Joint FAO/IAEA Programme
Nuclear Techniques in Food and Agriculture

Plant Breeding & Genetics Newsletter

https://www.iaea.org/topics/plant-breeding
https://www.fao.org/agriculture/fao-iaea-nuclear-techniques/en/

ISSN 1564-2569

No. 55, July 2025

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To Our Readers

Cover design: Mauricio Godoy, IAEA

As we reach the midpoint of 2025, it is my pleasure to share with you the latest news, updates and achievements from the Plant Breeding and Genetics Subprogramme of the Joint FAO/IAEA Centre. This edition comes at a time of scientific progress, on-going strategic planning, and institutional growth—reflecting our continued commitment to leveraging nuclear and related technologies for sustainable, resilient agriculture.

Over the past six months, we have concentrated our efforts on the development and strategic consultation of two new Coordinated Research Projects (CRPs). The first focuses on enhancing biodiversity to build climate resilience in both annual and perennial crops. The second addresses the growing threat of transboundary plant pathogens in root and tuber crops. Both CRPs emerged from intensive expert consultations and stakeholder dialogue, underscoring the relevance and urgency of our work in supporting Member States to address pressing and emerging agricultural challenges.

A special session during the consultations gathered expert suggestions for shaping future activities on plant breeding and genetics. Key recommendations included prioritizing traits for mutation breeding based on a balance of impact and feasibility. Experts advised initiating work with simpler traits before advancing to more complex ones, keeping in mind that most induced mutations are recessive. They also emphasized the importance of considering the agricultural system, especially for traits like herbicide resistance—and noted that the type of physical mutagen used may affect whether a mutation is dominant or recessive. Identifying causal mutations was also highlighted as a critical step for generating useful insights.

This edition presents highlights from those expert discussions and explores the enabling technologies that continue to shape our work. From speed breeding and radiation-induced mutagenesis to digital phenotyping and AI-driven trait selection, these tools are accelerating the development of improved crop varieties and enhancing their resilience to climate extremes, disease, and environmental stressors.

We are pleased to feature several timely and insightful contributions from our partners and Member States in this edition. These include:

- "Methods and Solutions for Digital Phenotyping in Plant Breeding" – This article explores how digital phenotyping, driven by advances in sensors, robotics, and AI, overcomes the limitations of traditional manual phenotyping. The approach provides scalable, rapid, and reliable data collection to support complex breeding decisions and ecosystem-level adaptation.
- "Plant Breeding Accelerated by Heavy-Ion Mutagenesis: Specific Examples from Japan" – Highlighting more than 90 new varieties developed through ion beam irradiation, this piece explains the influence of Linear Energy Transfer (LET) on mutation efficiency and genetic outcomes, including the isolation of high-yield rice genes.
- "Advancing Breeding Technologies to Boost Productivity and Resilience in Vegetatively Propagated Crops: The Case of Cassava and Beyond" – Focusing on crops of high economic and food security importance, the article explores how novel breeding approaches are being used to overcome propagation and genetic constraints in clonal crops.

As part of our broader mandate, we have actively engaged in several international fora to share knowledge, build partnerships, and advocate for science-based solutions. I had the honour of attending the 3rd International Laâyoune Forum on Biosaline and Arid Land Agriculture, where I was contributing to the Plenary Session "Cutting-Edge Science Towards Improving Crop Resilience to Drought and Salinity". I also delivered a keynote address on "Climate-Smart Plant Breeding: Leveraging Nuclear Techniques and Innovative Approaches for Marginal Environments", underlining the vital role of induced mutagenesis in developing drought- and salinity-tolerant crops for challenging agroecosystems.

I also contributed to the Steering Committee of the Partenariat pour le Coton (Cotton Partnership), supporting sustainable cotton production in the C-4+ countries. Discussions focused on establishing financing mechanisms across the cotton–textile–garment value chain and on the design of a dedicated fund for capacity building and technical support, with the Joint FAO/IAEA Centre participating in reviewing the draft Terms of Reference (ToR).

Another important achievement was our move into the new Plant Breeding and Genetics Laboratory in Seibersdorf, constructed under the ReNuAL2 initiative, the project that led to renovations of the nuclear applications laboratories. This modern facility marks a new era for our work, enabling expanded research, enhanced training capabilities, and deeper scientific collaboration to serve our global community.

The Plant Breeding and Genetics subprogramme of the Joint FAO/IAEA Centre also participated in the FAO Global Agri-Food Biotechnologies Conference in Rome, 16–18 June 2025. Ms. Pooja Bhatnagar-Mathur, Head of the Plant Breeding and Genetics Laboratory, spoke on "Mutation Breeding 2.0," highlighting R&D advances linking mutation and precision breeding. Two posters on coffee breeding and banana disease diagnostics presented by Mr. Radiras Nkurunziza and Mr. Venkatesh Jelli, two young researchers at PBGL. Additionally, Mr. Sharath Chandran, a PhD researcher competed in the Biotech Innovation Challenge, presenting the "Nuclear-augmented Microbial Consortia (NuMiC)" innovation for sustainable banana disease management.

We look forward to contributing to the global dialogue on agri-food biotechnology and showcasing the impactful R&D that the FAO/IAEA Joint Centre carries out with global partners to support Member States for both farmer- and consumer-centric traits/products for food and agriculture.

Our team has also seen important changes. We warmly welcomed Dr. Mohamed Abdelrahman to our laboratory team and extended our deep appreciation to Dr. Norman Warthmann, who parted from the Joint Centre and whose contributions have left a legacy.

As always, I would like to take this opportunity to thank our readers, collaborators, and partners—for your continued interest, trust, and support. Your engagement motivates us to pursue excellence, to share impactful results, and to drive forward innovation in support of global food and nutrition security.

We remain committed to keeping you informed-providing updates, celebrating success stories, and highlighting the transformative potential of nuclear and biotechnological advances in agriculture. Together, we are not only improving crops—we are reinforcing the systems that sustain lives, livelihoods, and ecosystems.

As the African proverb remind us, “If you want to go fast, go alone; if you want to go far, go together.” We invite you to continue walking this journey with us—deepening collaboration, exchanging ideas, and co-creating solutions for a more resilient and food-secure world.

Thank you for being an integral part of this journey. We look forward to what lies ahead.

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Staff News

Welcome

Mr Mohamed Abdelrahman (Egypt) joined the Plant Breeding and Genetics Laboratory (PBGL) as a plant genetics and molecular breeding consultant in February 2025. His career began in 2006 at Kochi University, Japan, specializing in classical and molecular breeding methods. From 2010 to 2011 he worked as a research assistant at the Africa Rice Center's Rice Biotechnology Laboratory. He also completed a two-month training at the International Rice Research Institute (IRRI) in the Philippines. He obtained his PhD in 2013, developing new rice lines harboring genomic region linked to yield performance under water-deficit conditions.

Abdelrahman conducted postdoctoral research at the Research Institute for Development (IRD), France (2016-2017), utilizing capture sequencing to study genetic diversity in African and Asian rice genotypes. He further advanced his research at the Chinese Academy of Agricultural Sciences, China (2019-2020), utilizing genome-editing for developing high quality and disease-resistant rice.

In Egypt Abdelrahman works as a molecular breeder at the Agricultural Research Center, Ministry of Agriculture, where he has contributed to the development of different high-yielding rice cultivars resistant to biotic and abiotic stresses. He is also committed to capacity building, having trained numerous graduate students, technicians and specialists from across Africa.

His interdisciplinary expertise includes biostatistics, bioinformatics and molecular breeding, with current research emphasizing biotechnology approaches to improve crop resilience to biotic and abiotic stresses, aiming for sustainable crop production in challenging environments.

Farewell

Ms Yiting Chen (China) joined the PBG laboratory in September 2024 as a consultant for four months. Yiting holds a BSc and a MSc in Agriculture Soil and Water Engineering from Northwest A&F University, China, and is now working on her PhD at the University of Copenhagen in Denmark. There, Yiting focuses on modelling stomatal conductance and water use efficiency of wheat and tomato plants in response to climate change. At PBGL, Yiting investigated the physiological responses of wheat (C_3) and sorghum (C_4) plants to elevated CO_2 concentration and drought stress. Given her previous experience working on the plant physiology, Yiting was able to quickly design a detailed experiment required to compare the physiological characteristics between two different type of crops and finished a thorough report, including necessary guidelines and recommendations. Yiting will finish her PhD in October 2025 and hopes to continue her research to develop a more precise and specialized physiological model for better predicting the responses of plants to climate change.

Ms Siti Norvahida Hisham (Malaysia) joined the Plant Breeding and Genetics Laboratory in July 2024 as an intern under IAEA Marie Sklodowska-Curie Fellowship programme. She is grateful to the programme for this opportunity of a lifetime and had an amazing year working with the PBGL team. She was welcomed with open hands and is now leaving with a fulfilled heart. Trusted with the 'Seeds in Space' project, her supervisor and lab head, Pooja Bhatnagar-Mathur, provided her with a platform to assemble a screening procedure for *Arabidopsis thaliana*, complete guidance from Joanna, supported by Mirta, Susu and Adel regarding facilities and resources, administered by Francisca and Karynne, Norman, Venki and Radi continuously giving input to consider and to all the previous PBGL fellows and interns who kept her company and made her days in Seibersdorf more cheerful. She wishes she had more time to learn about plant pathology from Friederike, Hassan and Sharath and plant breeding from Anupama. It has been her pleasure to be given a chance to learn from each one of the beloved PBGL team members. Siti is eternally grateful to her loved ones for their endless support that enabled her to be here.

It is with mixed feelings that we bid farewell to our colleague and friend, **Mr Norman Warthmann**, who recently concluded his tenure with the Plant Breeding and Genetics Laboratory.

Norman has been an integral part of our team, serving as a Molecular Geneticist with deep expertise in molecular biology, genomics, and breeding. During his time at PBGL, he played a vital role in advancing our laboratory's mission, contributing significantly to both research and capacity building. His leadership in genomics research and molecular breeding has not only strengthened our internal capabilities but also had a far-reaching impact through his training of fellows and Member State researchers.

Through his stewardship of technical cooperation and coordinated research projects, Norman has helped bridge the gap between cutting-edge science and practical applications, supporting the use of modern molecular and genomic tools in mutation breeding pipelines across our Member States. His work in developing methodologies and guidelines for technology transfer has set a strong foundation for future innovations, and his efforts in managing bioinformatics and research infrastructure have greatly enhanced the lab's operational excellence.

His collaborative spirit, integrity, and commitment to excellence have left an indelible mark on the lab. Simply put, we have been fortunate to count him among us. As he takes on new responsibilities, we know he will continue to make a meaningful impact on global agricultural systems.

Thank you, Norman, for your years of dedication, innovation, and leadership. We wish you every success and happiness in this exciting new chapter of your journey.

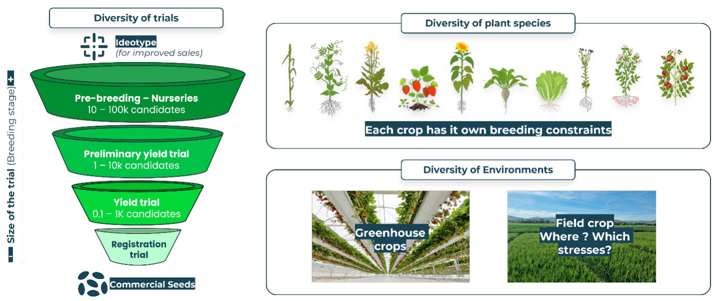
Feature Articles on Advanced Technologies in Crop Improvement

Methods and Solutions for Digital Phenotyping in Plant Breeding: From Scaling Up Trait Assessments to Phenomics-Based Prediction

Nicolas Cheviet, Rhianna McAneny

Introduction

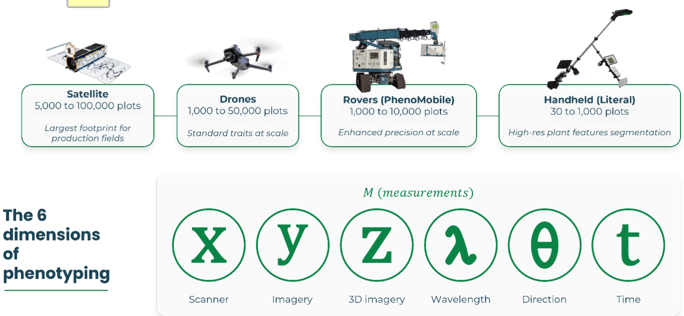
Traditional manual phenotyping has long been the bottleneck in plant breeding: labor-intensive, costly, and prone to inconsistency. Ten years ago, breeders relied almost exclusively on hand measurements - height, biomass, visual scores - which limited sample sizes and statistical power (Gano et al., 2024; Quirós Vargas et al., 2019; M. Weiss et al., 2020). As the demand for higher genetic gain intensified, researchers began exploring image-based methods, first with static cameras and then with drones, to capture canopy traits at scale (Yang and Zhai, 2022). Today, thanks to advances in sensor technology, robotics, and artificial intelligence, digital phenotyping through imaging solutions deliver dozens of quantitative and qualitative traits rapidly, reliably, and cost-effectively to optimize new varieties' selection (Qiao et al., 2022) while adapting to the complexity of plant breeding to address the challenges of the entire ecosystem.



Technological Evolution in Digital Phenotyping

a. Sensor and Platform Innovations

Digital phenotyping is based on the principle of the six dimensions of phenotyping – interpreting a signal in one or multiple dimensions to access different types of information about your crop. These dimensions are accessible with sensors that can be integrated in vectors or tools enabling repeatable data capture over time. Here's a non-exhaustive list of vectors to date:



Satellite imaging: In the early days of high-throughput phenotyping and remote sensing agriculture, satellite imagery played a huge role in allowing researchers accessing traits and heterogeneity maps at scale. Satellite imagery offers large-scale, cost-effective monitoring for high-throughput phenotyping, capturing temporal and spatial dynamics across entire breeding trials or production fields (Pinto et al., 2023; Zhang et al., 2020). Multispectral and hyperspectral sensors aboard satellites quantify vegetation indices, canopy cover, biomass proxies, and more overtime. Although spatial resolution is coarser than UAVs, satellites enable frequent revisit cycles (Roy et al., 2021) and global coverage, facilitating multi-environment comparisons and long-term trend analysis.

Drone Imaging: Off-the-shelf drones equipped with RGB and multispectral cameras (e.g., Mavic 3M) allow breeders to survey research plots from the air. Drones offer flexible, good resolution phenotyping solutions by capturing detailed RGB, multispectral, thermal, and LiDAR data at plot or plant level (Gano et al., 2024; Yang et al., 2017). They enable consistent and repeatable surveys to quantify precisely canopy structure, biomass proxies, stress responses, and growth dynamics. Autonomous flight planning and RTK geo referencing streamlines accurate image acquisition, while integration with AI-powered models enhances trait extraction for on-time decision-making during the season.

Flexible Pole Systems: To capture fine-scale variation in small plot trial or on a targeted population, Hiphen developed Literal with the French technical institute Arvalis. Literal is a telescopic pole harnessed by an operator, carrying synchronized RGB and NIR sensors (De Solan et al., 2024). Literal fills the gap between manual scoring in the field and UAV surveys, enabling precise traits extraction like wheat head density assessment to support and validate yield estimations.

Ground-based Rovers: The PhenoMobile represents the cutting edge in field phenotyping. These ground robots navigate autonomously, integrating LiDAR, hyperspectral, thermal, RGB, Multispectral and high-power flash modules to measure stress indicators (water deficit, disease symptoms) under controlled illumination, delivering highly repeatable data to tackle very specific agronomic challenges (Frédéric Baret et al., 2019).

b. Controlled-Environment and Post-Harvest Systems

Portable Quality Analysis – PhenoLite: A handheld unit combining an RGB camera and a dedicated mobile app, allowing its operator to perform rapid quality assessments of fruits and vegetables during harvest, streamlining post-harvest quality assessment workflows.

High-Throughput Phenotyping Stations – PhenoStation: Designed for greenhouses labs and industrial facilities, PhenoStation scales up PhenoLite's capabilities with larger screening throughput, multiple sensor arrays (3D, Hyperspectral, Thermal…), integrated weighing, and tailor-made designs to fit operational and logistic constraints.

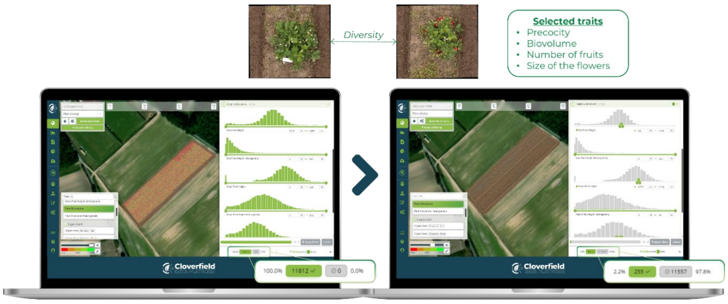
c. Advances in AI and Data Analytics

Recent advances in artificial intelligence, especially deep learning and computer vision—have transformed digital plant phenotyping by automating complex trait extraction from vast image datasets. Convolutional neural networks now segment organs (leaves, flowers, etc…) (Guo, 2023) and start helping quantifying traits like leaf area (Marie Weiss et al., 2020; M. Weiss et al., 2020), chlorophyll content, and stress symptoms at the organ level with great accuracy, even though it's still work in progress to make this available for multiple crops as training datasets needs to be deep and diverse (David et al., 2023). Also, multimodal models fusing RGB, multispectral, thermal, or LiDAR data to predict yield and resilience weeks before harvest are starting to being available and help deliver even more value from the sensors data, while transfer learning enables rapid adaptation across different species and environments. So overall, recent AI innovations help speed up the development and delivery of high-throughput, scalable, and reproducible measurements, empowering breeders to accelerate selection cycles, enhance data-driven decisions, and drive genetic gain more efficiently during the selection process.

