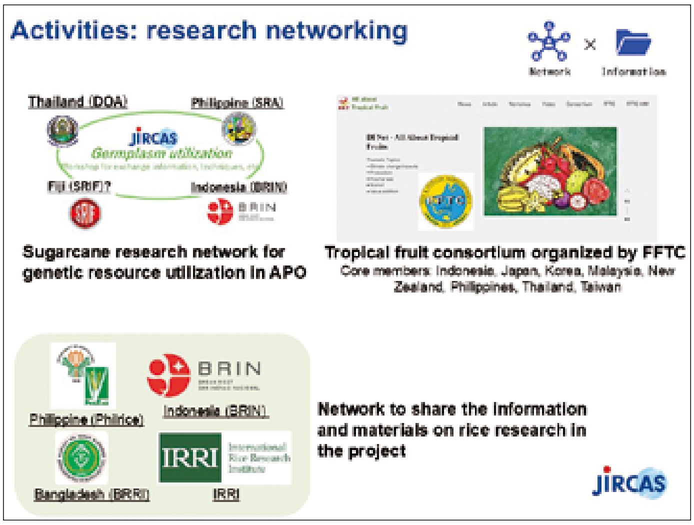
On-site trial of rice breeding materials in Indonesia (evaluation of 'Ciherang' based lines improved for AWD)



Activities: From genetic resources to information resources

Databases of *Erianthus* and Mango genetic resources (2023)
https://www.jircas.go.jp/en/database/erianthus
https://www.jircas.go.jp/en/database/mango/mango-top

Sugarcane wild relatives and tropical rice will be published (FY2024 and 2025, respectively)



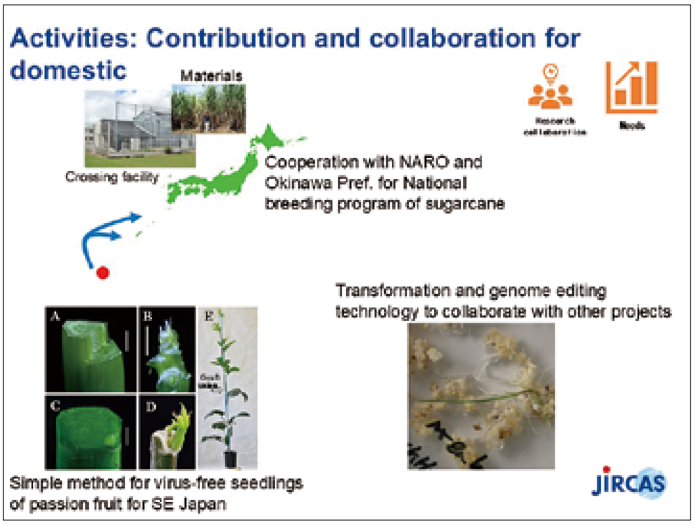
Activities: research networking

Sugarcane research network for genetic resource utilization in APO

Tropical fruit consortium organized by FFTC

Core members: Indonesia, Japan, Korea, Malaysia, New Zealand, Philippines, Thailand, Taiwan

Network to share the information and materials on rice research in the project

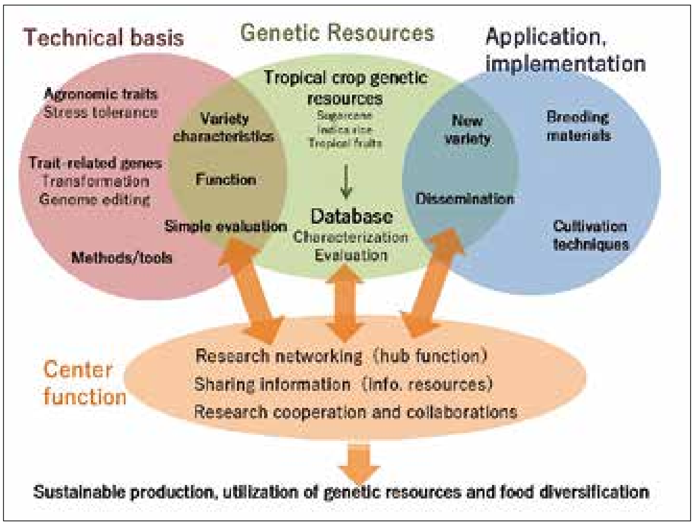


Activities: Contribution and collaboration for domestic

Cooperation with NARO and Okinawa Pref. for National breeding program of sugarcane

