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

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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

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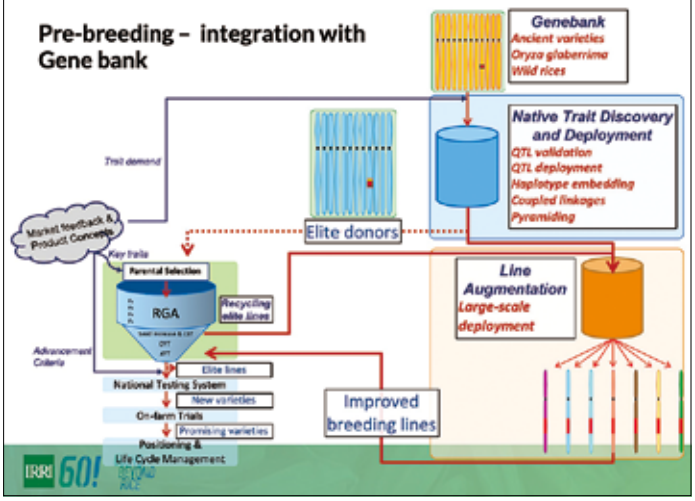
International Rice Genebank

- 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

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

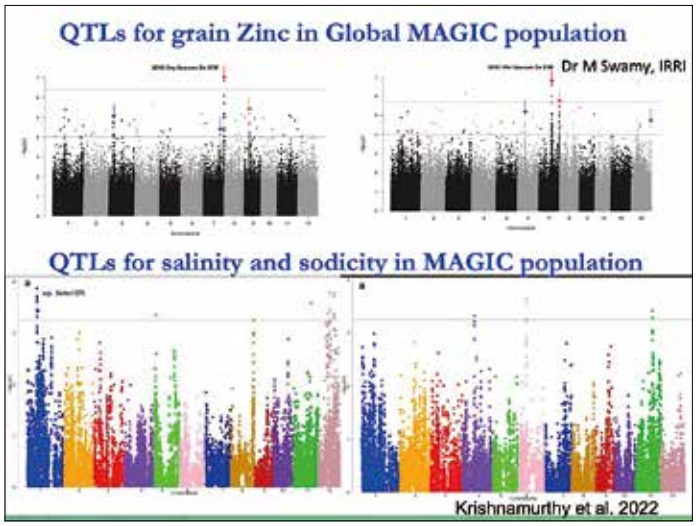
Use of genetic resources in breeding

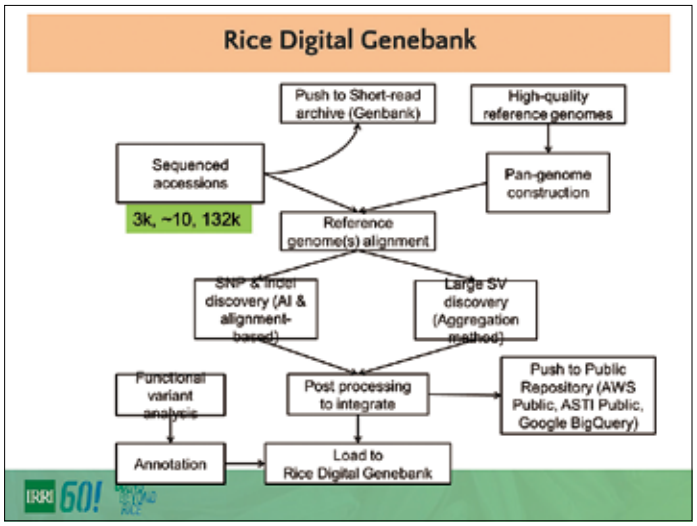
Quantitative trait
- Genomic selection

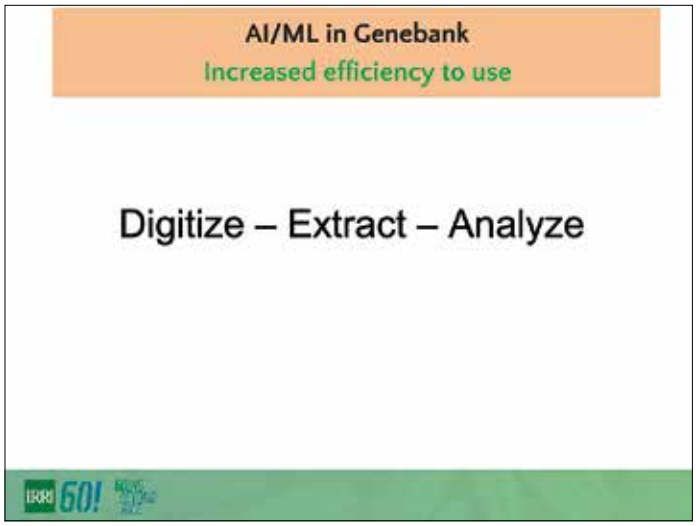