Impact on Breeding Programs

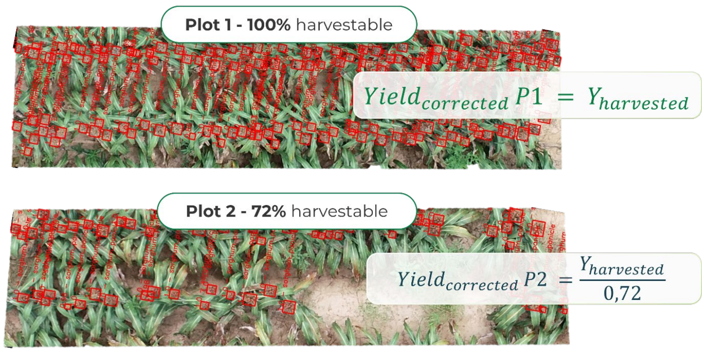
a. Accelerating Early-Stage Selection in Nurseries

In typical F_1 nurseries with >10,000 lines per trial, manual pre-screening is impractical. Using drone imagery processed in the Cloverfield data platform, breeders can filter the top 10% of candidates—those closest to an ideal ideotype—in under 15 minutes. These lines are tagged for subsequent in-depth field testing, dramatically reducing labor and speeding the pipeline.



b. Yield Correction in Advanced Trials

Advanced yield trials suffer from spatial heterogeneity and border effects that bias manual yield estimates. By computing traits such as plant gaps, border effect indices, and harvestable area, Hiphen's analytics refine genotype performance estimates, considering G×E interactions to strengthen selection decisions.

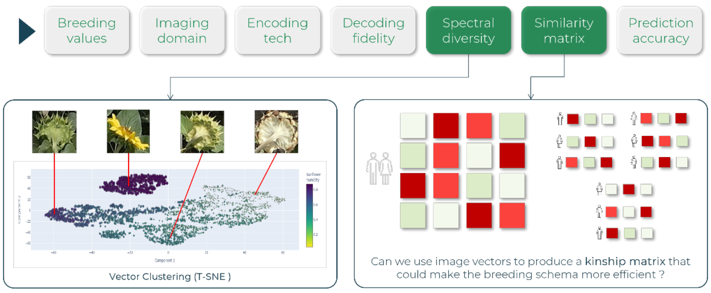


c. Registration Trials and Product Launch Support

Standardization and repeatability are critical when registering new varieties. Hiphen's imagery and trait outputs serve as objective proof of performance, enabling seed companies to compile robust dossiers for regulatory submissions and marketing, supported by quantitative visual evidence.

d. Phenomics-Based Prediction

By encoding image-derived spectral signatures into high-dimensional feature matrices, and training AI models to map diversity and find similarities, breeders can predict later-season traits—such as grain yield, disease resistance or fruit aspect—at early growth stages. This phenomic prediction approach reduces field cycle times and guides crossing decisions with greater foresight in combination with genomic selection.



Performance Metrics & Adoption

- Scale of Operation: Over the last ten years, Hiphen has processed >12,000 drone flights, screening more than 25 million plots across 23 countries for dozens of public and private sector clients.
- Data Volume: Each campaign routinely generates Gigabytes of imagery, which Hiphen's Cloverfield Data Platform ingests, processes, and manages to deliver actionable insights to the breeders.
- Trait Diversity: With ~70 traits available, clients enrich their data streams to build integrated G×E models, combining genomics with phenomics to streamline their selection process.

Despite this progress, widespread adoption faces hurdles: managing massive data flows, standardizing protocols across stakeholders, training users, and justifying up-front investment. Hiphen addresses these by offering intuitive interfaces, comprehensive training ("enablement"), and participating in EU-funded and international research consortia to refine workflows and learn from a great diversity of users and use cases.

Challenges and Future Directions

- Data Integration: Harmonizing phenomic and genomic datasets remain non-trivial. Tools for joint analysis of these heterogeneous data types will be crucial.
- Standardization: Establishing community standards for sensor calibration, trait definitions, and metadata to ensure cross-study comparability.
- Scalability: Developing more compact, cost-effective, real-time sensors and edge-computing solutions to reduce data latency.
- User Adoption: Enhancing user experience and minimizing technical barriers through plug-and-play hardware and AI-driven "auto-analysis" pipelines.

Hoping that the next decade will see digital phenotyping evolve from specialized projects into routine breeding practices with greater emphasis on real-time in-season decision support for the breeders.

Perspectives and Conclusion

Digital phenotyping has moved from experimental proof-of-concept to a core component of modern plant breeding. Hiphen's integrated product suite—drones, robots, handheld devices, and data platforms—addresses the full spectrum of breeder needs, from early-generation nurseries to final registration trials and even post-harvest quality control and shelf-life assessments. By enabling rapid, objective, and high-throughput trait measurement, these tools accelerate genetic gain, reduce bias, and enrich data for advanced analytics.

Looking ahead, the seamless integration of phenomics, genomic, and environmental data will drive even more accurate predictions and targeted breeding strategies. Yet, preserving the experiential knowledge of breeders and agronomists is paramount: digital tools should augment, not replace, human expertise. Through ongoing innovation, collaboration with public research institutes, and a relentless focus on usability, Hiphen will continue to empower the plant-breeding community to meet the challenges of tomorrow's agriculture.

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Plant Breeding Accelerated by Heavy-Ion Mutagenesis

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Introduction

We have studied heavy-ion mutagenesis and developed new breeding techniques using heavy-ion irradiation in the RI-Beam Factory (RIBF). Linear energy transfer (LET) is an important factor for ion-beam mutagenesis. LET is the energy an ionising particle gives the target, for example, plant tissue, per unit path length along its track. We found the optimal LET for mutation induction, designed as LETmax, was 30 keV/mm in Arabidopsis (Kazama et al, 2008). Heavy-ion beams with different LET induce different types and sizes of mutations (Kazama et al, 2011and 2017, Hirano et al, 2012 and 2015). Whole-genome analysis with high-throughput sequencing is now a powerful tool for characterising the nature of induced mutations and identifying the causative genes. Heavy-ion accelerator facilities that have been used for breeding purposes are RIBF, the Takasaki Ion Accelerators for Advanced Radiation Application (TIARA) and the Wakasawan Energy Research center Multipurpose Accelerator System with Synchrotron and Tandem (W-MAST) in Japan. More than 90 new varieties have been developed using ion beam irradiation in those three facilities. In this article, we introduce the mutation effect of LET in rice, its influence on genetic mutations, and the isolation of high-yield genes. We also introduce research on sweet potato for practical use.

Phenotype		M_2	M_3	
		Candidate	Fixed	Segregated
Plant height	Tall	9	1	0
	Dwarf	24	6	3
Flowering	Early	3	2	0
	Late	1 (Sterile)	-	-
Grain size	Large	7	1	0
Leaf color or shape	Stripe	11	2	6
	Narrow	1	0	1

Table 1. Rice mutants selected in the paddy field induced by Ar-ion irradiation

LET effect of mutation rates and mutation types

High-LET radiation, such as ion beams, causes more localised, dense ionisation within cells than low-LET radiation. Low-LET radiation produces secondary radicals throughout the cell nucleus and causes more single-strand breaks than double-strand breaks in irradiated DNA. In contrast, high-LET radiation densely deposits its energy in a localized region along the particle path and causes marked DNA damage, breaking both the DNA strands and the histones. Those clusters of DNA damage can only be repaired incompletely by the cells, which induce mutations. The ion particles can vary in mass from a simple proton to a uranium atom. Although the alpha ray can be considered a helium ion beam, ion beams are usually generated through ion accelerators. A heavier, highly charged ion is selected with a low velocity when a high LET is required. A higher LET means a lower dose is needed in plants to achieve the same biological effect

(Kazama et al, 2008; Abe et al, 2021), and dose in Gy is proportional to the LET in keV/mm and the number of particles. The number of ions passing an area decreases at the same dose when the LET is high. Therefore, we predicted that there was an appropriate LET for mutagenesis.

We irradiated dry rice seeds with a combination of LET of 23-650 keV/mm and doses of 5-200 Gy and observed the survival rate in M_1 plants and the frequency of chlorophyll-deficient mutants in M_2 lines. Figure 1 shows the highest mutation rate at doses for each LET.

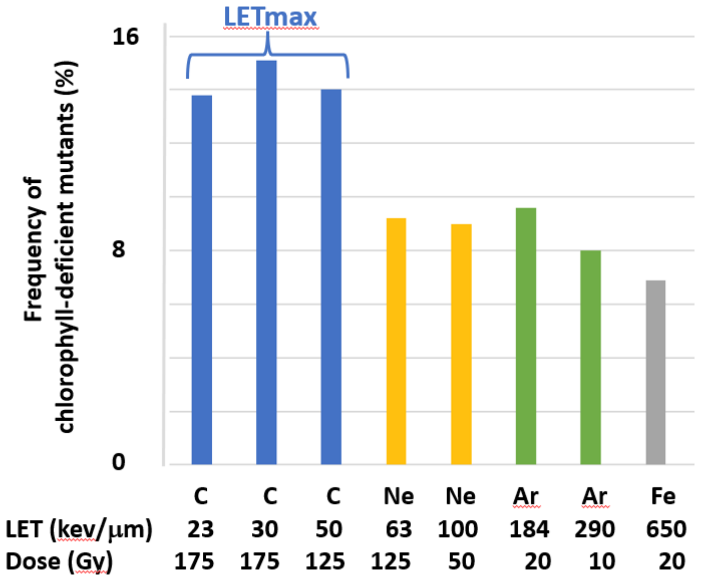

Figure 1. Optimum LET for mutation induction in rice

These irradiation conditions were in the dose range that did not reduce the survival rate, and the LETmax for C-ion that gave the highest mutation rate was 23-50 keV/mm (Hayashi et al, 2016 and 2018). Subsequently, mutants were selected in the M_2 plants, and the causative genes of mutant lines with stable traits in the M_3 plants were isolated using PCR-based mutation analysis, whole-exome and whole-genome analysis. We performed a detailed study on the molecular nature of DNA alterations induced by heavy-ion irradiation with different LET using the mutant's causative gene. As a result, there was no difference in the mutation types induced by gamma-ray irradiation and C-ion irradiation with 23-30 keV/mm, and most of the mutations were small deletion less than 100 bp (Morita et al, 2009 and 2021, Figure 2).

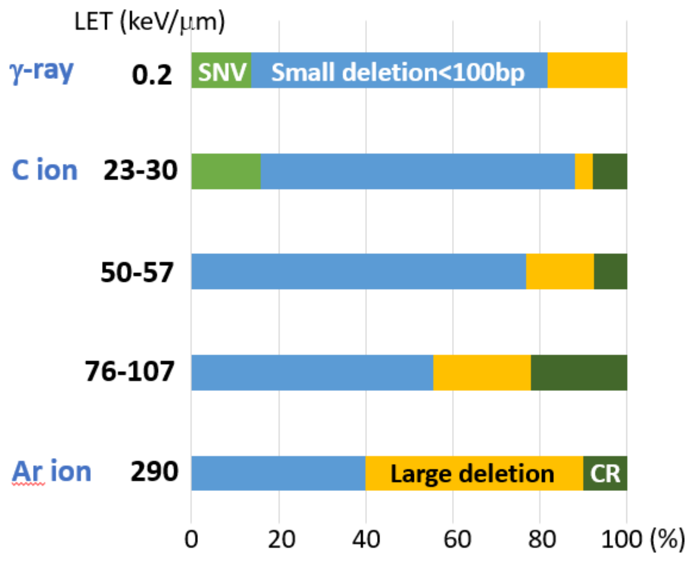

Figure 2. Comparison of mutation types in rice mutants

Furthermore, the proportion of small deletions decreased, and the proportion of large deletions and chromosomal rearrangements increased as the LET increased from 50–57 keV/mm (Morita et al, 2021) to 76–107 keV/mm (Sato et al, 2007 and 2008, Ishikawa et al, 2012, Oono et al, 2020) with C-ion irradiation, and 290 keV/mm with Ar-ion irradiation. Ar-ion beam at 290 keV/mm, which has a highly lethal effect, showed the proportion of small deletions was low, while that of large deletions and chromosomal rearrangements was high (Morita et al, 2021). From these results, LETmax is effective for mutation breeding because of its high mutation rate. Since most mutations involve small deletions, these are sufficient to disrupt a single gene. Thus, irradiation can efficiently generate knockout mutations of a target gene and can be applied to reverse genetics. On the other hand, when you aim for a trait that has yet to appear, argon irradiation is recommended, as this induces multiple gene disruptions and chromosome rearrangements.

Identification of a novel rice gene conferring high yield using mutants

Imbibed seeds of rice (*Oryza sativa* ssp. japonica 'Nipponbare') were irradiated with Ar ions (5 Gy, 290 keV/µm), and M_2 populations were grown in the field for mutant screening. A total of 678 M_2 lines (40 individuals per line) were cultivated, resulting in the selection of various mutants exhibiting diverse phenotypes such as plant height, heading date, seed morphology, and leaf colour and shape (Table 1). Among the selected mutants, the Ar5-76 line, which had longer seeds than 'Nipponbare', was identified and subjected to detailed analysis. Although the number of panicles, grains per panicle, and fertility rate were similar to those of 'Nipponbare', the 1000-grain weight increased due to an increase in seed length. Consequently, Ar5-76 showed a higher yield per unit area than 'Nipponbare', with increases of 1.08-fold in 2014 and 1.16-fold in 2016. (Morita et al., 2019).

We performed whole-genome sequencing (WGS) analysis to identify the causative gene for the long-grain phenotype. Mutations were detected using a bioinformatics pipeline (Ichida et al., 2019). A total of 247 mutations were identified, 15 located in genic regions, and 12 were found to be homozygous. The types of mutations included nine missense mutations, one frameshift mutation caused by a 1-bp deletion, one in-frame deletion caused by a 6-bp deletion, and one SNV at a splice donor site. To perform linkage analysis, we grew F_2 plants obtained from a cross between 'Nipponbare' and the mutant, and harvested their seeds individually from each F_2 plant. Using the average seed length from each F_2 plant as an indicator, the gene Os06g0675200, which harboured a frameshift mutation caused by a 1-bp deletion, was found to be linked to the long-grain phenotype. A screenshot using IGV software confirming the 1-bp deletion in the Os06g0675200 gene is shown in Figure 3. Using the CRISPR/Cas9 system, we generated transgenic plants with a 1-bp insertion in the Os06g0675200 gene of 'Nipponbare'. As the transgenic plants produced longer seeds, we confirmed that this gene was responsible for the long-grain phenotype and named it *long grain 1* (*lin1*).

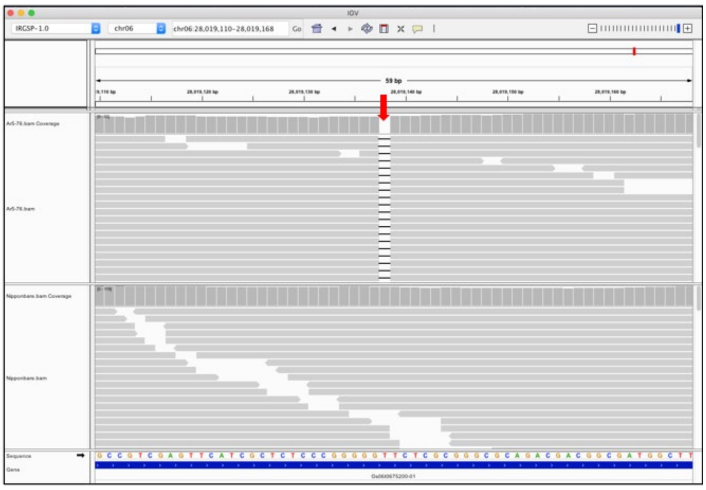

Figure 3. A 1-bp deletion in the Os06g0675200 gene visualized using IGV software

Introducing mutations into the *LIN1* gene will confer a long-grain phenotype and potentially increase yield. Therefore, using the TASUKE genome browser (http://ricegenomes.dna.affrc.go.jp/, currently offline), we examined the presence or absence of mutations in the *LIN1* gene across 25 rice varieties, including 15 temperate japonica, 9 indica, and 1 aus variety. Among these, the *LIN1* gene sequence was identical to that of 'Nipponbare' in all 15 temperate japonica and 6 indica varieties. In contrast, 3 indica varieties and 1 aus variety shared a common SNP (T to C) that results in a single amino acid substitution. Although the effect of this SNP on seed length remains unclear, introducing mutations into the *LIN1* gene in varieties with the same sequence as 'Nipponbare' may enhance yield.

Sweet potato breeding by heavy-ion irradiation

Sweet potato (*Ipomoea batatas* [L.] Lam.) is one of the most important food crops and plays a critical role in food supply and safety worldwide. In Japan, many sweet potato cultivars are grown for various applications, such as table use, processed foods, and alcohol and starch production, and these were basically bred by cross-breeding. However, sweet potato is a hexaploid plant (2n = 6x = 90) with a large and highly polymorphic genome, and the most cultivars of sweet potato show cross- and self-incompatibility. These characteristics prevent efficient breeding. Heavy-ion beam mutagenesis has been attempted to expand genetic variation and accelerate the development of new cultivars in sweet potato.

In vitro cultured shoots with an axillary bud of 'Beniharuka', which is widely cultivated for table use in Japan, were irradiated with C ions (30 keV/µm) and Ar ions (184 keV/µm). Regenerated shoot from each irradiated bud was regarded as an independent irradiated line, and the irradiated lines were maintained *in vitro* (Figure 4).