Transformation and genome editing technology to collaborate with other projects

Simple method for virus-free seedlings of passion fruit for SE Japan



Sustainable production, utilization of genetic resources and food diversification

Acknowledgements

Thank you very much for the cooperation and collaborations

Thank you for your attention

www.jircas.go.jp

Panel Discussion

Panel Chair: **Yasunari Fujita**
Program Director/Food, JIRCAS

Speakers:

Sarada Krishnan
Director of Programs, Global Crop Diversity Trust, Bonn, Germany

Toshihiro Hasegawa
Executive Scientist, Institute for Agro-Environmental Sciences, National Agriculture and Food Research Organization (NARO), Japan

Yukari Nagatoshi
Project Leader, Biological Resources and Post-harvest Division,
Japan International Research Center for Agricultural Sciences (JIRCAS), Japan

Hiroshi Ehara
Director, International Center for Research and Education in Agriculture,
Nagoya University, Japan
Professor, Graduate School of Bioagricultural Sciences, Nagoya University, Japan

Prakit Somta
Associate Professor, Department of Agronomy, Faculty of Agriculture at Kamphaeng Saen,
Kasetsart University, Nakhon Pathom, Thailand

Venuprasad Ramaiah
Research Unit Leader, International Rice Research Institute (IRRI), Philippines

Yoshihiro Matsuoka
Professor, Graduate School of Agricultural Science, Kobe University, Japan

Shinsuke Yamanaka
Director & Project Leader, Tropical Agriculture Research Front (TARF),
Japan International Research Center for Agricultural Sciences (JIRCAS), Japan


JIRCAS International Symposium 2024
Resilient Genetic Resources for Food Security in the Era of Global Boiling
JIRCAS
Panel Discussion
Panel Chair: Yasunari Fujita


Sarada Krishnan


HASEGAWA Yoshihiro
NARO


NAGATOSHI Yukari


EHARA Hirosh


Prakit


Venuprasad Ramaiah

Panel Discussion (35 min- 16:50-17:25)
Panel Session Theme: Resilient Genetic Resources for Food Security in the Era of Global Boiling – Opportunities and Challenges for Conservation and Utilization

FUJITA Yasunari: I am Yasunari Fujita, Program Director of JIRCAS' Food Program.
We are currently facing intertwined crises of biodiversity loss, environmental degradation, and malnutrition. Our food systems depend on genetic resources, and their conservation and use require urgent action.

There is a boost to the scientific debate to promote resilient crops, and the technology for their use is rapidly evolving, and the momentum needed to accelerate that opportunity.

First, we will discuss how to unlock the potential of resilient non-major crops.

Dr. Krishnan, in your keynote speech, you shared a historical perspective and future prospects for the conservation and use of genetic resources. Can you tell us more specifically global discourses on the opportunities to unlock non-major crop genetic resources in the age of global boiling?