Qualitative traits
- Introgression

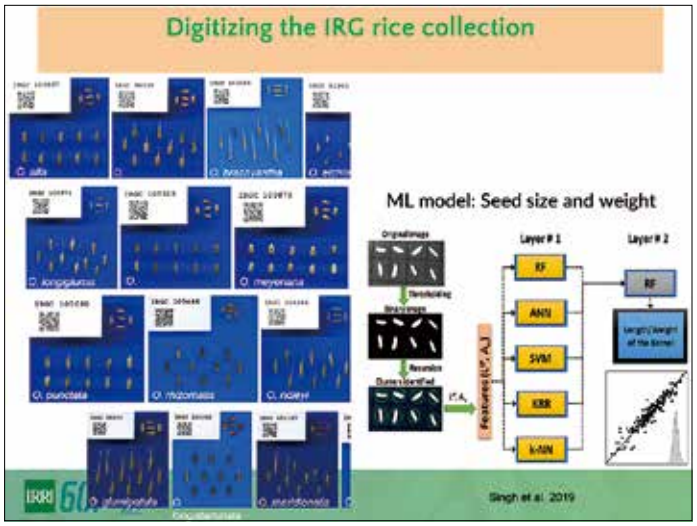
Genebank – specialized stocks – phenotype – genotype – analysis – loci – introgress

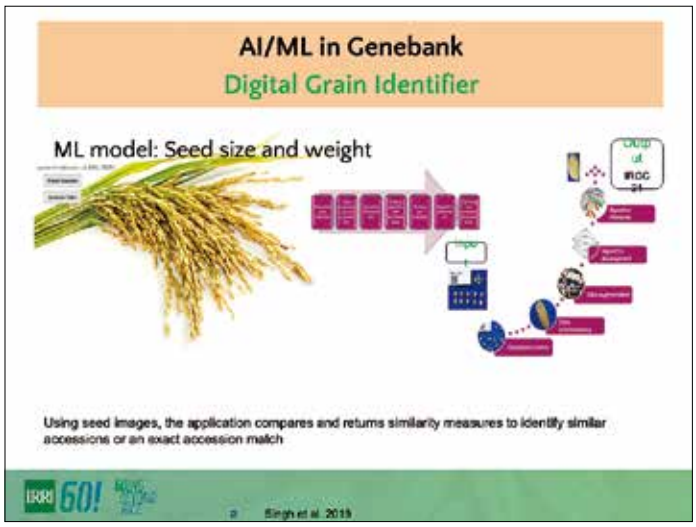
Specialized stocks
- Biparental mapping populations – several dozens
- Diversity panels – RDP, 3K
- MAGIC – indica, japonica, global, MAGIC+, heat, Bio
- NAM
- CSSLs - 2,000 CSSLs from 24 donors of AA-genome species

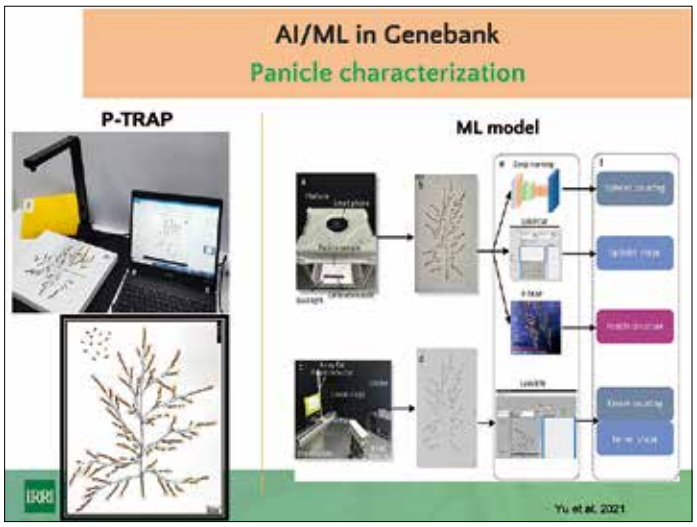

QTLs for grain Zinc in Global MAGIC population
Dr M Swamy, IRRI
QTLs for salinity and sodicity in MAGIC population
Krishnamurthy et al. 2022