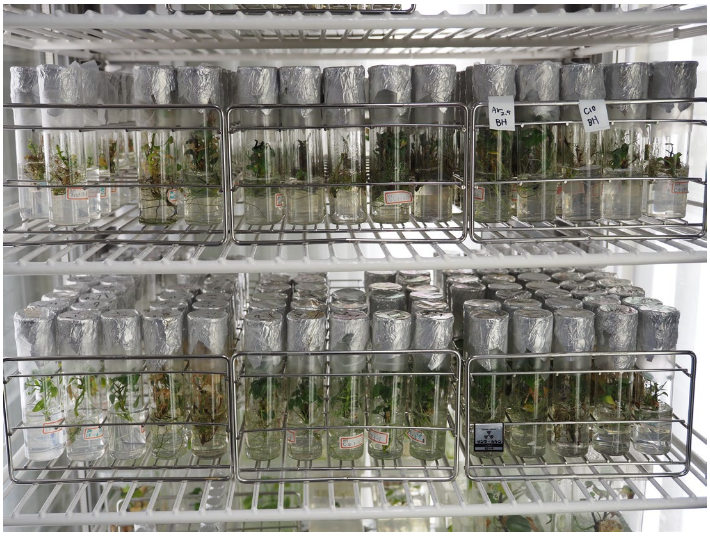

Figure 4. Heavy ion irradiate lines maintained in vitro

In the field screening, some irradiated lines showed inhibited or no storage root phenotype, and the high-yield mutant candidates were also obtained (Figure 5; Park et al, 2022). One irradiated line showed decreased

DNA content and inhibition of storage root formation during the early developmental transition stage (Park et al, 2023). These results suggest that heavy-ion beam mutagenesis effectively broadens the range of the phenotypes corresponding to storage root formation in hexaploid sweet potato. The irradiated lines are valuable genetic resources for the breeding and functional study of the mechanism of storage root formation.

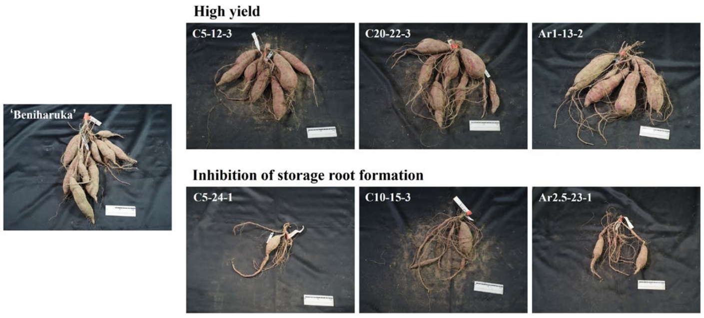

Figure 5. Phenotypes of storage root in heavy-ion irradiated lines

Future Perspectives

Innovations in molecular biology techniques, such as DNA and RNA sequencing, have made it possible not only to search for homozygous causative genes but also to clarify the structure of chromosomal rearrangements, including large-scale deletions, and changes in gene expression levels due to structural changes. It is also possible to elucidate phenomena that were previously difficult to discover. The number of fragmented chromosomes increased with Ar-ion (290 keV/µm) and Fe-ion (640 keV/µm) irradiation, and some of these fragments are shown to be heritable （Ishii et al, 2025). Large heterozygous deletions result in incomplete dominance (Ikoma et al, 2025). The new combination of genes and promoters resulting from large deletions induces immature amino acid production and changes the phenotype. Duplication mutations cause dominant traits. Mutants have become increasingly useful and important in modern genetic studies, when combined with genome editing techniques, the discovery of genes that control important traits and revealing the functions and mechanisms underlying their operation.

We revealed that deletion sizes were similar between different LETs (100 to 290 keV/µm) that their upper limit was affected by the distribution of essential genes. The LET 100 keV/µm is enough to disrupt tandemly arrayed genes in Arabidopsis genome (Ishii et al, 2024). We performed whole-genome analysis of a new unshu mandarin cultivar, 'Harushizuka', developed using Ne-ion irradiation (62 keV/µm), and successfully created DNA markers for cultivar identification. On the other hand, a new method was reported for selecting irradiated C-ion beam orchids that did not change in characteristics, and then using the mutation sites to create DNA markers for cultivar identification to develop new cultivars (Furukawa et al, 2024).

Two large heavy-ion accelerator facilities with industrial applications in mind, HIAF in China (Huizhou) and RAON in Republic of Korea (Daejeon), have begun operation. The number of facilities capable of conducting heavy-ion beam experiments for mutation breeding will likely increase in Asia. The RIKEN Nishina Center is a member of the Mutation breeding network, and ion-beam irradiation experiments can be conducted as a collaborative research project. We will continue to work with physicists to support users and aim to become a global hub for heavy-ion breeding technology. A special issue on research into mutation induction using ion beams has been published in the December 2021 issue of CYTOLOGIA (Japan Mendel Society, https://www.jstage.jst.go.jp/browse/cytologia/86/0/_contents/-char/en). If you are interested in this technology, please take a look

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Advancing Breeding Technologies to Boost Productivity and Resilience in Vegetatively Propagated Crops: The Case of Cassava and Beyond

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1. Introduction

In vegetatively propagated crops (VPC), individuals with superior performance can be clonally reproduced for commercial exploitation without genetic variation. As a result, farmers immediately benefit from the genetic advantages of outstanding clones. However, vegetative reproduction enhances the incidence of pests and diseases because planting material often acts as both a source of inoculum and an efficient means of pathogen dispersal.

Clonal reproduction enables the isolation of genetic variation among siblings within a given half- or full-sib family from the micro-environmental conditions affecting individual plant growth. Such an approach is not feasible in sexually propagated crops unless the progenitors are inbred - in which case, however, there is no genetic variation within the family. Measuring genetic variation within families allows a test for epistasis a strategy that is generally not applicable in grain crops. Despite this advantage, it has not been widely exploited except in cassava.

VPC also present significant challenges for breeders. Self- or cross-incompatibility is common in certain VPC, which are often polyploid, complicating both breeding efforts and quantitative genetic analyses (Jansky and Spooner, 2018). Additionally, the elimination of deleterious alleles in polyploid species is particularly difficult.

2. Breeding clonal crops

Most VPC have been bred through phenotypic mass selection (Ceballos et al., 2015; Jansky and Spooner, 2018; Lindqvist-Kreuze et al., 2024). The progenitors are typically highly heterozygous, and breeders focus on identifying individual genotypes with exceptional performance which are then clonally multiplied and eventually released as varieties. Genetically, clones are hybrids.

Inbreeding depression, heterosis and non-additive genetic effects are often significant for complex traits in VPC (Bradshaw, 2007; Ceballos et al., 2015; Gopal, 2014; Gurmu et al., 2018; Mendez de Paula, 2020). A common limitation of VPC is their generally poorly developed population structures compared to grain crops. No heterotic patterns have been identified, and as a result - despite its importance - heterosis remains unpredictable and its exploitation inefficient.

Farmers benefit from the full range of genetic effects - additive, dominance, and epistatic - when cultivating outstanding clones (Jennings and Iglesias, 2002). However, most conventional recurrent selection systems, including genomic selection, are limited in their ability to maximize the frequency of favourable gene combinations, whether within or between loci. While the genetic superiority of elite clones can be fully exploited by farmers, a considerable proportion of that superiority - particularly non-additive genetic effects - is lost when those clones are used as progenitors in breeding programs. Reciprocal recurrent selection has the potential of exploiting heterosis (Lindqvist-Kreuze et al., 2024; Mendes de Paula et al., 2022). However, the most efficient strategy to exploit heterosis is using inbred progenitors derived from gene pools from different heterotic groups (Mikel, 2008).

Cassava, an important crop, has the advantage of being diploid and can serve as a model for the breeding of other VPCs.

3. Boosting productivity and resilience: conventional strategies

Phenotypic mass recurrent selection remains the backbone of breeding VPC, including cassava. Several innovations that have been introduced to enhance the efficiency of conventional breeding are briefly described below.

3.1 Manipulating flowering biology

The vegetative reproduction of VPC has relaxed the need for their efficient sexual reproduction. Crossing elite progenitors and obtaining botanical seeds from sexual crosses in VPC is often challenging, time-consuming, labor-intensive, and ultimately costly.

Cassava's flowering biology has negatively impacted its genetic improvement. Once flowering is induced, buds located just below the inflorescence begin to sprout, allowing continued plant growth (Alves, 2002; Jennings and Iglesias, 2002). As a result, each flowering event triggers branching. While some genotypes flower early and frequently (3-5 times during a growth cycle), others flower infrequently, late, or not at all. Both flowering and branching patterns in cassava are highly heritable traits. Farmers prefer erect, non-branching types because they facilitate cultural practices, and the planting material is easier to transport and can be stored for longer periods which is a critical adaptation to climate change. However, this preference presents a significant challenge for breeders, as genotypes with erect plant architecture tend to flower late and infrequently.

Extending the photoperiod with red light, applying plant growth regulators, and/or pruning branches to enhance apical dominance of the inflorescences have successfully allowed manipulating the reproductive biology of cassava. These methods have shortened the duration of each breeding cycle, reduced the costs associated with crossing nurseries, and made the introduction of inbreeding in cassava possible (Hyde et al., 2024; Pineda et al., 2020a; 2020b).

3.2 Focused breeding objectives

Throughout the late 20th century, cassava breeding projects primarily focused on increasing productivity and enhancing resistance to diseases and pests. However, little attention was initially given to quality traits, which are fundamental for farmer and consumer acceptance and present critical opportunities for innovation. As a result, the released varieties, while highly productive, often lacked the essential quality attributes needed to meet the diverse requirements of ethnic food preparations made from cassava roots (Dufour et al., 2021). Consequently, the adoption of improved varieties is significantly lower when cassava is used for direct human consumption compared to its use in starch production, animal feed, or ethanol (Ceballos et al., 2021).

Over the past two decades, four clearly defined cassava product profiles have gradually emerged:

a) enhanced nutritional quality; b) good cooking quality (fresh or processed) for human consumption; c) high and stable dry matter yield for industrial applications and animal feed; and d) specialized starch quality traits (such as low amylose) for various industrial uses. More importantly, these product profiles provide a set of clearly defined breeding goals.

Starch quality traits have a significant influence on functional properties. These traits offer valuable opportunities for developing high-value specialty cassava varieties and inherently strengthen the linkages between farmers, and processors/industry. Inducing mutations and screening germplasm collections are effective strategies for identifying or creating such desirable traits in cassava (Ceballos et al., 2021). Social, economic and environmental implications strongly justify the development of varieties with natural or induced tolerance to herbicides.

3.3 Introduction of inbreeding

Dewey (1966) stated that "*the full potential and effectiveness of a plant-breeding program can be realized only when the reproductive, genetic, and breeding behaviour of a species is known and understood."* Early efforts to develop homozygous cassava were interrupted because, during the process, genotypes with early branching - associated with early flowering - were inadvertently favoured. This led to a plant phenotype that was highly undesirable (Ceballos et al., 2015). However, it is now possible to self-pollinate cassava and there is no longer a biological barrier to producing fully inbred cassava. Breakthrough research is also underway in potato breeding, focusing on the use of inbred progenitors (Lindhout et al. 2011; Lindqvist-Kreuze et al., 2024; Zhang et al., 2021).

By default, inbreeding reduces genetic load, and useful recessive traits can be readily identified. Marker-assisted selection (MAS) has traditionally been limited to simple, monogenic traits, particularly through the accelerated backcross introgression that requires inbred progenitors (Xu & Crouch, 2008). Trait introgression is very inefficient when heterozygous progenitors are used. Inbred lines enhance the efficiency and adaptability of breeding programs by reducing the time and cost involved in developing new varieties with specific desirable traits (Zhang et al., 2021, 2024). Moreover, inbreeding enhances the efficiency of genomic selection and the accuracy of predictive estimates (Melchert et al., 2025). The exploitation of heterosis is also greatly facilitated by inbreeding, as within-family variation becomes negligible and additive variation between inbred lines is increased (Ceballos et al., 2015).

4. Boosting productivity and resilience: new technologies

In the past three decades a great diversity of technologies have been developed and gradually implemented in cassava and other VPC.

4.1 Genetic transformation and gene editing.

Cassava transformation date back to the 1990s. More recently, CRISPR-Cas9-mediated gene editing became an important protocol for the introduction of desirable genetic variability in cassava. Efforts spanned various areas, including detoxifying cyanides, increasing herbicide resistance, root starch content and quality traits, leaf retention, resistance to viral and bacterial diseases, cold tolerance, and nutritional quality (Liu et al., 2011; Ma et al., 2025; Zhang et al., 2011). To date, no genetically modified or gene-edited cassava varieties have been released. Governmental regulations heavily oversee food products derived from biotechnology, with only a select few countries permitting their usage (Turnbull et al., 2021).

Despite the limited deployment of germplasm developed through genetic transformation or gene editing, these technologies have proven effective in validating the expression of target traits at specific loci in the cassava genome.

4.2 Genomic selection

Genomic selection (GS) uses genotypic and phenotypic data for estimation of genomic breeding values (GEBV), expediting the development of superior cassava varieties. Previous efforts have been made to assess the breeding values of progenitors using large phenotypic databases (Ceballos et al., 2016). GS technology holds substantial promises for fast-tracking progress in cassava breeding, especially in clonally propagated crops, where it has demonstrated significantly higher genetic gain compared to phenotypic selection, particularly when halving the generation cycle (de Oliveira et al., 2012), particularly for traits controlled by the additive genetic variance.

Several articles have reported results of ongoing work implementing GS in cassava. As predicted, the relative importance of non-additive genetic effects (such as dominance and epistasis), along with the substantial within-family variation, hinders the overall impact of this technology particularly for yield (Ceballos et al, 2015; 2021; de Andrade et al., 2019; Phumichai et al. 2022; Wolfe et al., 2016a; 2016b).

4.3 Identification of Germplasm Carrying Useful Traits

There is a valuable opportunity to apply molecular tools for identifying useful traits hidden within germplasm collections. Eco-TILLING, a technique that explores natural genetic variation in populations, has proven effective in plants for detecting SNPs associated with variation in specific target loci (Comai et al., 2004).

Eco-TILLING is like a “molecular sieving” of DNA extracted from accessions in germplasm collections. Its application in cassava is fully aligned with the need for focused breeding objectives described above. This strategy requires a clear definition of target genes that have been identified because of their usefulness. Duitama et al. (2017), conducted preliminary screening of accessions from CIAT’s germplasm collection targeting natural variation for herbicide tolerance and starch biosynthesis traits. Other target traits could be low cyanogenic potential or haploid inducer(s).

5. Concluding remarks

Basic knowledge in key areas relevant to breeding vegetatively propagated crops (VPCs) remains limited. In cassava, for instance, advances in manipulating flowering, as well as in understanding embryo development and pollen tube growth, have only been achieved recently. While significant resources are currently being directed toward molecular breeding, these efforts often proceed in the absence of essential knowledge that continues to limit progress in VPC improvement. Additionally, critical expertise within the scientific community is gradually being lost. For example, preparing sections for microscope analysis requires not only technical knowledge but also a level of craftsmanship that is increasingly rare. Similarly, the number of experts capable of accurately interpreting these sections (e.g., for embryo development studies) is rapidly declining.

Innovative molecular approaches have typically been developed for grain crops, which rely on efficient sexual reproduction and are generally bred using inbred progenitors - conditions that are often not met by VPC. Molecular breeders offer valuable tools for tracking genes in segregating populations. However, developing useful varieties requires not only the ability to track genes but also to control how they segregate. The challenges of trait introgression in VPC underscore the urgent need to address the critical limitations that continue to hinder their breeding. It is, therefore, fundamental that innovative and conventional approaches are properly integrated. Technology-driven decisions do not always lead to the most effective approaches for developing successful varieties.

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Partnership, Collaboration and Knowledge Sharing

Experts Meeting on Future Perspectives in Plant Breeding and Genetics using Nuclear Techniques and Consultancy Meeting for New Coordinated Research Projects (CRPs)

Vienna, Austria, 17-21 March 2025

The Consultancy Meeting for the new Coordinated Research Projects entitled "Building Resilience to Climate Change: Enhancing Biodiversity in Annual and Perennial Crops with Nuclear Innovations" and "Developing Enabling Technologies for Improved Plant Health using Nuclear Techniques - Transboundary Pathogens Affecting Roots and Tubers" was held from 17 to 21 March 2025 at the Vienna International Centre, Austria. These Consultancy Meetings were conducted in parallel with the "Experts Meeting on Future Perspectives in Plant Breeding and Genetics using Nuclear Techniques".

The Experts Meeting brought together international experts from diverse fields to discuss the contribution of mutation breeding in vegetatively propagated crops research and development. Topics discussed included: current breeding approaches, nutritional quality enhancement, emerging and transboundary pests and diseases, as well as promising new technologies.

A special session was dedicated to collect experts' suggestions for future Plant Breeding and Genetics activities. Experts provided several key recommendations during the meeting. When it comes to selecting critical traits for mutation breeding, they emphasized the importance of balancing impact and feasibility. Traits such as herbicide resistance should be considered from an agricultural system perspective, and it is advised to begin with simpler traits before progressing to more complex ones, with a reminder that most mutations are recessive. Additionally, the type of physical mutagens used can influence whether mutations are dominant or recessive and identifying causal mutations could provide valuable insights.

Regarding the key crops for mutation breeding, experts suggested focusing on crops such as yam, mango, cacao, and orphan crops with limited genetic variation. They also highlighted the potential of edible fungi, algae, polyploid crops with complex genomes, and medicinal plants. The use of microbes for food processing was noted as another promising area as well as looking for complementarity with existing CGIAR and other international agricultural research organizations' initiatives.

To accelerate the efficiency and impact of mutation breeding, the experts recommended leveraging emerging technologies like genomics, phenomics, and artificial intelligence. Developing frameworks for identifying and tracking mutations, creating mutation catalogues, and using precise, affordable phenotyping methods were among the suggested approaches. Furthermore, experts recommended focusing on reverse genetics and standardizing methods for identifying chromosomal rearrangements.

For integrating mutation breeding into national and global breeding programs, experts proposed focusing on high-value diseases and crossing systems. They suggested leveraging connections with organizations like the FAO and using initiatives like "Seeds without Borders" in Asia and Africa to promote seed exchange, with a strong emphasis on quality control and capacity building.