Sarada Krishnan: Thank you for the question. You know, in my talk I did talk about an initiative, a global initiative called the VACS initiative, which stands for Vision for Adapted Crops and Soils. And this initiative is through the US Department of State and headed by Dr. Cary Fowler, who was the 2024 World Food Prize Laureate. So, for the VACS initiative, the objective is to improve nutrition, food security, and resilience to climate change through the development and cultivation of climate-resilient and demand-driven crops, while also prioritizing soil conservation as the foundation of soil health. So, the VACS through the US government, they have an implementer's group, the Crop Trust along with the CGIAR led by CIMYTT. The IFAD and FAO are the main implementing partners. So last year we got funding through the VACS initiative from the Norwegian government to develop programs for opportunity crops in Africa. So, we're calling that program a BOLDER, which is under a BOLD project, which BOLDER stands for "Building Opportunities for Lesser known Diversity and Edible Resources. So, we are currently working in four African countries which are Benin, Ghana, Uganda and Tanzania. And the way we do I showed the four pillars. So, we look at conserving and utilizing crop diversity research, evaluation, breeding, seed systems development as well as policy-enabling environment. So, we have all these four countries. We have selected 2 crops each based on stakeholder consultation. So, we work with farmers of seed suppliers and all of the different stakeholders, bringing them together to identify these crops because we need buying from everyone to improve the crop. And so that is one of the projects. And recently we got funding from the German government as well as Irish government, and we have developed a funding facility called the Power of Diversity funding facility. So next year we'll initiate the Power of Diversity pilot project and the five additional countries and three in Africa which are Rwanda, Nigeria and Zambia and then one in Asia which it will be India and then in Latin America and Colombia. So, we will use almost the same process, and we will start working on all of these five-year projects because to see impact you need a little bit of time to make sure that seed systems are developed. All of these things are in place. So that is our project that we are currently working on. Thank you.

FUJITA Yasunari: Thank you, Dr. Krishnan. Dr. Nagatoshi, from a resilience and nutrition point of view, quinoa is a very interesting crop. How do you think the lessons from quinoa will contribute to advancing research of resilient crops?

NAGATOSHI Yukari: Thank you for asking the important point. As already mentioned by Dr. Sarada, using unutilized crops, I say orphan crops, are very important for future food and nutritious security. In this point, I think the progress of our quinoa research including establishment of the breeding platform and also finding the involved in useful agronomical trait will provide a road map for utilization for the other orphan crops, I hope so. In addition, for major crop, I think new findings from quinoa or the other orphan crops are useful for their improvement as presented in this symposium, maize and rice, major crop research is at the forefront of the plant science. But I strongly believe that we will find new mechanism or new genes involved in high nutritious content or stress tolerance from quinoa. So, I expect these findings to give a new hint for major crop improvement. Thank you.

FUJITA Yasunari: Thank you, Dr. Nagatoshi. Prof. Ehara, sago can be grown in poor environments, but can you talk about the innovation and policy challenges and opportunities needed to unlock its potential?

EHARA Hiroshi: Thank you, Dr. Fujita. About the very important questions, first, I'd like to talk about the innovation. Recently the NGO and supporting/partner organization in Indonesia, they would like to expand the opportunity to utilize the sago palm. One of the new challenges is to plant the sago palm at the post mining site. So, for the deep devegetation, because of the post mining of the area, we'd have a serious problem in the soil. Such kind of opportunities expanded to say utilization will be expanding. However, when we increase the opportunity to utilize sago palm, of course, sago starch production will be increased, but at the same time, the amount of the residue also will be increased. Actually, at this moment, almost half of the stored carbohydrate starch in the trunk will remain after such extraction in the residue. So, how we can utilize such remaining resource will be one of the very important agenda. For finding the better solution, we are working with our former international students. For example, to produce the biodegradable material, the seeds, like the styrofoam-like material. However, to expand the opportunity to utilize the residue, probably much easier access devices should be prepared. So, another example is for producing the organic fertilizer utilizing the sago, the residue. So our partner in the Sulawesi island, they're trying to utilize such organic fertilizer for the post mining of the area. So, this will be one of the recent challenges. So, then it's about the policy. So, we expected the new challenge from the producing country. We introduced the one example from Indonesia, so the government of Indonesia started to support the development of the infrastructure for the sago starch, sago-producing area. Because the center of the sago production area will be very far from the large city, it will be difficult to provide the material for the consumers. That's why they started to select several provinces to support, to develop their infrastructure. Yesterday I heard a news from the Philippines, our partner organization in the Philippines, they got the new budget to utilize sago resource, to be one of the components for their ecology services just like the Satoyama activities. Such kind of new trial from the support, the local and central government, will be already launched so we'd like to support their activity together with our partner organizations.