Rice Digital Genebank
Push to Short-read archive (Genbank)
High-quality reference genomes
Sequenced accessions
3k, ~10, 132k
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
P-TRAP
ML model
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

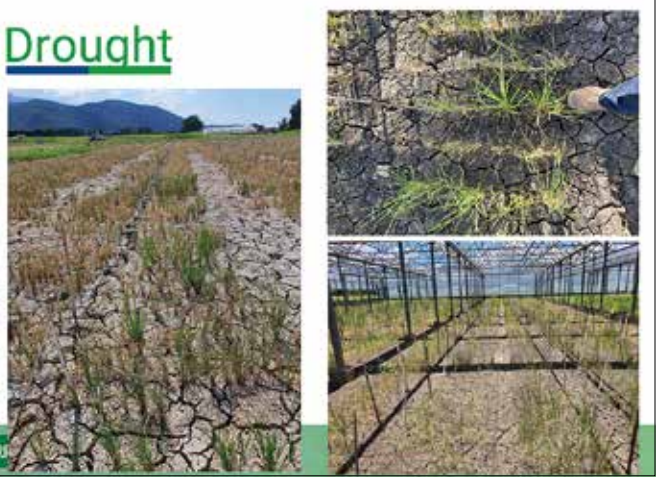
Flood tolerance screening-summary

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

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

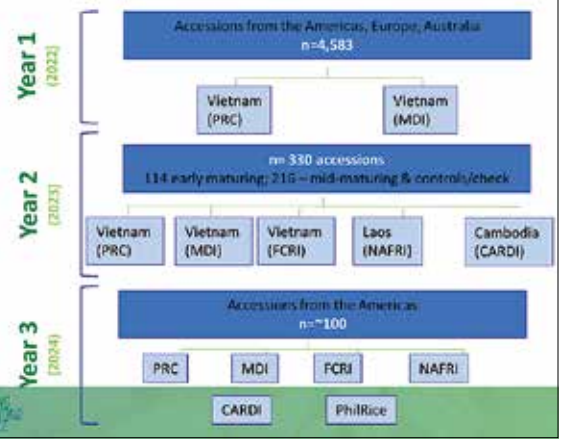
Time: 1/10th
Cost: 1/16th

Drought



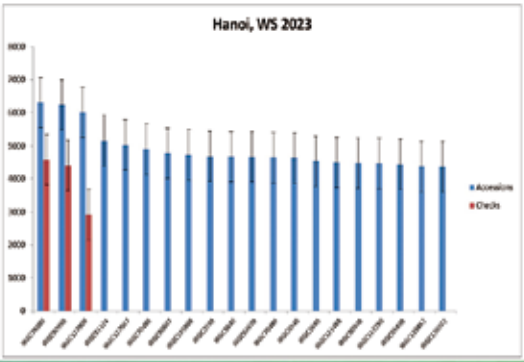
Salinity tolerance

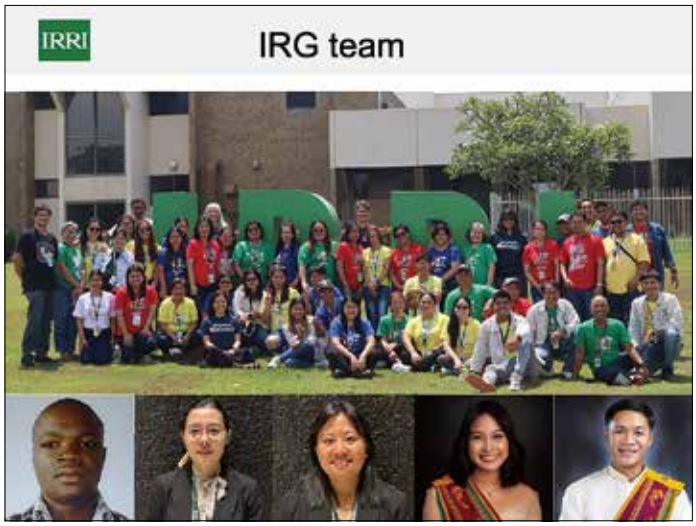
Exploiting GxE



Participatory accession selection

Grain yield of genebank accessions, Vietnam, WS 2023




IRRI
IRG team


Collaborators/
contributors