Lastly, for strengthening capacity-building activities, the experts identified several opportunities for collaboration, including training in statistics, experimental design, speed breeding, and mutation breeding. They also recommended creating a common platform for bioinformatic data analysis and facilitating information sharing under CRPs to improve knowledge dissemination and research collaboration.

These recommendations collectively focus on advancing mutation breeding to improve crop resilience, food security, and foster global research partnerships.

Vienna International Centre (VIC) Daughters' Day 2025 Celebration

Vienna, Austria, 24 April 2025

This event aimed to engage adolescent girls from various schools in Venna in educational activities aimed at improving crop production through nuclear applications and biotechnologies, thereby addressing climate change-related food security challenges. The event aimed to show how innovative mutation breeding technologies can help mitigate the effects of droughts, rising temperatures, and increased disease incidence, ensuring adequate food supply.

The celebration included a brief video on how nuclear techniques and biotechnologies are applied in crop improvement, showcasing achievements in Member States and encouraging young girls' interest in science and sustainable agriculture. Over forty-five adolescent girls participated in a hands-on demonstration of bananas and coffee from the Plant Breeding and Genetics laboratory.

Strengthening Sustainable Cotton Partnerships: IAEA Participation in the Cotton Partnership Steering Committee

Cairo, Egypt, 28-29 April 2025

The Joint FAO/IAEA Centre's Plant Breeding and Genetics (PBG) Section participated in the Steering Committee of the *Partenariat pour le Coton* (Cotton Partnership) to support sustainable cotton production in C-4+ countries.

Ms Fatma Sarsu, Acting Section Head, represented the IAEA in discussions focused on financing mechanisms for the cotton-textile-garment value chain, review of the draft Terms of Reference , and a proposed dedicated fund for capacity building and technical activities. The IAEA's ongoing work with C-4+ countries on climate-resilient crop production was highlighted, along with its proposed role in supporting sustainable cotton practices through nuclear techniques.

Key outcomes included agreement on a dedicated fund, a roadmap for finalizing the Terms of Reference, and plans to celebrate *World Cotton Day 2025* at FAO Headquarters in Rome, coinciding with FAO's 80th anniversary in October. The mission reinforced FAO's and IAEA's commitment to advancing sustainable agriculture in the cotton sector and strengthening partnerships with C-4+ countries.

Strengthening Collaboration with ICARDA for Sustainable Agriculture in Drylands

Rabat, Morocco, 15-16 May 2025

Ms Fatma Sarsu, Acting Section Head of the Plant Breeding and Genetics (PBG) Section at the Joint FAO/IAEA Centre, participated in the International Center for Agricultural Research in the Dry Areas' (ICARDA) Agricultural Field Day and the inauguration of the Speed Breeding Facility. The visit aimed to strengthen collaboration under the CGIAR-IAEA Memorandum of Understanding (MoU) and explore joint research opportunities.

During the event, Ms Sarsu engaged in fruitful discussions with ICARDA staff, national agricultural research system (NARS) representatives, and members of ICARDA's Board of Trustees. Key outcomes of the mission include agreement on the development of a collaborative project titled "*Enhancing Genetic Improvement of Chickpea, Lentil, and Faba Bean Using Nuclear Techniques for Herbicide Resistance and Mechanized Harvesting in Dryland Agro-Ecosystems*".

The project will focus on developing improved varieties of chickpea, lentil, and faba bean with enhanced traits - specifically, herbicide resistance and suitability for mechanized harvesting - by applying induced mutagenesis and complementary biotechnologies. This collaboration marks an important step toward advancing climate-resilient and sustainable agricultural practices in dryland regions.

Joint FAO/IAEA Participation in the 3rd International Laâyoune Forum on Biosaline and Arid Land Agriculture

Laâyoune, Morocco, 20-22 May 2025

The Joint FAO/IAEA Centre's Plant Breeding and Genetics (PBG) Section was represented at the 3rd International Laâyoune Forum on Biosaline and Arid Land Agriculture. Ms Fatma Sarsu, Acting Section Head, participated as a panelist in the Plenary Session *Cutting-Edge Science Towards Improving Crop Resilience to Drought and Salinity* and delivered a keynote address titled "*Climate-Smart Plant Breeding: Leveraging Nuclear Techniques and Innovative Approaches for Marginal Environments*".

Ms Sarsu's interventions highlighted the critical role of nuclear technologies, such as induced mutagenesis, in accelerating the development of drought- and salinity-tolerant crops for biosaline and arid agroecosystems. Success stories from Joint FAO/IAEA projects were shared, along with perspectives on integrating nuclear techniques with genomics, speed breeding, and phenotyping for enhanced crop improvement.

The forum attracted over 200 participants, including leading scientists, researchers, institutional leaders, and development partners. Ms Sarsu engaged in bilateral discussions with key stakeholders, notably representatives from Mohammed VI Polytechnic University (UM6P), to explore collaborative opportunities under the IAEA framework. Discussions focused on aligning research priorities, identifying target crops, and establishing pathways for technical cooperation or a coordinated research project to enhance crop resilience in challenging environments.

This mission strengthened partnerships, raised the visibility of the Joint FAO/IAEA Programme's work in climate-smart agriculture, and laid the foundation for impactful future collaborations, including a potential visit by UM6P representatives to the IAEA.

Coordinated Research Projects (CRPs)

Project Number	Ongoing CRPs	Project Officers
D22006	Enhanced Biotic-stress Tolerance of Pulses Towards Sustainable Intensification of Cropping Systems for Climate-change Adaptation (2019–2024)	A. Hingane F. Sarsu
D24014	Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops (2021–2025)	I.K. Bimpong F. Sarsu
D24015	Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development (2022-2027)	P. Mathur F. Sarsu
D23033	An Integrative Approach to Enhance Disease Resistance Against Fusarium Wilt (*Foc* TR4) in Banana – Phase II	C. Zorrilla P. Mathur
E43041	Application of Nuclear Techniques to Improve and Evaluate Nutritional and Health Benefits of Underutilised Crops	K. Bimpong V. Owino
D24016	Accelerated Genetic Improvement of Key Dryland Millets for Climate Change Adaptation	F. Sarsu A. Hingane
D24017	Induced Mutation for Accelerated Varietal Development in Cowpea for Africa	P. Mathur F. Sarsu
D24018	Building Resilience to Climate Change: Enhancing Biodiversity in Annual and Perennial Crops with Nuclear Innovations	C. Zorrilla F. Sarsu

CRP D22006: Enhanced Biotic-stress Tolerance of Pulses Towards Sustainable Intensification of Cropping Systems for Climate-change Adaptation

Project Officers: A. Hingane, F. Sarsu

The objective of this CRP is to increase the productivity of three key pulse crops: chickpea, cowpea, and lentil, which together constitute 40% of global pulse production. Mutation induction and genomics technologies are deployed to enhance the resistance of chickpea to the pod borer *Helicoverpa armigera*, cowpea to the pod borer *Maruca vitrata*, and lentil to combat *Stemphylium blight*.

Specific research objectives are: (1) to generate genetic diversity in chickpea, cowpea and lentil through mutagenesis for resistance to *Helicoverpa armigera, Maruca vitrata* and *Stemphylium botryosum*, respectively; (2) to develop and/or refine phenotyping tools to facilitate precise and efficient selection of biotic-stress resistance in selected pulse crops; and (3) to develop genomic tools for accelerated variety development for the selected pulse crops and associated traits of interest.

Over a period of four years, this mutant population (M1-M4) was evaluated in field conditions along with check for natural pod damage, number of pods per plant, laboratory bioassays (artificial feeding on pods/leaves), and biochemical parameters. Following thorough evaluation across seasons, 31 putative mutants were identified. These M4 mutants were further tested at four hotspot locations (Uttarakhand & Punjab-Northern Zone; Andhra Pradesh & Telangana-Southern Zone) in India for pod borer resistance and other diseases.

Based on preliminary results from two locations (M4) - Nandyal, Andhra Pradesh, and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Telangana - they have identified two promising mutant lines: ICCL86111-B-638-8 with erect type and ICCL 86111-B-8-4 series mutant line with spreading type morphology, exhibiting resistance to pod borer and major diseases compared to the wild/non-mutant line (ICCL 86111, with short stature and less spreading type).

CRP D24014: Development of Integrated Techniques for Mutation Breeding in Vegetatively Propagated and Horticultural Tree Crops

Project Officers: I.K. Bimpong, F. Sarsu

This CRP focuses on developing innovative genetic resources and technologies to accelerate breeding in vegetatively propagated crops (VPCs) and horticultural tree crops (HTCs). The approach involves inducing genetic diversity, ensuring chimera-free regeneration, and utilizing functional genomics. The project aims to produce stable mutant clones free from chimeras that possess desirable traits, as well as to publish protocols for phenotyping and genomic analysis to benefit Member States.

Since its commencement in 2021, participating research teams have achieved notable progress. At the University of Ghent in Belgium, researchers have successfully standardized protocols for cultivating large-scale *in vitro* shoots from olive explants, facilitating large-scale mutagenesis efforts and improving success rates. The CRP is also investigating the use of slow-release plant growth regulator nanoparticles and auxin beads to induce adventitious shoot or root meristems *in vitro*, leading to successful root regeneration.

At *Centro IFAPA "Alameda del Obispo"* in Spain, twelve early olive cultivars have been identified and subjected to mutation induction. Additionally, mutant cassava clones developed through the CRP have been tested in collaboration with International Institute of Tropical Agriculture (IITA) in northern Zambia, demonstrating moderate tolerance to both cassava brown streak disease (CBSD) and cassava mosaic disease (CMD), as assessed by the team in Uganda.

Furthermore, project participants from Uganda and Ghana have standardized single-cell regeneration techniques, which can be shared with interested Member States to accelerate cassava breeding and fundamental research in VPCs. The CRP has also contributed to capacity building by supporting the graduation of four MSc students, along with two MSc and two PhD students currently engaged in various stages of their research.

CRP D24015: Radiation-Induced Crop Diversity and Genetic Associations for Accelerating Variety Development

Project Officers: P. Mathur, F. Sarsu

A status update meeting of the FAO/IAEA CRP D24015 was held from 2 to 9 April 2025. The progress made in the activities of the project was reviewed, to summarize the outputs, assess the outcome, and to identify areas to be further investigated and recommend further actions to be taken by both the FAO/IAEA and participating countries. Participants discussed the progress made since the last Research Coordination Meeting (RCM) for 2025 annual reports and brainstormed on potential publications.

CRP D23033: An Integrative Approach to Enhance Disease Resistance Against Fusarium Wilt (*Foc* TR4) in Banana - Phase II

Project Officers: C. Zorrilla, P. Mathur

This CRP is aimed at improving disease resistance in banana and developing microbes with enhanced beneficial activities through induced mutagenesis for the management of Fusarium wilt (*Foc* TR4) disease. Specific research objectives are (1) to generate induced genetic diversity in bananas using physical mutagenesis for developing resistance; (2) to generate functional genomics tools and methodologies for understanding the mechanisms of disease resistance using available resistant germplasm that will contribute to markers' development and gene editing; (3) to develop rapid and reliable diagnostic protocols for field detection of the pathogen; and (4) to develop protocols for physical mutagenesis of microbes for enhanced biocontrol and plant growth promotion activities, and evaluation against the disease.

The CRP intends to expand results obtained by a previous CRP that focused on screening methods by including new aspects such as biological control and disease detection.

The project had its third Research Coordination Meeting (RCM) in May 2025 in virtual mode. Participants have shared their progress and discussed how to enhance their results by exchanging experiences and collaboration among them and with the Joint FAO/IAEA Centre.

CRP D23033 participants are working collaboratively to develop knowledge and technologies that will be published and disseminated. The outputs of this project will include validated protocols for field detection of the pathogen, protocols for cell and tissue culture of different banana and plantain varieties, mutant lines of banana and plantain with resistance to banana Fusarium wilt (*Foc* TR4), and microbial strains for biocontrol as part of an integrative approach to contribute to the management of this disease.

CRP E43041: Application of Nuclear Techniques to Improve and Evaluate Nutritional and Health Benefits of Underutilized Crops

Project Officers: K. Bimpong, V. Owino

Malnutrition as a result of nutrient deficiencies, especially for micronutrients (e.g., iron, zinc, calcium, vitamin A, thiamine, riboflavin) and essential amino acids, is associated with almost 50% of mortality among children under five years of age, especially in Low- and Middle-Income Countries.

For example, iron deficiency affects at least 30% (2 billion) of the world's population; it is associated with anemia, decreased work capacity, impaired immune and endocrine function, and impaired physical and cognitive development in children. Underutilized crops can be used to enhance nutrition security as they have higher concentration of nutrients, including protein, vitamins, and minerals.

Mutation breeding is a routine method in plant breeding and has contributed to the development of new varieties with desired traits. However, nutritional benefits of most nutrient-enhanced underutilized crop varieties have not been evaluated adequately since the focus of mutation induction has been on enhancing crop yield. This CRP aims to fill this gap by generating robust evidence on the nutritional value and health efficacy of underutilized crops among vulnerable groups in Asia and Pacific, Africa, Latin America and Europe. This approved CRP is an innovative cross-disciplinary approach to improving and evaluating the nutritional benefits of underutilized crops between NAFA-Plant Breeding and Genetics (PBG) and IAEA's Nutritional and Health-Related Environmental Studies (NAHRES) Team.

CRP D24016: Accelerated Genetic Improvement of Key Dryland Millets for Climate Change Adaptation

Project Officers: F. Sarsu, A. Hingane

The CRP is aimed to develop novel genetic stocks of key dryland millets using mutation breeding and biotechnologies to accelerate the development of new varieties for food and nutrition security and climate-change adaptation. Specific objectives are (1) to generate genetic diversity in selected millets with improved nutrition and quality traits, and improved resilience to biotic/abiotic stress through induced mutation for better adaptation to climate change; (2) to develop/adapt phenotyping tools for precise screening/selection of mutant lines with the desired traits in selected millet crops; (3) to develop genomic tools for delivery of novel induced variation to accelerate genetic gain in millet improvement. The First Research Coordination Meeting (RCM) for the Coordinated Research Project (CRP) on Accelerated Genetic Improvement of Key Dryland Millets for Climate Change Adaptation was held virtually from 7 to 11 October 2024.

NEW CRP D24017: Induced Mutation for Accelerated Varietal Development in Cowpea for Africa

Project Officers: P. Mathur, F. Sarsu

The CRP aims at piloted enhancements of high-performing crop varieties of cowpea to create improved genetic variation with emphasis on trait deployment and accelerated delivery of novel induced variation to core breeding efforts. The nuclear -induced genetic variation integrated with novel and more effective functional genomics approaches will be used to identify superior alleles and deploying them in the breeding pipelines supporting the adaptation of legume cropping systems to rapid climate change.

The objectives are to strengthen the ability of the Joint FAO/IAEA Centre and its Member States to develop and test emerging technologies in mutation induction, genomics, and big data to facilitate the accelerated development of crop varieties for food security and climate-change adaptation.

NEW CRP D24018: Building Resilience to Climate Change: Enhancing Biodiversity in Annual and Perennial Crops with Nuclear Innovations

Project Officers: C. Zorrilla, F. Sarsu

A new CRP project has been launched. The consultancy meeting took place at the Vienna International Centre, Austria, from 17 to 21 March 2025, and the project was approved by the CCRA on 7 May 2025.

The primary focus of CRP D24018 is on addressing the limited biodiversity in crops that are resilient to climate change and can contribute to a nutritious and diverse diet. To tackle this challenge, the project aims to develop tools and knowledge that enhance crop diversity and accelerate the selection process through nuclear innovations. The discussion identified cassava and taro (annual crops), as well as citrus and avocado (perennial crops), as priority crops. Key traits of interest include tolerance to abiotic stress (such as drought and salinity), herbicide resistance, and improved nutritional quality. The project will involve several key components, including mutation breeding, *in vitro* culture, rapid generation advancement, as well as screening for stress tolerance and quality traits. If extended beyond five years, it will also incorporate functional genomics for analyzing mutant-derived traits. Expected outputs include protocols and breeding materials or mutant populations.

Potential participants span across various regions, including countries in Africa (e.g. South Africa, Nigeria, Ethiopia), Latin America and the Caribbean (e.g. Argentina, Mexico), Asia and the Pacific (e.g. India, Indonesia, Australia), Europe and beyond (e.g. Spain, UK) and USA. Experts recommended a five-year implementation period for the project, involving technical contracts with advanced institutions and research contracts with developing countries. They also emphasized the importance of training sessions to ensure consistent methodologies across all participating institutions.

NEW CRP: Building Resilience to Climate Change: Enhancing Biodiversity in Annual and Perennial Crops with Nuclear Innovations (D24018)

Cinthya Zorrilla, IAEA Department of Nuclear Sciences and Applications

The FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture is calling on research institutes to join a new Coordinated Research Project (CRP) on the development of tools to improve resilience in annual and perennial vegetatively propagated crops. This project has a time frame of one year, with possibility to be extended up to 5 years in a yearly basis as per funds availability.

Introduction

Climate change poses a significant threat to global food security by disrupting crop production through unpredictable weather patterns, declining yields, and increased vulnerability to biotic and abiotic stresses. The limited availability of climate-resilient, nutritionally diverse crop varieties restricts the food system's ability to adapt to changing conditions and access to diverse, sustainable and nutritious diets to growing populations.

Focusing on research that contributes to the improvement and adaptation of vegetatively propagated crops is essential for several reasons. Vegetatively propagated crops (VPCs), annuals such as cassava and taro; and perennials such as citrus and avocado, are particularly vulnerable to the effects of climate change due to their genetic uniformity, making them highly susceptible to disease outbreaks and stresses.