FUJITA Yasunari: Prof. Ehara, thank you for your good news. Next, Dr. Somta, despite its socioeconomic importance, mungbean has a low yield and is susceptible to biotic and abiotic stresses. You talked about technological advances in overcoming stress tolerance. What conditions can accelerate and enable the development of more resilient varieties?

Prakit Somta: OK, thank you for the question. I think the availability and the easy accessibility to the diverse genetic resource will be the key to rapid development of the climate resilience cultivars. And also, for example, in my case that I showed in my presentation, we screened a lot of the germplasm for the salt tolerance, thousands of germplasms. But finally, we got one from one mungbean, only one accession that shows the resistance and now we are using it for the development of the new cultivar with salt tolerance. And also, for the minor crops such as the mungbean. The wide availability of the reference genome and the genomic tools are really important to push forward the new cultivar development.

FUJITA Yasunari: OK. Thank you, Dr. Somta. So, in conclusion, thank you for such interesting topics. As policies such as the Vision for Adapted Crops and Soils or VACS initiative attempt to unlock the secrets of quinoa's high nutritional value and stress tolerance and use them to create a resilient crop, along with the innovation of policies related to the sago palm. Also, the issue of the gap between traditional breeders and plant biotechnologists.

And we move to the next, on harnessing resilience in major crops. To ensure food security, it is essential to ensure the resilience of staple crops, the opportunities and trade-offs for the use of genetic resource diversity, the development of the latest technologies, and the need for international initiatives.

So next, I would like to ask the panelists about the opportunities and challenges of harnessing resilience in major crops.

Dr. Hasegawa, you talked about the IPCC's viewpoint on the significance of genetic resources in adapting to climate change. Can you tell us about the urgency of adapting research for major crops like wheat and rice to ensure food security under the scenarios of climate change and global population growth?

HASEGAWA Toshihiro: Thank you, Fujita-san for the question. The urgency of adaptation, adapting to climate change is actually immense as its impacts from floods, heat, the outbreaks of the pest and diseases are already threatening global food security. So, mitigating these negative impacts from biotic and abiotic stresses is a primary adaptation measure with these genetic improvements serving as a critical component, but enhancing this stress tolerance is a key, but it's increasingly difficult. The hurdle is going up and up as the intensity and frequency of these extreme events are rising with every degree of warming. We must acknowledge that we are approaching, unfortunately, the adaptation limits for the maintaining yields and the rising environment pressures, so this is alarming. So, we need to make really strong efforts to mitigate the climate change at the same time.
For staple crops like wheat and rice, there's another really serious concern, that is, the yield potentials. The yield potentials are unfortunately showing some signs of plateauing, particularly rice and wheat. It is a contrast to some other major crops like maize and soybean that show us almost consistent growth. And that's also alarming, so we need to highlight urgent efforts to boost the yield potentials at the same time. And to do that, we also do the ordinary research breeding program, but at the source, at the same time, we need some program that even leverages some of the positive side of climate change. For instance, rising temperature, also rising CO2, so those are the issues that can be leveraged in some way to enhance yield potential. But at the same time, I also would like to mention something about the minor crops or underresearched crops, they are as important as major crops as they provide important source of nutrients. And they are really underresearched, diversifying cropping system not just for major crops, another key issues to be resilient against climate change. So, I think I'll just reiterate what the speakers said, the importance of these minor crops. But finally, that said, the genetic improvements alone are not sufficient to address all the full spectrum of challenges posed by climate change. And we need a comprehensive approach, one that integrates advanced breeding with better resource management and sustainable farming practices in resilient infrastructure. By taking these coordinated and urgent action, we can build a more resilient agricultural system capable of securing the food supply for a growing population in an increase in volatile climate. Thank you.

FUJITA Yasunari: Thank you, Dr. Hasegawa. You mentioned the importance of a comprehensive approach and to building a more resilient agriculture system, that is a very important thing, thank you. Prof. Matsuoka, wheat has been domesticated for a long time. Modern species have lost the potential for resilience that wild species possess. What do you think about that possibility, or how would you balance the loss of desirable traits of modern species?

MATSUOKA Yoshihiro: OK. Thank you for the question. And then my simple answer is that the possibility of wheat germplasm is priceless, basically limitless because in the genus Triticum and Aegilops, there are about 30 species and each species is a reservoir of alleles that may not exist in bread wheat. And then if we can transfer these alleles to bread wheat, they should provide some new novel phenotypes in bread wheat. Each of these species has the potential. We have at least 30 species. So, this is the reason why I think the wheat germplasm is priceless and countless, are limitless. And then I would like to add that we need to do more pre-breeding in order to achieve our goals to save our next generation from hunger. Thank you.

FUJITA Yasunari: Thank you, Prof. Matsuoka, and thank you for telling me the importance of the wild wheat in wheat improvement. So, Dr. Ramaiah, rice is cultivated in a wide range of growing areas, thus the development of new varieties needs to meet the challenges of each local environment. Your presentation highlighted the potential of using technologies such as AI to optimize GxE. In turn, what strategies do you think are necessary to make more use of Genebank?

Venuprasad Ramaiah: Thank you for the question. There are two among the several strategies I presented, which are AI application in the gene bank era and how we can better exploit GxE to utilize gene and genetic resource tools. These are two separate topics. Going forward, maybe AI can come in to even help us with optimizing those GxE, but right now we are not there yet. Among other strategies that are relevant for us as an international center is you have to remember we are not the only institute doing this type of work, so there are plenty of other researchers who are actually doing similar work in the national program, so we can enhance their program by enhancing the access of the genetic resources to these. So, at IRRI, every year we send out 25 to 30,000 samples globally, and there are lot of other users that we have to also tackle to understand their needs to come up with strategy how to better serve them, that is one of our strategies. To attend this, what we do is every few years, mostly five years, we conduct a user survey and try to understand -- What is the trend? What are the users looking for? So, our recent survey was just around the pandemic time and then one interesting thing which came out was going forward, the users want wild species in more, they are more interested in that before to address climate change. This is the message that we got. And one of the other recommendations was that from a gene bank perspective, wild species are difficult to manage and there is very less amount of seed production, so we give very less in our center. We give only 50 seeds, many times the partners want more. So, since the wild species is going to become much more important going forward, we said, okay, let us tackle this strategy. So, we now have a revamped regeneration system for the wild species at IRRI so that now we can produce more seeds. And then we are able to attend to their needs. So, this is one of the strategies that we are following. Also, to make the genetic resources much more amenable, we have to make sure that the system in which we provide this material is smooth. Currently there are some bottlenecks. We are much better, but still there is lot of bottlenecks to solve. It is not as easy, sometimes their request takes months before the seed is provided and available to the researcher. So, there are few steps we can address that.

Then also, I think this was pointed out by others, the current information system, database systems that genebanks handle somehow are not so user friendly unfortunately and I myself, I'm a user, and I have this complaint myself. So, what are the ways in which we can make the information easily accessible? So here again AI can come in and then there are now we are developing what is called as chat bots where the users can just communicate with the system and they get the required information and so that it becomes faster, easily available. Right now, we have to run pillar to post to access certain information and then see what I want. So, these are some of the additional strategies in addition to what I mentioned in my talk, which could further help to make the genetic resources more useful and available to the users.

FUJITA Yasunari: Dr. Ramaiah, thank you for the important comment and about promoting the gene bank by improving the user demand and user friendliness. And thank you for providing us with very interesting topics on the importance of a comprehensive approach to building a more resilient agricultural system, the importance of wild wheat in wheat improvement, and on promoting the use of gene banks by improving the end user demand and user friendliness.

Dr. Yamanaka, in your presentation, taking advantage of its subtropical environment, JIRCAS has been conducting research on the conservation and utilization of tropical genetic resources through international joint research over the past 50 years. What are some of the best lessons for the future of international collaboration of genetic resources?