General Description

This new CRP project is aimed at developing key technologies for crop improvement of vegetatively propagated crops (cassava, taro, citrus, and avocado) including nuclear-based induced genetic diversity (using radiation to create mutations and expand variability), effective micropropagation methods, rapid generation advance (RGA) to accelerate breeding cycles, advanced phenotyping and genotyping tools to identify superior mutant lines with enhanced tolerance/resistance to abiotic stresses, as well as improved nutritional quality. By focusing on improving these crops' resilience to abiotic stress and enhancing their nutritional qualities, together with rapid generation advance approaches, we can contribute to sustainable, climate-resilient food systems that benefit smallholder farmers, global markets, and communities worldwide.

Inducing mutations to create heritable variations has been a longstanding method for enhancing various traits in numerous crops, including those that are vegetatively propagated. However, most mutant varieties are seed propagated with reduced applications in vegetatively propagated crops due to the requirement of well-established micropropagation methods. Therefore, mutation breeding using *in vitro* cultured clones shows significant potential for further diversifying the genetic base of crops such as cassava, taro, citrus, and avocado.

The application of Rapid Generation Advancement (RGA) in vegetatively propagated crops presents a new promising strategy to shorten breeding cycles through physiological interventions such as modified lighting, temperature control, and the use of induced mutagenesis to obtain early, profuse and/or synchronous flowering clones. This approach is particularly relevant for crops like taro and cassava with limited and inconsistent flowering hampers crossbreeding efforts for trait transferring. In citrus and avocado, the breeding process is further constrained by long juvenile periods, early flowering varieties would contribute to faster breeding schemes. Avocado poses additional challenges due to its asynchronous flowering behavior - where male and female phases occur at different times - complicating both controlled pollination for breeding and fruit production. RGA using physiological methods and mutagenesis can significantly reduce the time required to develop and release improved, climate-resilient, and high-yielding crop varieties.

Vegetatively propagated crops are vital for nutritious and diverse diets, but their qualities vary widely. Improving these crops involves enhancing nutritional profiles and reducing antinutrients. Near-infrared (NIR) spectroscopy and other spectroscopy methods are key technologies that allow rapid, non-destructive analysis of nutritional components as well as antinutrients. Once adequate calibrations have been conducted; these technologies support high-throughput phenotyping in breeding programs.

Rapid, reliable, and affordable methods of screening for abiotic stress tolerance. Imaging methods can contribute to accelerate the evaluation of crops to determine the variation in their response to stresses and identify outstanding mutant lines. The protocol developed will use rating/scoring methods, measurements of physiological variables, among other methods.

Functional genomic technologies are essential for identifying candidate genes and uncovering the genetic basis of traits induced by mutations in the target crops. These technologies help establish precise genetic associations, enabling a deeper understanding of trait expression. Additionally, bioinformatics tools can assist breeders in conducting more efficient and targeted selection, while also contributing valuable insights to the broader scientific community regarding the genetic architecture of these crops.

Target Crops

Cassava, a hardy crop well-suited to poor soils and low-input farming, is a crucial source of carbohydrates in many tropical countries, where it is vital for food security. Its adaptability to climate stress, including drought, makes it an ideal crop for smallholder farmers in regions facing climate challenges. Enhancing its nutritional quality - such as reducing cyanogenic glycosides and boosting carotenoids - could significantly improve food security. Conventional breeding is challenging due to limited flowering in erect varieties delaying the obtention of seedlings.

Taro is grown by resource-poor farmers and valued for its nutritional qualities, but the presence of irritants like calcium oxalate limits its broader adoption. With climate change affecting rainfall patterns and pests, improving taro's resilience to these stressors is critical, particularly in Sub-Saharan Africa, where it is a staple food. Limited research funding and inadequate breeding facilities in many taro-growing regions result in reduced number of improved varieties and insufficient knowledge on flowering induction or manage controlled pollination.

Citrus, including oranges, mandarins, and lemons, is one of the most important fruit crops globally, contributing significantly to food systems and economies. However, citrus breeding faces challenges due to complex genetics, pollination inefficiencies, and susceptibility to pests and diseases. Developing improved rootstocks and varieties that are more resilient to environmental stressors would ensure sustained production.

Avocado, often considered a "superfood" due to its rich nutritional content, is experiencing growing global demand. Avocados are highly sensitive to water and salinity stresses. However, avocado breeding is challenged by long regeneration periods, low pollination efficiency, and complex flowering behavior. Addressing these challenges through improved breeding techniques and genetic diversity would not only increase avocado yields but also enhance fruit quality and contribute to a diverse diet.

CRP Objectives

This CRP is aimed at developing technologies that will enhance diversity of local varieties of annual and perennial vegetatively propagated crops by making them more nutritious and resilient to climate-related challenges.

The specific research objectives are:

1. To establish and optimise protocols for micropropagation and mutation induction in target crops.
2. To develop protocols for rapid generation advance (RGA).
3. To establish and optimise rapid and easy to apply protocols to screen for adaptation to stresses.
4. To develop and optimise protocols for screening quality traits (nutritional/antinutritional, cooking, health promoting).
5. To establish and optimise protocols for functional genomics using mutant lines

The expected outputs of the project are:

- Protocols for micropropagation and mid-term conservation using cells, tissue, micrografting, among other techniques,
- Protocols for mutation induction including initial preparation of material/explants and radiosensitivity testing to determine the adequate doses,
- Protocols for adequate regeneration of materials after irradiation,

- Mutant lines regenerated after chimera elimination and ready for screening,
- Protocols developed for RGA to obtain M2 populations in crops with limited flower production,
- M2/M3 mutant lines obtained using RGA for the evaluation of recessive traits,
- Protocols for earliness, flower induction and/or flower synchronization evaluation in mutants,
- Mutant lines tested for earliness, flower induction and/or flower synchronization,
- Rapid, reliable and easy to apply protocols developed to screen for enhanced water use efficiency using nuclear-based, imaging-based and other methods under field conditions,
- Mutant lines tested for abiotic stress tolerance,
- Protocols for nutrients and anti-nutrients quantification in annual crops using rapid but reliable methods such as near-infrared, visible spectroscopy, etc,
- Protocols for nutrients and consumer preference in fruit trees using near-infrared methods and consumer panels,
- Mutant lines tested for quality traits (high nutrients, low anti-nutrients, etc.),
- Protocols for functional analysis and bioinformatic pipelines established,
- Lines with mutation-induced traits evaluated for identification of candidate genomic regions.

How to join this CRP

Up to fifteen technical and research contracts are expected to be awarded, with a minimum of two contracts per specific research objective.

Research institutes with demonstrated expertise in the targeted technologies or active breeding programmes in the relevant crops are encouraged to apply and contribute to the development and validation of the proposed technical packages.

Coordination and technical oversight will be provided by the scientific secretary from the IAEA's Plant Breeding and Genetics Section, in collaboration with the Plant Breeding and Genetics Laboratory.

Priority will be given to proposals addressing two or more specific research objectives. Proposals in functional genomics should have existing mutant germplasm, infrastructure and data analysis capabilities already in place.

Research organizations interested in joining the CRP must submit their Proposal by e-mail to the IAEA's Research Contracts Administration Section (Research.Contracts@iaea.org), by **15 July 2025**, using the appropriate template on the CREA web portal (https://www.iaea.org/services/coordinated-research-activities/how-to-participate).

The IAEA encourages institutes to involve, to the extent possible, women Chief Scientific Investigators and young researchers in their proposals. For further information related to this CRP, potential applicants should use the contact form under the CRP page (https://www.iaea.org/projects/crp/d24018).

Technical Cooperation Field Projects

Project Number	Country/Region	Title	Technical Officer(s)
BDI5005	Bangladesh	Enhancing Productivity of Staple Crops Using Nuclear-derived Technologies	P. Mathur with SWMCN
BKF5024	Burkina Faso	Improving Food Crops through Mutation Breeding and Best Soil and Nutrient Management to Ensure Food Security	F. Sarsu with SWMCN
BOT5025	Botswana	Improving Selected Vegetable Crops and Cereals through the Use of Mutation by Speed Breeding Techniques	I.K. Bimpong
BUL5020	Bulgaria	Increasing the Yield and Quality of Main Vegetable Crops through Nuclear Technology to Withstand the Impacts of Climate Change	C. Zorrilla
CAF5015	Central African Republic	Improving Productivity of Maize and Developing Resistance to Fall Armyworm Using Radiation-Induced Novel Genetic Diversity - Phase II	F. Sarsu
CHI5055	Chile	Strengthening the National Cooperation Network in the Use of Nuclear Techniques in Plant Breeding Programmes	C. Zorrilla
COD5031	Democratic Republic of Congo	Using Nuclear Techniques to Improve Crop Productivity for Maize, Soybeans and Beans, as well as Food Safety Testing Capabilities	I.K. Bimpong with FSC
COL5026	Colombia	Enhancing Crop Productivity of Creole Potato Using Nuclear and Related Techniques	I.K. Bimpong with SWMCN
COL5027	Colombia	Strengthening the Detection and Management of Quarantine Pathogens by Implementing Molecular Methods and Mutation Breeding Techniques	C. Zorrilla
COS5038	Costa Rica	Developing Resistance to Fusarium Wilt in Bananas and Contributing to the Integrated Management of the Disease through the Application of Mutation Breeding Techniques	C. Zorrilla
ECU5034	Ecuador	Improving the Resilience of Bananas to their Major Diseases through Mutation Breeding Techniques	C. Zorrilla
ERI5013	Eritrea	Improving Food Crop Varieties through Mutation Breeding and Related Technologies	I.K. Bimpong
ERI5017	Eritrea	Enhancing Productivity by Improving Seed Crops Relevant for Food Security and Income through Mutation Induction and Related Breeding Technologies	C. Zorrilla
INT5158	Interregional	Strengthening Member State Capacities to Combat Banana Fusarium Wilt (TR4) through Early Detection, New Resistant Varieties, and Integrated Management	C. Zorrilla
IRA5015	Iran, Islamic Republic of	Enhancing Capacity of National Producers to Achieve Higher Levels of Self-Sufficiency in Key Staple Crops	F. Sarsu with FSC *and* SWMCN
IRQ5023	Iraq	Utilizing Nuclear Technology to Improve Key Legume Crops for Climate Change Adaptation	I.K. Bimpong
JAM5015	Jamaica	Strengthening National Capacities for the Introduction of the Sterile Insect Technique for Pest Control, Mutation Breeding of Crops and Post-Harvest Treatment of Agricultural Produce Using a Self-Contained Gamma Irradiation Facility	I.K. Bimpong
KAM5007	Cambodia	Improving Cotton for Enhanced Resilience to Climate Change	I.K. Bimpong
KUW5006	Kuwait	Improving Barley and Sorghum Production Under Harsh Environmental Conditions Using Mutation Breeding Techniques	F. Sarsu
LAO5006	Lao PDR	Enhancing Crop Production with Climate Smart Agricultural Practices and Improved Crop Varieties	F. Sarsu with SWMCN

Project Number	Country/Region	Title	Technical Officer(s)
LES5012	Lesotho	Improving Productivity of Potato and Sorghum through Mutation Breeding and Best Soil, Nutrient and Water Management Practices	I.K. Bimpong
LIR5004	Liberia	Enhancing Rice and Vegetable Crops' Productivity through the Use of Mutation by Speed Breeding for Food Self-Sufficiency and Income Generation	I.K. Bimpong
MAG5026	Madagascar	Enhancing Rice and Maize Productivity through the Use of Improved Lines and Agricultural Practices to Ensure Food Security and Increase Rural Livelihoods	F. Sarsu with SWMCN *and* IHS
MAK5010	North Macedonia	Improving Dry Bean Productivity and Tolerance to Diseases and Drought by Use of Nuclear Techniques	F. Sarsu
MAR5029	Mauritius	Improving Landraces of Crucifers (Cauliflower and Cabbage) and Carrot through Mutation Breeding and Biotechnology - Phase II	F. Sarsu
MAU5029	Mauritania	Improving Rice and Sorghum through the Application of Nuclear Techniques	I.K. Bimpong
MLI5031	Mali	Improving Rice Productivity through Mutation Breeding and Better Soil, Nutrient and Water Management Practices	I.K. Bimpong with SWMCN
MLW5006	Malawi	Developing Drought Tolerant, High Yielding and Nutritious Crops to Combat the Adverse Effects of Climate Change	C. Zorrilla
NAM5020	Namibia	Enhancing Staple Crop Yields, Quality, and Drought Tolerance through Broadening Genetic Variation and Better Soil and Water Management Technologies	F. Sarsu with SWMCN
NEP5009	Nepal	Enhancing Climate Resilient Field Crops Production Systems for Food Security by using Nuclear and Molecular Techniques	I.K. Bimpong
NER5025	Niger	Improving Food and Biological Hazard Detection, Food Preservation and Mutation Breeding	I.K. Bimpong with FSC
PAK5023	Pakistan	Strengthening and Enhancing National Capabilities for the Development of Climate Smart Crops, Improvement in Animal Productivity and Management of Soil, Water, and Nutrient Resources Using Nuclear and Related Techniques	F. Sarsu with SWMCN
PAL5011	Palestine	Enhancing Food Security via Nuclear Based Approaches	I.K. Bimpong with SWMCN
PAR5012	Paraguay	Evaluation of Varieties and Advanced Mutant Lines against Biotic and Abiotic Stress Conditions to Mitigate the Effects of Climate Change in Crops	C. Zorrilla
PER5034	Peru	Improving Yellow Potato and Coffee Crops through Mutation Breeding Techniques	F. Sarsu
PHI5036	Philippines	Providing an Innovative Platform for Germplasm Utilization for Rainfed and Irrigated Lowland Rice Ecosystems - Phase I	A. Hingane
QAT5008	Qatar	Developing Best Soil, Nutrient, Water and Plant Practices for Increased Production of Forages under Saline Conditions and Vegetables under Glasshouse Using Nuclear and Related Techniques	F. Sarsu with SWMCN
RAF5092	Regional Africa	Enhancing Agricultural Productivity for Improved Food Security in Africa	F. Sarsu
RAS5088	Regional Asia	Enhancing Crop Productivity and Quality through Mutation by Speed Breeding (RCA)	F. Sarsu
RAS5094	Regional Asia	Promoting Sustainable Agricultural and Food Productivity in the Association of Southeast Asian Nations Region	C. Zorrilla with FSC *and* SWMCN
RAS5098	Regional Asia	Improving the Resilience of Crops to Climate Change through Mutation Breeding - Phase II (SAPI)	C. Zorrilla

Project Number	Country/Region	Title	Technical Officer(s)
RAS5099	Regional Asia	Developing Climate Smart Crop Production including Improvement and Enhancement of Crop Productivity, Soil and Irrigation Management, and Food Safety Using Nuclear Techniques (ARASIA)	I.K. Bimpong with SWMCN
RLA7027	Regional Latin America	Applying Nuclear Technology in Agriculture, Water Resource Management and the Environment in Caribbean Member States (CARICOM)	I.K. Bimpong
RER5024	Regional Europe	Enhancing Productivity and Resilience to Climate Change of Major Food Crops in Europe and Central Asia	F. Sarsu
SAF5016	South Africa	Promoting Mutation Breeding of Vegetables to Improve Rural Livelihoods - Phase I	N. Warthmann
SIL5024	Sierra Leone	Improving Rice and Cassava Production Using Nuclear Related Techniques	I.K. Bimpong with SWMCN
SRL5050	Sri Lanka	Supporting Genetic Improvement of Tea	F. Sarsu
STK7001	Saint Kitts and Nevis	Building National Capacity for the Application of Nuclear Science and Technology	I.K. Bimpong
SUD5041	Sudan	Enhancing Productivity and Quality of High Value Crops through Improved Varieties and Best Soil, Nutrient and Water Management Practices	F. Sarsu with SWMCN
SWA5002	Eswatini, Kingdom of	Improving Adaptability of Cowpea to Climate Change through Mutation Breeding	I.K. Bimpong
SWA5003	Eswatini, Kingdom of	Improving Cowpea for Enhanced Resilience to Climate Change	I.K. Bimpong
TOG5004	Togo	Improving Crop Productivity and Agricultural Practices through Radiation Induced Mutation Techniques	I.K. Bimpong with SWMCN
TUN5031	Tunisia	Developing Cereal and Legume Mutants for Improving Food Security and Farmers' Resilience to Climate Change	F. Sarsu
UGA5043	Uganda	Improving Cassava and Rice Disease Resistance through Mutation Breeding Techniques	I.K. Bimpong
URT5037	Tanzania, United Republic of	Developing Rice Varieties with Resistance to Rice Blast and Salinity Tolerant Using Mutation Breeding and Biotechnology Techniques	F. Sarsu
URT5039	Tanzania, United Republic of	Mutation Breeding for Improved Productivity, Nutritional Quality, and Pest and Disease Resistance in Cotton and Common Beans - Phase I	C. Zorrilla
VEN5023	Venezuela	Improving Banana Productivity through Mutation Breeding Techniques for Enhanced Disease Resistance	C. Zorrilla
YEM5016	Yemen	Enhancing Sorghum and Legume Crop Productivity through Induced Mutations with Supportive Breeding and Biotechnologies - Phase II	I.K. Bimpong
ZAM5035	Zambia	Enhancing Resilient AgriFood Systems through Improved Crop Varieties and Soil Management Practices	I.K. Bimpong
ZIM5027	Zimbabwe	Enhancing Food Security by Developing and Disseminating High Yielding Climate Resilient Mutant Crop Varieties	A.J. Hingane

Forthcoming Events

National Training Course

Strengthening the Detection and Management of Quarantine Pathogens by Implementing Molecular Methods and Mutation Breeding Techniques - COL5027

Mosquera, Colombia, 7-11 July 2025

Project Officer: Cinthya Zorrilla

Project Objective: Plant pathogens pose a major challenge to crop production worldwide, with significant implications for international trade and food security. This project aims to implement a comprehensive strategy for managing quarantine diseases that affect key food crops in the country by strengthening official control measures through the use of advanced molecular techniques for accurate detection of quarantine pathogens, and by developing improved potato genotypes using radiation-induced genetic variation.

Course Objective: This training will provide an overview of plant pathogens, focusing on *Xylella fastidiosa*, *Candidatus Liberibacter solanacearum*, and *Candidatus Phytoplasma* spp. It will cover the biology, epidemiology, management, hosts, and vectors of these bacteria, along with sampling techniques for symptomatic and asymptomatic plants and potential vectors. Participants will learn methods for bacterial isolation, DNA extraction from plants and insects, and various molecular detection techniques, including PCR, Real-Time PCR, and RPA.

The course will contribute to identify these pathogens at the level of species and subspecies contributing to taking adequate decisions for prevention and management.

Regional Training Course

Farmer Participatory Variety Selection Approach in Plant Mutation Breeding - RAS5099

Muscat, Oman, 10-21 July 2025

Project Officer: I.K. Bimpong

Project Objective: Support the transfer of knowledge and expertise among ARASIA participating countries and collaborate to enhance the production of major food crops with improved performance and better resilience to climate change through mutation breeding and combined biotechnologies, in order to contribute to food security in ARASIA participating countries.

Course Objective: Enhance capacities on the principles and practices of farmer participatory varietal selection in plant breeding. Participants will learn how to engage farmers in the selection and evaluation of crop varieties based on local preferences and needs. Through this approach, farmers will be empowered to actively participate in the breeding process, fostering the development of crop varieties that are well-suited to local conditions and preferences.

National Training Course

Mutation Breeding for Improved Productivity, Nutritional Quality, and Pest and Disease Resistance in Cotton and Common Beans - Phase I - URT5039

Mwanza, Tanzania, 21-25 July 2025

Project Officer: Cinthya Zorrilla

Project Objective: Create variability by mutation induction that can be used for trait screening under field and laboratory conditions for common beans (improved nutrition) and cotton (disease resistance).

Course Objective: Train participants in basic statistical analysis methods that will support the selection of best performing materials for diverse traits to be evaluated in common bean (yield, cooking time, iron content) and cotton (yield, fiber quality).

The training will focus on data preparation, experimental design across different stages of plant research, and multi-environment testing with an emphasis on genotype-by-environment interactions and selection. It will also include hands-on sessions using R/RStudio for data analysis and visualization, equipping participants with practical skills for managing and analyzing agricultural research data.

National Training Course

Approaches in Mutation Breeding: Double Haploidy and Speed Breeding in Legumes - BOT5025

Gaborone, Botswana, 28 July-8 August 2025

Project Officer: I.K. Bimpong

Project Objective: Support the development and deployment of seeds of improved mutant cowpea varieties that are high-yielding and drought-tolerant contributing to food security in the country.

Course Objective: Provide participants with advanced knowledge and practical skills including supporting the development and dissemination of high-yielding, drought-tolerant mutant cowpea varieties, promoting their adoption among farmers, enhancing food security, and strengthening local seed systems. By mastering these techniques, participants will be equipped to develop improved legume varieties with enhanced traits such as yield, nutritional content, and stress tolerance, contributing to food security and agricultural sustainability.

Task Force Meeting in Climate-Smart Crop Breeding in Africa

Hawassa, Ethiopia, 4-8 August 2025

Project Officer: F. Sarsu

This Task Force Meeting, held under the FAO/IAEA Atoms4Food Initiative, aims to foster regional dialogue and cooperation in advancing climate-smart crop breeding across Africa. Organized alongside a regional consultation and expert meeting, the event will bring together a diverse group of scientists, policymakers, and project partners from across the continent.

The primary objectives of the meeting are to:

- Facilitate technical discussions on the status, progress, and future direction of climate-resilient crop breeding efforts.
- Assess current challenges, opportunities, and regional priorities through expert consultation.
- Align ongoing project activities with agreed priorities to ensure effective implementation and impact.

The meeting will also explore opportunities for technology transfer, collaborative innovation, and strategic support available through the Atoms4Food Initiative, which promotes the application of nuclear and related technologies for sustainable agricultural transformation. The goal is to strengthen food security, resilience, and productivity in the face of climate change across Africa.

National Training Course

Speed Breeding Techniques for Crop Improvement and Molecular Tools for Mutation Detection - NEP5009

Katmandu, Nepal, 4-15 August 2025

Project Officer: I.K. Bimpong

Project Objective: Enhance climate-resilient field crop production systems for food security by utilizing nuclear and molecular techniques, with a focus on strengthening researchers' capacity in plant mutation breeding, particularly in selection, phenotyping, and related methodologies to develop improved crops tailored to the country's needs.

Course Objective: Equip participants with skills in applying double haploidy techniques and speed breeding (MbyS) to accelerate crop development, enabling rapid fixation of desirable traits. Additionally, it will introduce molecular technologies for detecting novel induced mutations in stress-tolerant mutants, enhancing capacity for efficient crop improvement and resilient variety development.

National Training Course

Rapid Generation Advancement Techniques and Mutation Detection using Molecular Tools in Cereals - LIB5004

Monrovia, Liberia, 11-22 August 2025

Project Officer: I.K. Bimpong

Project Objective: Develop improved rice varieties that are high-yielding and salinity-tolerant contributing to food security in the country.

Course Objective: Enhance awareness of nuclear techniques through training in mutation breeding. Participants will learn about mutation induction, breeding schemes, selection methods, and laboratory protocols. The program includes lectures, demonstrations, and practical sessions to develop skills in rapid generation advancement, effective handling of segregating populations in targeted crops and detecting novel mutations, ultimately accelerating breeding for resilient crop varieties in Liberia.

National Training Course

Innovative Approaches in Mutation Breeding: Data Analysis and Experimental Design Methods - KAM5007

Phnom Penh, Cambodia, 18-22 August 2025

Project Officer: I.K. Bimpong

Project Objective: Support the development of improved cotton varieties that are high-yielding and drought-tolerant contributing to food security in the country.

Course Objective: Provide participants with specialized training in developing effective data analysis and experimental design strategies to optimize mutant breeding lines, improving accuracy in selecting desirable traits, enhancing efficiency in their breeding programs, ensuring robust data interpretation, and facilitating the development of high-performing, climate-resilient mutant varieties through precise and systematic approaches. By acquiring these skills, participants will contribute to sustainable cotton production in challenging environments.

Fourth Research Coordination Meeting (RCM)

Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops (CRP24014)

Beijing, China, 18-22 August 2025

Project Officer: I.K. Bimpong

The CRP's goal is to assist Member States' National Agricultural Research Systems (NARS) in accelerating the development of new varieties of vegetatively propagated crops (VPCs) and horticultural tree crops (HTCs) through advanced technology packages. The project will build on existing efforts by developing *in vitro* mutation induction techniques, screening methods, and functional genomics tools for disease resistance in cassava, potatoes/sweet potatoes, and olives. The CRP includes researchers from thirteen countries as well as advanced institutions. The fourth Research Coordination Meeting (RCM) for CRP D24014 will evaluate the progress and discuss final-year work plan activities for 2025-2026. The event will discuss and review the progress made in research activities in the development of standardized screening protocols to enable precise and efficient development of new genetic resources and technologies for accelerated breeding in VPCs and HTCs through induced genetic diversity, chimera-free regeneration, and functional genomics since the third RCM, as well as consolidate the work plan for the following cycle.

National Training Course

Empowering Farmers Through Participatory Breeding and Variety Promotion - MAU5029

Rosso, Mauritania, 26-30 August 2025

Project Officer: I.K. Bimpong

Project Objective: Address the development and deployment of seeds of improved rice varieties that are high-yielding and tolerant to saline conditions contributing to food security in the country.

Course Objective: Actively involve farmers in the breeding process to ensure the development of rice varieties better adapted to local conditions, identify and promote high-yielding and resilient rice varieties, enhance farmers' knowledge and acceptance of new rice varieties, and foster sustainable, community-driven agricultural practices through participatory breeding.

Advanced Mutation Breeding techniques for Improvement of Nutritional Quality

Faisalabad, Pakistan, 6-18 October 2025

Project Officer: F. Sarsu

Project Objective: Contribute to the alleviation of malnutrition in the Regional Cooperative Agreement (RCA) Government Parties (GP) through biofortification of food crop varieties. Through this project, the protocol to develop biofortification food crop germplasm and varieties will be established and shared within all participating GPs. Such methodology and crop varieties could significantly benefit the large, undernourished population in Asia and Pacific region in a long-term range

Course Objective: Build Member States' capacity in using advanced mutation breeding to enhance crop nutritional quality. Through theoretical and practical sessions, participants will gain skills in mutation induction, trait selection, and nutritional profiling to support the development of biofortified varieties addressing micronutrient deficiencies.

The course will cover advanced mutation techniques (physical, chemical, and genome editing tools like CRISPR/Cas9), genetics of nutritional traits, mutation screening, and quality assessment of biofortified crops. It will also address breeding program design, regulatory frameworks, and socioeconomic aspects.

Regional Training Course

Farmers' Participatory Plant Breeding Approach to Enhance Climate Resilience and Improve Local Varieties - RAF5092

Kinshasa, Democratic Republic of the Congo, 13-17 October 2025

Project Officer: F. Sarsu

Project Objective: This initiative falls under RAF5092, part of the Atoms4Food Initiative, a collaborative effort between the IAEA and FAO to strengthen agricultural resilience and food sovereignty in Member States.

Course Objective: Strengthen national capacity in applying the Farmers' Participatory Plant Breeding (FPPB) approach to develop crop varieties better adapted to local environments and farmers' needs. By engaging farmers directly in the selection process, the course fosters demand-driven innovation, enhances adoption of improved varieties, and supports sustainable agriculture in the face of climate change. It also focuses on developing new varieties through mutation breeding and combining advanced technologies, such as molecular tools and genomics, to accelerate the breeding process and ensure genetic gains that are both resilient and responsive to local challenges.

National Training Course

Improving Banana Productivity through Mutation Breeding Techniques for Enhanced Disease Resistance - VEN5023

Maracay, Venezuela, 13-17 October 2025

Project Officer: Cinthya Zorrilla

Project Objective: Obtain promising mutant lines of bananas, plantains and topochos that present resistance and/or tolerance to diseases; especially to *Fusarium oxysporum* f. sp. *Cubense* Tropical Race 4 (*Foc* TR4).

Course Objective: The training program will cover a comprehensive range of topics focused on molecular techniques in banana research. It will begin with lectures and hands-on demonstrations detailing the process of DNA extraction, followed by an in-depth exploration of the procedures used to obtain molecular markers in banana. Participants will also engage in practical sessions on analyzing molecular marker results to interpret genetic variation observed. The training will include guidance on the next steps for identifying mutant regions through advanced techniques such as qPCR, sequencing, and other molecular tools. Case studies showcasing successful applications of molecular markers in identifying banana mutants will be presented to illustrate real-world outcomes. Additionally, the training will provide a thorough overview of the materials and equipment required for the demonstrated methodologies, along with practical recommendations for utilizing existing facilities and resources efficiently.

National Training Course

Basics of Experimental Design Methods and Data Analysis in Mutation Breeding - YEN 5017

Kuala Lumpur, Malaysia, 15 October-15 November 2025

Project Officer: I.K. Bimpong

Project Objective: Enhance National Food Security through the Development of Climate Smart Crops and the Improvement of Livestock Productivity Using Nuclear Techniques.

Course Objective: Train participants with modern skills in designing and implementing statistically rigorous pre-field and field screening methods, enhancing the accuracy and efficiency in selecting superior mutant lines for crop improvement. This training also aims to improve decision-making processes and accelerate the development of high-performing, resilient crop varieties.

National Training Course

Farmer Participatory Variety Selection in Mutation Breeding - SIL5024

Rokupr, Sierra Leone, 21-25 October 2025

Project Officer: I.K. Bimpong

Project Objective: Support the production of major food crops with higher yields, improved quality, and better resilience to climate change through mutation breeding and combined biotechnologies, in order to contribute to food security in the country.

Course Objective: Actively involve farmers in the breeding process to ensure the development of mutant cassava varieties better adapted to local conditions, identify and promote high-yielding and resilient mutant cassava varieties, enhance farmers' knowledge and acceptance of new mutant cassava varieties, as well as foster sustainable, community-driven agricultural practices through participatory breeding.

Fourth Research Coordination Meeting (RCM)

Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development (CRP24015)

Virtual, 28-31 October 2025

Project Officer: P. Mathur

This CRP addresses Member States' needs with emerging trends in the field of mutation breeding: (1) newer mutagen sources; (2) establishment of genetic associations for marker-assisted breeding, gene editing, and potentially, genomic selection; and (3) bioinformatic platforms and computational tools for trait analysis. The fourth Research Coordination Meeting (RCM) for CRP D24015 will be held virtually via Microsoft Teams from 28 to 31 October 2025. The meeting will review the progress made in the activities of the project, summarize the outputs, assess the outcome, identify areas to be further investigated and recommend further actions to be taken by both the FAO/IAEA and participating countries for the coming year.

Regional Training Course

Application of Tissue Culture (DH) in Crop Improvement and Molecular Breeding Methods - RAS5099

Jakarta, Indonesia, 16-25 November 2025

Project Officer: I.K. Bimpong

Project Objective: Support the transfer of knowledge and expertise among ARASIA participating countries and collaborate to enhance the production of major food crops with improved performance and better resilience to climate change through mutation breeding and combined biotechnologies, in order to contribute to food security in ARASIA participating countries.

Course Objective: Foster capacity development in the application of tissue culture techniques, specifically Doubled Haploidy (DH), in crop improvement. Participants will learn how to utilize DH for rapid crop breeding and genetic improvement. Additionally, the course will cover the principles and methodologies of molecular breeding and marker-assisted selection, empowering participants to integrate cutting-edge biotechnological tools in crop improvement programs.

Past Events

Regional Meeting

Finalization of the ARASIA Concept Proposal for Feasibility Study on Establishing a Regional Seed Bank - RAS5099

Vienna, Austria, 17-20 February 2025

Project Officer: I.K. Bimpong

Project Objective: Support the transfer of knowledge and expertise among ARASIA participating countries and collaborate to enhance the production of major food crops with improved performance and better resilience to climate change through mutation breeding and combined biotechnologies, in order to contribute to food security in ARASIA participating countries.

Meeting Objective: Develop a proposal for feasibility studies to explore the establishment of a regional seed bank in ARASIA countries, with potential funding from the OPEC Fund for International Development. The proposal includes assessing the feasibility of establishing a seed bank to preserve diverse mutant plant genetic resources, enhancing collaboration among ARASIA countries in agricultural research, and strengthening climate resilience through mutant seed conservation. During the meeting, Mr Bimpong delivered a presentation and led the discussions and finalization of the proposal.

Seventeen participants (six women and eleven men researchers) from eight ARASIA participating counties, as well as one international expert, attended the meeting.

First Coordination Meeting

Using Mutational Biofortification for Improving the Nutritional Quality of Food Crops - RAS 5101

Vienna Austria, 17-21 February 2025

Project Officer: Fatma Sarsu

Meeting Objective: The kick-off meeting of the Regional Cooperative Agreement (RCA) Project RAS5101 was held from 17 to 21 February 2025 in Vienna, Austria. The meeting aimed to review the national capacity and workplans of the RCA Government Parties (GPs) in mutation breeding for the improvement of nutritional quality in food crops, and to establish a comprehensive project workplan.

The meeting was attended by National Project Coordinators (NPCs) or senior members of national project teams from sixteen Government Parties in the Asia and Pacific region, including Bangladesh, Cambodia, China, India, Indonesia, Republic of Korea, Lao PDR, Malaysia, Mongolia, Myanmar, Nepal, Pakistan, the Philippines, Sri Lanka, Thailand, and Vietnam. In total, sixteen participants were present (four women and twelve men). Additionally, Mr Ricardo Francisco Oliva Perez (Consultant, Plant Breeding and Genetics Section, Joint FAO/IAEA Centre), the Programme Management Officer (PMO), and the Lead Country Coordinator (LCC) also attended the meeting.

During the meeting, national situations and workplans were presented and reviewed. The regional workplan was also discussed and agreed upon, providing a clear roadmap for project implementation. Participants discussed existing challenges and knowledge gaps in their respective countries.

National Training Course

Mutation Breeding for Improved Productivity, Nutritional Quality, and Pest and Disease Resistance in Cotton and Common Beans - Phase I - URT5039

Arusha, Tanzania, 24-28 February 2025

Project Officer: Cinthya Zorrilla

Project Objective: Create variability by mutation induction that can be used for trait screening under field and laboratory conditions for common beans (improved nutrition) and cotton (disease resistance).

Course Objective: The training covered basic concepts related to mutation breeding, such as mutation induction, radiosensitivity testing, population advance at early and advanced generations, screening methods, among others relevant for the mutation breeding process.

The training brought together a total of twenty-four participants (ten women and fourteen men researchers) from diverse institutions in Tanzania.

National Training Course

Evaluation of Varieties and Advanced Mutant Lines against Biotic and Abiotic Stress Conditions to Mitigate the Effects of Climate Change in Crops - PAR5012

Asuncion, Paraguay, 24-28 February 2025

Project Officer: Cinthya Zorrilla

Project Objective: Develop mutant lines with tolerance to biotic and abiotic stresses, as well as improve nutritional quality in several crops including soybeans, beans, and Stevia.

Course Objective: Acquaint participants of the main methods for evaluation of stress tolerance in plants. Additionally, use this knowledge to screen for water stress tolerance in breeding material of cowpea and soybean developed by induced mutations.

This training included topics such as basic concepts of water stress tolerance in plants, methods of screening for water stress, case studies of successful application of the methods presented in roots and tubers, and practical sessions in the application of screening methods and data analysis.

A total of eighteen participants (five women and thirteen men researchers) participated in the course.