YAMANAKA Shinsuke: Thank you very much for your comment and question, Dr. Fujita. So, during these fifty years, of course, I don't know about 50 years ago, but we have many experiences and learned so much from our research activities. The first point to be mentioned regarding the handling of genetic resources in international collaborative research is that international attitudes toward genetic resources have changed drastically in the last 20-30 years. As you know, the CBD, The Convention on Biological Diversity, adopted at the Rio Summit in 1992, reconfirmed the sovereign rights of the country of origin and regulated compliance with national laws and regulations. In addition, in 2010, the Nagoya Protocol was established under the CBD which establishes laws and regulations concerning opportunities for the access to genetic resources and the fair and equal benefit-sharing, ABS arising from their utilization. Besides the CBD and the ABS, the ITPGR-FA, International Treaty on Plant Genetic Resources for Food and Agriculture was also adapted at FAO. And these three treaties have been signed and are in effect even in Japan. As long as JIRCAS is conducting research activities on genetic resources with international collaboration, it is a law that must be complied with, and those who handle genetic resources are required to take the utmost care in their handling of genetic resources. We also take sufficient preparation and prior coordination into account when introducing and providing genetic resources. At the moment, some developing countries have not yet developed domestic laws that correspond to these international treaties, but we think that more careful procedures will be required in the future, as they will no doubt be strictly applied in all countries. Considering the current situation, it is not easy to introduce genetic resources from overseas to Japan in the future, and the genetic resources that have been already introduced in the past and are currently in our possession will become extremely valuable.

FUJITA Yasunari: Dr. Yamanaka, thank you for the important comment increasing the usefulness of currently held genetic resources and through the entry into force of the Nagoya Protocol. We don't have enough time. Is there anyone who has any questions about the presentations or panel discussion at this symposium? Only one question. So, is there any?

Questioner:
To all the speakers, thank you very much for wonderful talks. I'm very inspired to all the sessions you gave. My question is really to everyone, now this is about research as usual, but when do we shift this to crisis management? I'm from the Norin Chukin Research Institute, which is agricultural and forestry central bank’s research institution, which means I am in the position to advise the Japanese farmers what we should be doing and from the talk today, I think the climate change is really serious and it’s going to be even more serious because the fossil subsidies is over $1 trillion and it's not going to decrease and all majors are not going to give up their rights and also the oil-producing countries are not going to give up their lives too. And the United States has elected Donald Trump to be the next president and that he's going to protect the fossil industry. And US-UN climate change or SDGS are going to fail, meaning that we are going to face the big, big climate change very soon. And I think we need to be prepared. I mean, the farmers need to be prepared to change their seeds, their farming styles, the insect management and so, when and how are we going to advise is my question. Thank you.

FUJITA Yasunari: Thank you for your question. We don't have enough time but please answer Dr. Hasegawa.

HASEGAWA Toshihiro: I think the first thing is that we shouldn't give up. Curbing the climate change, well, that's one thing. The other thing is that the involvement of farmers' participation from the early step of this development of innovative technology is another issue. So, I think sharing information about how and what the impacts are that we are currently seeing? What is the technology that we can develop? And should be shared from the beginning with the farmers and in that way, the adoption of the technology can be much quicker. So hopefully we can provide more, better platforms to do to enhance this activity. Thank you. Very short answer.

FUJITA Yasunari: Do you have any comments from the panelists please?

Sarada Krishnan: Maybe I think we need to go into emergency situation now. I think we shouldn't be waiting because breeding takes such a long time, especially in, I mean, I work on coffee genetic resources. A coffee breeding program can take 25 to 30 years. So, we need to think about 2050 and beyond now. And we have all those predictions that we are doing. And looking at those predictions, if that is what is predicted, we need to start breeding now for 2050.

Venuprasad Ramaiah: Just to supplement to what Sarada mentioned, if you remember my slide about my last work in Vietnam. This is one strategy where best adapted material is provided to the hands of the user today. It's not about a promise of breeding a better line tomorrow, so that is one way in which genebanks can contribute to some of the crisis management scenario wherever possible.