National Training Course

Improving Banana Productivity through Mutation Breeding Techniques for Enhanced Disease Resistance - VEN5023

Maracay, Venezuela, 23-28 March 2025

Project Officer: Cinthya Zorrilla

Project Objective: Obtain promising mutant lines of bananas, plantains and topochos that present resistance and/or tolerance to diseases; especially to *Fusarium oxysporum* f. sp. *cubense* Tropical Race 4 (*Foc* TR4).

Course Objective: Train professionals from Venezuela in the concepts and methods used in the bioprospecting of biological control agents to mitigate the disease caused by *Fusarium oxysporum* f. sp. *cubense* Tropical Race 4 in banana, from sample collection to bioformulation. Additionally, one of the objectives of this training was to establish a strategy to develop biopesticides using native biological control agents against *Fusarium oxysporum* f. sp. *cubense* Tropical Race 4 in banana.

The training focused on the fundamentals and practical applications of biological control in agriculture. It covered the isolation, identification, and preservation of biological control agents, along with methods to evaluate their effectiveness against plant pathogens in different settings. Participants also explored successful case studies and learned about the development process of bioproducts for plant disease control.

A total of twenty-two participants (five women and seventeen men researchers) were a part of this training.

Second Research Coordination Meeting (RCM)

Accelerated Genetic Improvement of Key Dryland Millets for Climate Change (CRP24016)

Vienna, Austria, 7-11 April 2025

Project Officer: F. Sarsu

The second Research Coordination Meeting (RCM) for the IAEA Coordinated Research Project (CRP24016) on "Accelerated Genetic Improvement of Key Dryland Millets for Climate Change" was held from 7 to 11 April 2025 at the IAEA headquarters in Vienna, Austria. The event brought together ten participating scientists from Burkina Faso, China, India (two participants), Ethiopia, Namibia, South Africa, Sri Lanka, Slovakia, and the USA, as well as an observer from the Food and Agriculture Organization of the United Nations (FAO).

The meeting served as a dynamic platform for researchers to share progress, present early results, and chart the path forward. Discussions focused on deploying cutting-edge tools such as high-throughput digital phenotyping, genomics integration, and novel breeding technologies to accelerate the development of climate-resilient millet varieties. Special emphasis was placed on enhancing resistance to biotic and abiotic stresses and improving the nutritional profiles of millet to meet global health needs.

Beyond generating new scientific knowledge, this CRP is strengthening national capacities in plant breeding and genetics while supporting smallholder farmers through the development of adaptable, high-yielding, and resilient millet varieties. The project embodies a holistic, interdisciplinary approach, combining breeding, agronomy, climate resilience, value addition, market development, and policy advocacy.

The RCM also provided an opportunity to introduce advanced methodologies for identifying beneficial mutations, expediting screening processes, and facilitating multi-location trials. These collaborative efforts have sparked bilateral and multilateral partnerships, particularly in developing advanced mutant lines and applying genomics.

The meeting underscored the critical role of millet in ensuring food and nutritional security under changing climates, and the CRP's contribution to building sustainable and resilient food systems across Member States.

National Training Course

Advances in Mutation-Based Crop Improvement: Double Haploidy and Speed Breeding - ZAM5035

Luanda, Zambia, 5-9 May 2025

Project Officer: I.K. Bimpong

Project Objective: Enhance resilient Agrifood systems through improved crop varieties and soil management practices for the country.

Course Objective: Train participants in applying double haploidy techniques to accelerate mutation breeding, enhance skills in speed breeding methods, facilitate rapid development of homozygous lines, and promote efficient crop improvement strategies for increased productivity and resilience in the country.

Thirty participants (ten women and twenty men researchers) attended the training.

Third Research Coordination Meeting (RCM)

An Integrative Approach to Enhance Disease Resistance Against Fusarium Wilt (*Foc* TR4) in Banana (CRP D23033)

Virtual, 5-9 May 2025

Project Officer: Cinthya Zorrilla

The CRP D23033 is a five-year CRP focused on the development of protocols, technologies, mutant lines and mutant beneficial microbes. The third year of the project was officially initiated with this virtual Research Coordination Meeting.

The contract and agreement holders in CRP D23033 gathered together to discuss the progress of each participating institution, exchange suggestions and comments, plan detailed activities for the third year of the project, and strengthen collaboration between different institutions to ensure the success of the project.

Overall, the project is progressing as planned. Most activities under each of the four specific objectives have been initiated or are in progress, pending activities correspond mostly to field related experiments that are expected to be conducted in the final two years of the project.

Main achievements include the identification of putative resistant banana clones to *Foc* STR4 to be screened also for *Foc* TR4 resistance, progress on the sequencing and identification of candidate genes associated to banana Fusarium wilt resistance, development of LAMP and Mini-PCR methods that will be validated under field conditions, as well as initial mutation induction on beneficial microbes and suitable irradiation methods.

A total of seventeen participants (five women and twelve men researchers) from thirteen institutions in twelve countries participated in the discussions. The Plant Breeding and Genetics Laboratory presented their work on activities that contribute to the overall CRP project objectives.

National Training Course

Enhancing Crop Stress Tolerance through Mutation Induction and Molecular Techniques - LES5012

Maseru, Lesotho, 19-23 May and 2-6 June 2025

Project Officer: I.K. Bimpong

Project Objective: The project addresses the development and deployment of seeds of improved root and tubers and cereals that are high-yielding and drought-tolerant contributing to food security in the country.

Course Objective: Enhance capacities to improve crop productivity on mutation induction and selection in crops for adaptation to extreme climatic conditions, enhancing skills in identifying stress-tolerant mutants, promoting the application of mutation breeding techniques, and building capacity in basic biotechnological tools for detecting novel induced mutations.

Thirty-five participants (twenty-two women and thirteen men researchers) attended the training.

National Training Course

Double Haploidy and Molecular Techniques for Mutation Based Crop Improvement - COD5031

Kinshasa, Democratic Republic of Congo, 2-13 June 2025

Project Officer: I.K. Bimpong

Project Objective: Support the improvement of crop productivity for maize, soybeans and beans, as well as food safety testing capabilities by using nuclear techniques.

Course Objective: Train participants in utilizing double haploidy techniques to accelerate crop breeding, enabling rapid development of homozygous lines. The course also aims to enhance skills in Next Generation Sequencing (NGS) for detecting novel mutations in stress-tolerant mutants, thereby improving breeding efficiency, promoting rapid variety development, and strengthening national capacity for sustainable crop improvement.

Thirty participants (ten women and twenty men researchers) attended the training.

Regional Training Course

Speed Breeding Techniques for Accelerated Crop Improvements - RAF5092

Tunis, Tunisia, 16-27 June 2025

Project Officer: F. Sarsu

Project Objective: This initiative falls under RAF5092, part of the Atoms4Food Initiative, a collaborative effort between the IAEA and FAO to strengthen agricultural resilience and food sovereignty in Member States. As part of this broader program, the training provided both theoretical knowledge and hands-on technical expertise in plant breeding and genetics, equipping participants with the tools needed to advance crop improvement efforts in the face of global challenges such as climate change

Course Objective: Enhance Member States' research capabilities in crop mutation breeding, focusing on speed breeding techniques such as double haploid technology, marker-assisted selection, and controlled artificial growth environments. It also explored phenotypic and genotypic linkages to improve the selection of mutant plant populations and lines. These advanced approaches are designed to accelerate breeding cycles, enabling the development of genetically stable, climate-resilient crop varieties that can withstand biotic and abiotic stresses-critical for global food security.

Thirty researchers attended the training, including eighteen women and twelve men.

National Training Course

Next-Generation Sequencing for the Discovery of Novel Induced Mutations and the Maintenance of Mutant Line Integrity - UGA5043

Kampala, Uganda, 23-27 June 2025

Project Officer: I.K. Bimpong

Project Objective: Develop disease resistance cassava and rice crops using mutation breeding techniques, aiming to enhance resilient varieties with improved yield and sustainability. This approach seeks to strengthen crop resilience against emerging diseases, ensuring food security and supporting sustainable agricultural practices.

Course Objective: Train participants in utilizing Next Generation Sequencing (NGS) techniques for detecting novel mutations in stress-tolerant mutants, while also covering best practices in maintaining breeding lines and designing experiments, thereby enhancing precision and efficiency in crop improvement programs.

Thirty participants (ten women and twenty men researchers) attended the training.

National Training Course

Techniques in Mutation Breeding and Introduction to Molecular Breeding - SWA5005

Mbabane, Eswatini, 23-27 June 2025

Project Officer: I.K. Bimpong

Project Objective: Strengthen participant researcher capacity in plant mutation breeding techniques, specifically in selection and phenotyping processes and related techniques in developing rice crops for the country.

Course Objective: Train participants in mutation breeding techniques for crop improvement, enhancing skills in identifying and selecting desirable mutants, introducing the application of Next Generation Sequencing (NGS) for detecting novel mutations, and promoting the development of stress-tolerant crop varieties to accelerate breeding programs and ensure food security in the country.

Twenty participants (ten women and ten men researchers) attended the training.

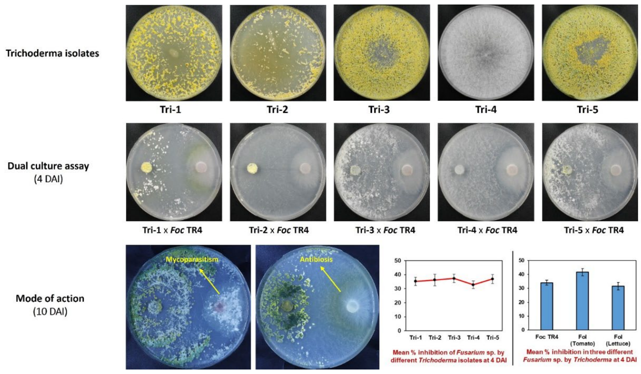
Developments at the Plant Breeding and Genetics Laboratory (PBGL)

Activities on developing sustainable tailored biological solutions

As previously reported, the Laboratory of Plant Breeding and Genetics initiated activities on developing sustainable tailored biological solutions combining nuclear mutagenesis techniques with consortium-based formulation methodologies to enhance biocontrol and plant growth-promoting traits of native microorganisms. Towards this, in addition to the bacteria reported in our last issue, the biocontrol potential of *Trichoderma* sp. is being exploited and improvised for enhancing its effectiveness against Fusarium wilt (strain TR4) in banana.

Five *Trichoderma* sp. were isolated from soils obtained from the rhizosphere of healthy bananas using Trichoderma selective media. The isolates were first assigned to the genus Trichoderma based on their growth and spore formation characteristics in the medium and later classified as *T. asperellum*, *T. harzianum*, *T. hamatum*, and *T. lixii* based on the ITS sequence. Due to the exceptionally high number of closely related species, these species are currently being validated with other phylogenetic markers.

To confirm their antagonistic properties, the Trichoderma isolates were subjected to a dual culture test against the *Foc* TR4 isolate. Six mm pieces of mycelium were cut from actively growing cultures of Trichoderma and *Foc* TR4, placed in opposite corners of Petri dishes, and allowed to grow for seven days at 27°C. The observations were evaluated based on the growth rate of the Trichoderma isolates, the percentage growth inhibition of *Foc* TR4, and the mode of action of the control of *Foc* TR4. Several isolates covered the plates within 3-4 days and completely inhibited the growth of the pathogen. Three isolates showed very high mycoparasitism, with these isolates overgrowing *Foc* TR4 and using it as a nutrient source. Two isolates showed very strong pigmentation in the medium, especially at the contact point between Trichoderma and *Foc* TR4, indicating potential growth inhibition through the process of antibiosis.



The next steps include, mutagenesis of the selected strains using X-rays, gamma radiation, or electron beams. Using a bacterial strain (*Priesta megaterium*), it has already been shown that gamma radiation produces mutants that grow faster and have a higher reproduction rate than the wild type. The next step is to screen the mutants for a better biocontrol activity.

In addition, efforts are being made to optimize assays to test mutant strains for biocontrol properties in a high throughput manner. This includes using in planta methods using "model species" as well as bananas. The dual culture plates using bacterial strains and *Foc* TR4, *F. oxysporum* f. sp. *lycopercici* and F. *oxysporum* f. sp. *lactucae* demonstrated several bacterial mutant strains inhibiting all three tested Fusarium oxysporum f.species under hydroponics and in-soil experiments with tomatoes and lettuce patho-systems. In two treatments with bacteria, faster seedling growth was observed. The most promising mutant strains are being planned to be tested in banana to compare the obtained results.

Climate Change Project

Climate change is anticipated to impose multiple stressors on plants. Future scenarios predict not only an increase in temperature and drought but also elevated CO_2 levels on Earth. Projections suggest that CO_2 levels could exceed 800 ppm by the end of the century, compared to the current level of around 400 ppm (NOAA, 2024).

To compare the effects of drought and elevated CO_2 stresses PBGL hosted Yiting Chen, a PhD student from the University of Copenhagen, and collaborated with SWMNCL on a joint pilot study assessing the impact of combined effect of drought and elevated

CO_2 on C3 and C4 plants. The study was based on published knowledge that C4 plants exhibit higher photosynthetic efficiency, water use efficiency, and transpiration rates under drought conditions compared to C3 plants (Tahmasebi & Niazi, 2021). This project was supported by the Permanent Mission of UK as Peaceful Use Initiative (PUI) on "Ensuring Food Security and Safety by Future-Proofing Dryland Crops under Climate Change".

Over forty-eight pots of each crop were grown in two different climate-controlled chambers (one with 400 ppm and one with 800 ppm of CO_2). Both chambers were maintained at 25°C, 60% relative humidity, a 16-hour photoperiod, and >500 µmol/m²/s PAR. Half of the pots were continuously watered, while the other half experienced progressive soil drying by withholding irrigation until stomatal conductance dropped to approximately 10% of that of the irrigated group. Furthermore, half of the plants received potassium (K) treatment, while the other half did not. All plants received 1.5g of nitrogen (applied as 15N-labeled urea) and 0.8g of phosphorus.

Periodical observation on various productivity parameters, physiological and biochemical parameters, yield and grain nutritional parameters was recorded. During the drought period, stomatal conductance, transpiration rate, relative water content (RWC), and chlorophyll content (SPAD) were measured. After drought stress period, plants were allowed to recover, and flowering and plant height were recorded. Upon maturity, the plants were harvested to weigh the dry biomass and assess the stem-to-foliage weight ratio.

Elevated CO_2 levels had a significant effect on wheat and sorghum, with higher biomass observed in both plants at 800 ppm. Sorghum plants showed larger and more foliage but experienced significantly delayed heading and anthesis at 800 ppm, with several not forming panicles. While drought stress significantly decreased biomass in both crops, K treatment significantly increased biomass and plant height in sorghum but did not demonstrate any effect in wheat.

Similarly, while combined drought and high CO_2 stresses significantly decreased stomatal conductance and transpiration rates in wheat, the stomatal conductance and transpiration rates in sorghum were much lower and stayed unaffected by drought. Similarly, both wheat and sorghum plants showed reduced RWC under combined stresses.

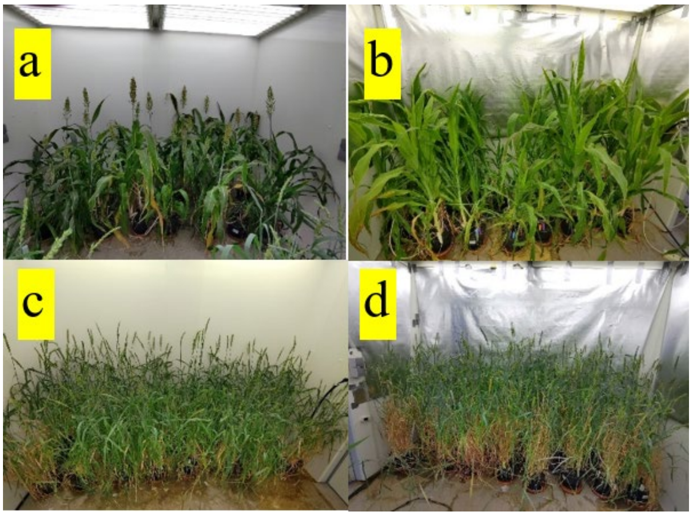


Figure 1 a) Sorghum at 400ppm, b) Sorghum at 800 ppm, c) Wheat at 400ppm, d) Wheat at 800 ppm

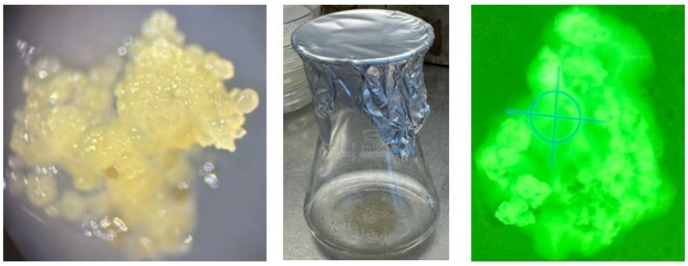
- Tahmasebi, A., & Niazi, A. (2021). Comparison of transcriptional response of C3 and C4 plants to drought stress using Meta-Analysis and Systems Biology Approach. Frontiers in Plant Science, 12. https://doi.org/10.3389/fpls.2021.668736
- NOAA. (2024, April 9). Climate change: atmospheric carbon dioxide. NOAA Climate.gov. https://www.climate.gov/news-features/understanding-climate/climate-change-atmospheric-carbon-dioxide

Advancing Mutation Breeding in Banana through Somatic Embryogenesis

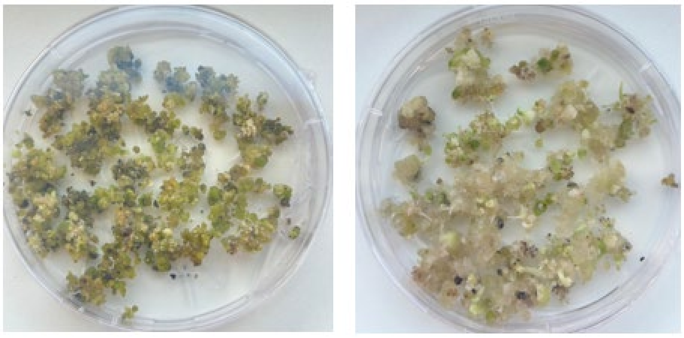
As part of its broader mission to improve mutation induction methods in vegetatively propagated crops, PBGL has expanded its work on *in vitro* regeneration using single cell derived systems. While banana is widely cultivated and propagated clonally, traditional methods of inducing mutations often result in chimeric tissues-plants carrying a mix of mutated and non-mutated cells. This heterogeneity makes it challenging to stabilize desired traits.

In order to address these issues, PBGL has initiated somatic embryogenesis protocols in banana, aiming to regenerate whole plants from single somatic cells. Somatic embryogenesis offers several important advantages in the context of mutation breeding. This approach helps avoid chimerism and results in more uniform mutant lines. During the past year, an initial protocol for inducing embryogenic callus from immature male flower explants of banana was successfully developed. These calli, once established, were maintained in culture and induced to form somatic embryos under specific hormonal and environmental conditions. Early regeneration results are promising, and banana plantlets have been regenerated from somatic embryos, showing the potential for scaling up this platform for mutation induction and genetic improvement. This advancement marks an important step forward in generating stable banana lines for future screening and breeding efforts.

A) Induction of somatic embryogenesis from immature male flowers.



B) Cell suspension



C) Somatic embryos regeneration

D) Germination of somatic embryos.

Table 1. Crop Irradiation Services

Request Number	Country	Request Type	Crop/Species
1797	Germany		*Brassica napus*
1798	Malawi	TC	Soybean
1799	The Netherlands		Ornamentals
1800	PBU		Banana
1801	UK		strawberry
1802	Cameroon	TC	Bean, sorghum
1803	Myanmar	TC	Rice, *Vigna radiata*
1804	Hungary		Ornamentals
1805	Tanzania	CRP	*Phaseolus vulgaris*
1806	Germany		*Euphorbia pulcherrima*, *Portulaca umbraticola*
1807	Tanzania		Rice, Sunflower
1808	Namibia	TC	Cowpea, Pearl millet

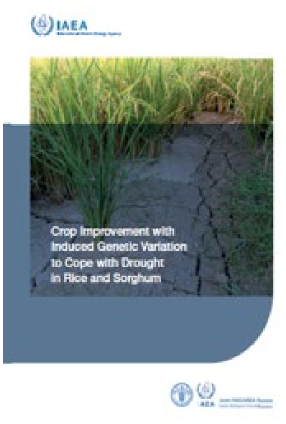
Table 1 lists the irradiation requests that PBGL has received so far (as of 2025-04-17). PBGL received 12 requests from 9 Member States across 14 different plant species covering a total of 34 accessions/varieties.

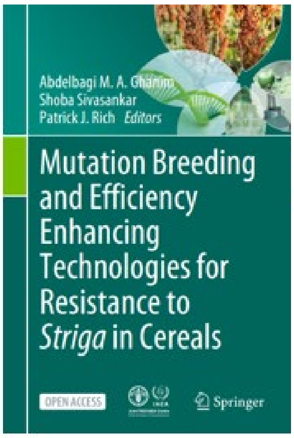
Table 2. Individual Training Activities at the Plant Breeding and Genetics Laboratory (PBGL)

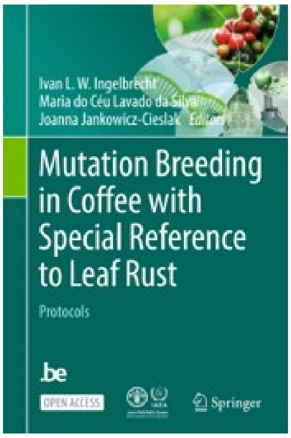
Name	Country	Status	Topic	Period
Mr Radisras NKURUNZIZA	Uganda	PHD-Consultant	Coffee mutation breeding	1 year
Mr Hassan MDUMA	United Republic of Tanzania	PHD-Consultant	Mutation breeding of African cooking banana for Fusarium Wilt resistance	1 year
Ms Siti HISHAM	Malaysia	Intern		1 year
Mr Sharat CHANDRAN	India	PHD-Consultant		1 year
Ms Danke ZHANG	China	Intern		1 year
Ms Matsikoane Malineo SEFOTHO	Lesotho	Fellow	1. Principles of mutation induction 2. Development and handling of mutant populations 3. Detection and selection of mutant plants 4. Introduction to mutation breeding efficiency enhancing technologies available at PBGL	3 months
Ms Puleng Mariam LETUMA	Lesotho	Fellow	1. Principles of mutation induction 2. Development and handling of mutant populations 3. Detection and selection of mutant plants 4. Introduction to mutation breeding efficiency enhancing technologies available at PBGL	3 months
Ms Margueritte OUEDRAOGO	Burkina Faso	Fellow	Molecular Breeding, including PCR, DNA extractions and QC (hands-on), Genetic/genomics/NGS, KASP marker genotyping and MAS	9 months

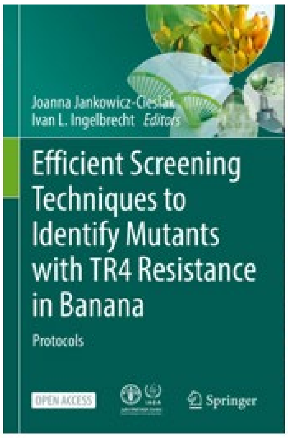
Publications

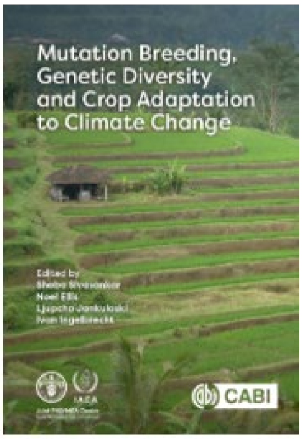
Books

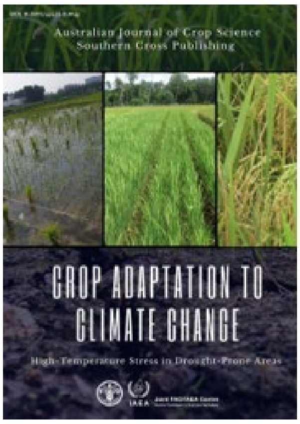


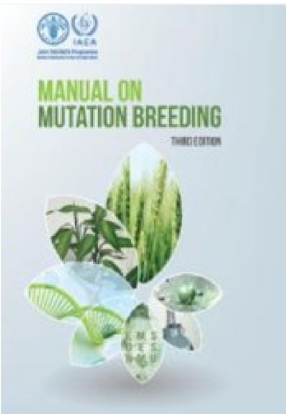


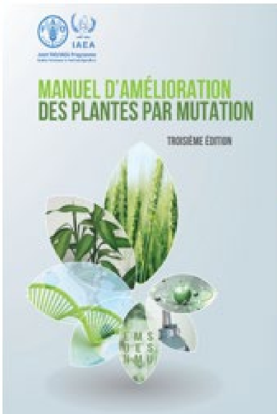


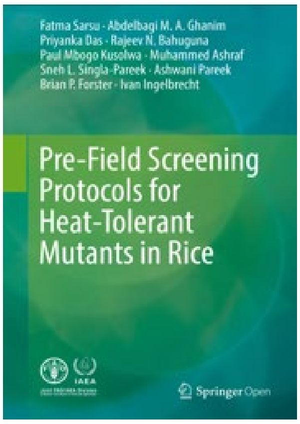












Crop Improvement with Induced Genetic Variation to Cope with Drought in Rice and Sorghum
Editors: F. Sarsu, S. Penna, S. Sivasankar
International Atomic Energy Agency, 2024
ISBN 978-92-0-135124-1 (eBook)
CRCP-IGV-004

Mutation Breeding and Efficiency Enhancing Technologies for Resistance to Striga in Cereals
Editors: Abdelbagi M. A. Ghanim, Shoba Sivasankar, Patrick J. Rich
Springer, 2023
ISBN 978-3-662-68181-7 (eBook)
Mutation Breeding and Efficiency Enhancing Technologies for Resistance to Striga in Cereals | SpringerLink

Mutation Breeding in Coffee with Special Reference to Leaf Rust
Editors: Ivan L.W. Ingelbrecht, Maria do Céu Lavado da Silva, Joanna Jankowicz-Cieslak
Springer, 2023
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Mutation Breeding in Coffee with Special Reference to Leaf Rust: Protocols | SpringerLink

Efficient Screening Techniques to Identify Mutants with TR4 Resistance in Banana
Editors: Joanna Jankowicz-Cieslak, Ivan L. Ingelbrech
Springer, 2022
ISBN 978-3-662-64915-2 (eBook)
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Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change
Edited by S. Sivasankar, T.H.N. Ellis, L. Jankuloski, I. Ingelbrecht.

CABI, 2021
ePDF 9781789249101

Crop Adaptation to Climate Change: High-Temperature Stress in Drought-Prone Areas
Guest Editors: F. Sarsu, B.P. Forster, S. Sivasankar
Australian Journal of Crop Science, Southern Cross Publishing, Volume 14, Number 8, 2021
DOI: 10.21475/ajcs.21.15.09.sp
https://www.cropj.com/full_issue_IAEA_AJCS.pdf

Manual de mejoramiento por mutaciones, Tercera edición
Editado por M.M. Spencer-Lopes, Forster, B.P., Jankuloski, L., Sub Programma de Mejoramiento de Plantas y Genética, División Conjunta FAO/OIEA de Técnicas Nucleares en Alimentación y Agricultura.Manu
ISBN 978-92-5-133741-7 © FAO, 2021
Manual de mejoramiento por mutaciones (fao.org)

Manuel d'amélioration des plantes par mutation, Troisième édition
Édité par. M.M. Spencer-Lopes, B.P. Forster et L. Jankuloski, Sous-programme de Génétique et d'Amélioration des Plantes
Division mixte FAO/IAEA des Techniques Nucléaires appliquées à l'Alimentation et à l'Agriculture.
ISBN 978-92-5-132932-0 © FAO, 2020
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Pre-Field Screening Protocols for Heat-Tolerant Mutants in Rice
Sarsu, F., Ghanim, A.M.A., Das, P., Bahuguna, R.N., Kusolwa, P.M., Ashraf, M., Singla-Pareek, S.L., Pareek, A., Forster, B.P., Ingelbrecht, I.L. Springer, 2018
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Development of Tolerant Crop Cultivars for Abiotic Stresses to Increase Food Security (IAEA-TEC DOC-1969)
Contributors: N.K.A. Amoah, B. Manneh and I.K. Bimpong.
ISBN 978-92-0-123321-9
ISBN 978-92-0-123221-2 (PDF)

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JANKOWICZ-CIESLAK, J., GOESSNITZER, F., INGELBRECHT, I.L.W. (2023) Chemical mutagenesis of mature seed of Coffea arabica L. var Venecia using EMS. In: Mutation Breeding in Coffee with Special Reference to Leaf Rust. Springer Nature.

NKURUNZIZA, R., JANKOWICZ-CIESLAK, J., WERBROUCK, S., INGELBRECHT, I.L.W. (2023) Use of open-source tools for imaging and recording phenotypic traits of a coffee (Coffea arabica L.) mutant population. In: Mutation Breeding in Coffee with Special Reference to Leaf Rust. Springer Nature.

WARTHMANN, N. (2023) Targeted Sequencing in Coffee with the Daicel Arbor Biosciences Exome Capture Kit. In: Mutation Breeding in Coffee with Special Reference to Leaf Rust. Springer Nature.

Conference Abstracts and Posters

2024

Vezzone, M., Dercon G.,Vlachou, C., Bhatnagar-Mathur, P. (2024). Response of dryland crops to climate change: Understanding the nexus between water and nutrient use efficiency, nutritional security, and food safety. Tropentag 2024, September 11 - 13, Vienna, Austria

2023

SUBRAMANIAN N, PILLAI S, ROONEY W, BAGAVATHIANNAN M, SIVASANKAR S (2023) Utilization of electron-beam mutagenesis for sorghum crop improvement. Global Sorghum Conference 2023, June 5-9, Montpellier, France

SIVASANKAR S (2023) Innovative plant breeding for climate-resilient crops. Invited plenary lecture at the 5th Mindanao Summit of the Philippine Phytopathological Society, Inc. - Southern Mindanao Division (PPS-SMD), June 9, 2023, Davao City, Philippines.

DHANASEKAR P, SOUFRAMANIEN J, DHOLE VJ, HINGANE AJ, SIVASANKAR S (2023) Physical mutagenesis for induction of resistance against *Maruca* pod borer in cowpea [*Vigna unguiculata* (L.) Walp]. Submitted to the International Conference on Pulses: "Smart Crops for Agricultural Sustainability and Nutritional Security" February 10-12, 2023, New Delhi, India.

SIVASANKAR S (2023) Induced genetic variation and mutation breeding for crop improvement at the Joint FAO/IAEA Centre. Invited talk at the 2nd International & 12th Biennial Conference of the Plant Breeding and Genetics Society of Bangladesh 2023, February 18-19, 2023, Dhaka, Bangladesh.

SIVASANKAR S (2023) The role of induced genetic variation in crop improvement towards food and nutrition security – a global context. Invited Keynote Lecture at the International Conference on Food and Nutrition Security (iFANS-2023) January 6-9, 2023, Mohali, India.

JAWDAT D., MOSTAFA O., JANKULOSKI L., SARSU F., MALEK M., MIR A.N. (2023) Mutation breeding, an affordable crop improvement strategy in challenging times: Barley mutation breeding projects in Syria and the urge for acceleration. The 3rd International Barley Mutant Conference- 8-10 October 2023, - Kurashiki, Japan

KIRYAKOV I., PETKOVA M., AZIZ S., MASHEVA V., SARSU F., TOMLEKOVA N. (2023) Phytopathology and molecular investigation of resistances to bacterial and fungal patogens in common bean mutant and breeding lines. 2-4 November 2023, Antalya, Türkiye.

AZIZ S., MLADENOV P., GULER U., ONAT B., PLANCHON S., TOPALOVA E., MASHEVA V., KIRYAKOV I., RENAUT J., SALIH B., SARSU F., TOMLEKOVA N. (2023) Drought stress tolerance in common bean mutant and breeding lines: Physiology and proteomics response. 2-4 November 2023, Antalya, Türkiye

JANKOWICZ-CIESLAK, J., WARTHMANN, N., ENRIQUE MORALES ZAMBRANA, A., VILJOEN, A., INGELBRECHT, I. (2023) Induced Mutagenesis of Banana for Resistance to Fusarium Wilt Tropical Race 4. The Plant & Animal Genome Conference (PAG), January 13 - January 18, San Diego, CA, USA.

WARTHMANN, N., MURRAY, K.D., MORALES ZAMBRANA, A.E., CONDE M.V., MORALES., L., ALI, A., GHANIM, A.M., BOREVITZ, J.O., INGELBRECHT, I. (2023) Mainstreaming Genomics: Protocols for Genome Re-Sequencing at the Population Scale. The Plant & Animal Genome Conference (PAG), January 13 - January 18, San Diego, CA, USA.

NKURUNZIZA, R., JANKOWICZ-CIESLAK, J., INGELBRECHT, I.L.W., WERBROUCK, S. (2023) In vitro tissue culture and genotyping innovations to accelerate mutation-assisted breeding of Coffea arabica. COPYTREE (European Network for Innovative Woody Plant Cloning - Cost Action 21157), Faculty of Chemistry, Universidad de Santiago de Compostela, 17 - 18 April 2023, Spain.

News Highlights

- Harnessing Science and Partnerships to Transform the Millet Sector: A Global Research Effort **(April)**
- COP29: Harnessing Science, Technology and Innovation (STI) for Climate-Resilient Agrifood Systems | IAEA **(November)**
- Small Islands, Big Impact: Improving Agriculture and Nutrition in Pacific Island States | IAEA **(November)**
- Keine Gentechnik, dafür Radioaktivität: Was in den österreichischen Labors der IAEA passiert - Technik - derStandard.at › Wissenschaft **(November)**
- 76. Innovations in Nuclear Sci - S/GWI's Innovation Station - Apple Podcasts **(October)**
- Despite climate extremes, Bangladesh improves harvests to feed a growing population | IAEA **(September)**
- The IAEA's successful field trial | IAEA **(September)**
- Enhancing mung bean and chickpea cultivation in Pakistan through nuclear techniques | IAEA **(September)**
- Seeds in space | IAEA **(September)**
- Can the harsh conditions of space breed more resistant crops for Earth? | Grist **(May)**
- COMESA countries upgrade laboratory diagnostic capacity to manage Fusarium TR4 - International Plant Protection Convention (ippc.int) **(May)**
- https://www.iaea.org/newscenter/news/fao-and-iaea-underscore-the-need-to-enhance-agrifood-systems-through-climate-resilient-and-nutrition-dense-crops **(April)**

Websites and Links

- Plant Breeding and Genetics Subprogramme: https://www.iaea.org/topics/plant-breeding
- Infographic on Mutation Breeding: https://www.iaea.org/newscenter/multimedia/videos/using-nuclear-science-to-boost-plant-biodiversity
- Mutant Variety Database: http://mvd.iaea.org
- Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture: https://www.iaea.org/about/organizational-structure/department-of-nuclear-sciences-and-applications/joint-fao/iaea-centre-of-nuclear-techniques-in-food-and-agriculture
- Plant Breeding Publications: Plant breeding publications | IAEA
- Food and Agriculture Organization of the United Nations (FAO): Home | Food and Agriculture Organization of the United Nations (fao.org)

Impressum

Plant Breeding and Genetics Newsletter No. 55

The Plant Breeding and Genetics Newsletter is prepared twice per year by the Plant Breeding and Genetics Subprogramme, Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture

International Atomic Energy Agency
Vienna International Centre, PO Box 100, 1400 Vienna, Austria
Printed by the IAEA in Austria, July 2024

25-03380