FUJITA Yasunari: Thank you. So, anyone has any question and comment? OK, thank you. Dr. Krishnan and Dr. Hasegawa, can you give us your final message on how the international community can promote genetic resource research to ensure food security in the era of global boiling? Dr. Krishnan, please?

Sarada Krishnan: Sure. So, genebanks around the world are the guardians of crop diversity and many genebanks are underfunded, which impacts the operations of the genebanks. So, if you go nationally, a lot of national genebanks are very under resourced and underfunded. And so that impacts the quality of the material that they're conserving in the genebanks. So, we need to ensure that genebanks are very well funded as well as well managed to make sure that they are meeting international standards. And that will ensure the diversity, the crop diversity is protected not just for our current generation, but for future generations.

HASEGAWA Toshihiro: Thank you. I will just reiterate what Yamanaka-san said. This international community is really important and respecting the safeguarding rights of local communities is really immensely important. Also, ensuring equitable access to those materials that are really important and in breeding really has to be accelerated, At the same time also it is critically important that effectiveness of these innovation must be evaluated across multiple dimensions. And so, economic, environmental, institutional and physical dimensions will be also important. So, I think the breeders and also the other scientists must collaborate very closely internationally to make this evaluation very effective. And also, we first bear in mind that these target environments are unfortunately changing, so the breeding targets will be changing all the time. So, I think we have to look ahead like Dr. Krishnan said, 30-40 years from now. So those are the target environments, so at the same time, we have to make 10 years efforts to curb the climate change. OK, I really conclude the sentence again. Don't give up trying to fight this climate change. Thank you

FUJITA Yasunari: Thank you, Dr. Krishnan and Dr. Hasegawa. And it's time. Thank you, all panelists, for this interactive and insightful discussion on today’s topic and the straightforward answers. We will retain the international research collaboration, and multidisciplinary approaches are important to build resilient food systems in the era of global boiling. Especially, we need to conserve and restore the diversity of nutritiously rich genetic resources and harness their inherent resilience to biotic and abiotic stresses. There are still a lot of challenges, but we will continue working hard to address them. Thank you to all of you who attended on-site and online, and we hope to see you again on future occasions. Finally, please give a round of applause to all the panelists.

Closing Remarks

YANAGIHARA Seiji

Vice-President, JIRCAS

Distinguished guests, all the participants here and online, good afternoon. I‘m Seiji Yanagihara, vice president of JIRCAS. As we conclude this year's symposium, I would like to take a moment to offer some closing remarks on behalf of the organizers.

First, I would like to deeply thank Dr. Sarada Krishnan and Dr. Toshihiro Hasegawa for your insightful keynote speeches today. And to express my gratitude to all the session speakers for your valuable contributions to this symposium. I would also like to thank everyone else for your active participation in this symposium. A little short in time for more questions or comments. I’m sorry about that.

The JIRCAS International Symposium is held every year with the aim of providing a forum for participants from national agricultural research institutes, universities, and international agricultural research organizations in developing regions to discuss and exchange ideas on the challenges facing agriculture, forestry, and fisheries in developing regions, as well as their sustainable development.

This year, as the global average temperature reaches an all-time high, we focused on research related to resilient genetic resources under the “global boiling” era. For over 50 years, JIRCAS has been working with partners to develop crops that can be sustainably cultivated even in poor agricultural environments in tropical and subtropical regions. However, dealing with “global boiling” is a new challenge. Thus, it is important to conserve and utilize genetic resource diversity for both genetic resources that have not been used until now and those that have already evolved in research and development. As discussed in today's lectures and panel sessions, I believe that the conservation and utilization of genetic resources in building resilient food systems is an area where international joint research is indispensable. I hope this symposium has provided an opportunity to explore further strategies for the conservation and utilization of genetic resources.

In closing, I would like to express my sincere gratitude to the Ministry of Agriculture, Forestry and Fisheries and the National Agriculture and Food Research Organization (NARO) for their support of the JIRCAS International Symposium. I would also like to express my appreciation to everyone involved in the planning and execution of this event.

Thank you very much.