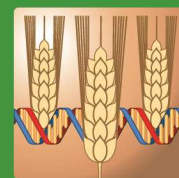




Joint FAO/IAEA Programme
Nuclear Techniques in Food and Agriculture

Plant Breeding & Genetics Newsletter



<https://www.iaea.org/topics/plant-breeding>

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SPECIAL ISSUE

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AWARDS IN PLANT MUTATION BREEDING AND ASSOCIATED BIOTECHNOLOGIES

VIENNA
20 SEPTEMBER 2021



*The Plant Breeding and Genetics Newsletter 48 is a special issue commemorating the **Achievement Awards in Plant Mutation Breeding and Associated Biotechnologies 2021**. Outstanding Achievement Awards, Women in Plant Mutation Breeding Awards and Young Scientists Awards were presented to 28 recipients. The Award Ceremony was held on 20 September 2021 as a Side Event of the 65th General Conference of the IAEA at the IAEA Headquarters in Vienna, Austria.*

To Our Readers

Dear Colleagues,

I am excited to announce this special issue of the Plant Breeding and Genetics (PBG) Newsletter that celebrates a very good year completed in close cooperation with, and providing technical support and services for, Member State Counterparts, amidst a continuing global pandemic.

An important highlight for PBG in 2021 was the Awards Ceremony held on 20 September for Achievements in Plant Mutation Breeding and Associated Biotechnologies. Awards were presented during a side event of the 65th regular session of the IAEA General Conference at the IAEA Headquarters in Vienna, Austria. The Ceremony recognized 28 recipient individuals, groups or institutions across **11 Outstanding Achievement Awards, 10 Women in Plant Mutation Breeding Awards and seven Young Scientists Awards**. This special issue of the PBG Newsletter commemorates key technical achievements that were recognized by these awards (pages 33–63).

An equally important output during the second half of the year was the rapid response to the request for help to **combat the banana Fusarium Wilt Tropical Race 4 (TR4) in the Andean Region**. Fusarium Wilt is considered the most important lethal disease of banana and is believed to have originated in Southeast Asia. It was first reported from Australia in 1876 prior to spread to other parts of the world. The disease caused by *Fusarium oxysporum* f.sp. *cubense* (Foc), Race 1, invaded banana-growing countries in Central and South America destroying plantations, wreaking havoc on the export industry. Discovery of genetic resistance to Race 1 in the banana variety Cavendish led to the disappearance of the disease for a while until the 1990s, when Cavendish began to succumb to a new race of the pathogen, tropical race 4 (TR4), first in Southeast Asia and then Australia. In subsequent decades, TR4 spread rapidly in different banana production systems in Asia, Africa and the Middle East, and was reported for the first time in Latin America in Colombia in 2019, and in Peru in April 2021. Responding rapidly to the request from the Andean Community, PBG in close cooperation with the IAEA Technical Cooperation programme, organized an Expert Mission at the Universidad Nacional Agraria La Molina during 25–28 October 2021. The Expert Mission brought together plant breeders, phytopathologists and phytosanitary officials from Bolivia, Colombia, Ecuador and Peru to develop an urgent workplan for the detection, containment and management of the disease. Requisitions were placed for urgent equipment and consumables, two regional training courses were planned for 2022, and a regional project was designed.

A **new Coordinated Research Project (CRP), Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development (D24015)** was approved

and a call for proposals is open based on a concept note prepared through a Consultants' Meeting. This CRP will address cutting-edge science central to the application of induced genetic variation for plant breeding and crop improvement in the coming years and decades. Its focus is on (1) determining the effect of different mutagen sources, including space radiation, on plant genomes and physiological attributes, (2) establishing genetic associations for obvious phenotypes to identify and use the molecular bases of mutations for marker-assisted breeding and gene editing, and (3) exploring the concept of genomic prediction in mutant populations.

The **CRP D24014** that was launched in 2021 on *Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops* held its first Research Coordination Meeting in September 2021 in virtual mode. The single-contract **CRP D20003** on *Impact Assessment of Mutant Rice Varieties Developed by the Bangladesh Institute of Nuclear Agriculture* was completed and part of the results have been published, with the remaining results in preparation for publication.

An agreement was signed with the Universidad Nacional Agraria La Molina, Peru, recognizing it as a **new IAEA Collaborating Centre on Plant Mutation Breeding and Associated Biotechnologies**. This Collaborating Centre agreement for a period of four years was signed at a side event during GC 65 in September 2021. A proposal by PBG for a workshop on *Plant Mutation Breeding* at the **International Plant and Animal Genome Conference (PAG XXIX, 8–12 January 2022)** has been accepted, and the workshop is scheduled for Tuesday, 11 January 2022.

PBG continued to provide technical support to the **implementation of 49 Technical Cooperation Projects (TCPs)**, of which 35 began in 2020, and to the **design of 35 new TCPs** planned for the 2022–23 cycle. In the endeavor to advance plant mutation breeding in the digital age, and to mainstream and standardize sophisticated statistical software for experimental design and analysis, a regional training course was implemented for the Asia Pacific Region under the TC project, RAS5088, during 22 November to 3 December 2021. This **regional training course on Digital Breeding Management Systems and Field Experimental Data Analysis** was delivered virtually to 30 trainees from 10 Member States.

R&D efforts at the PBG Laboratory during the second half of the year centered on continued development of the bioinformatic toolbox and advancing the research on banana TR4 resistance. The bioinformatic toolbox now address the plotting of allele frequencies, and identifying copy number variations, along with visualization of information. Under the previous CRP on banana wilt and coffee rust

(CRP D22005), the Laboratory had set up a mutation breeding programme with Cavendish bananas. A total of eight mutants have been identified with no symptoms upon inoculation with the pathogen. Genomic analysis of a putative mutant identified 28 deletions ranging from 100 kb to 1 Mb, and further analysis is in progress.

On the publications front, I am happy to announce the availability of (1) the book, *'Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change'* resulting from the FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology at 20210424108.pdf (cabi.org), and (2) the special issue of the Australian Journal of Crop Science, *'Crop Adaptation to Climate Change: High-Temperature Stress'*, resulting from a recently completed CRP under the same name, at [CROP ADAPTATION TO CLIMATE CHANGE: High-Temperature Stress in Drought Prone Areas](https://www.cropj.com) ([cropj.com](https://www.cropj.com)). Also published during the second half of the year is the IAEA TECDOC on *Development of Tolerant Crop*

Cultivars for Abiotic Stresses to Increase Food Security, that can be accessed at [IAEA-TECDOC-1969](https://www-tecdoc.iaea.org/TECDOC/TECDOC1969.html).

Finally, I am delighted to announce and welcome two new Technical Officers to PBG: Ms Anupama Hingane, who joined the PBG Laboratory in November 2021 from the Consultative Group on International Agricultural Research or CGIAR, and Ms Cinthya Zorrilla, who joined the PBG Section in November 2021 from the Universidad Nacional Agraria La Molina, Peru.

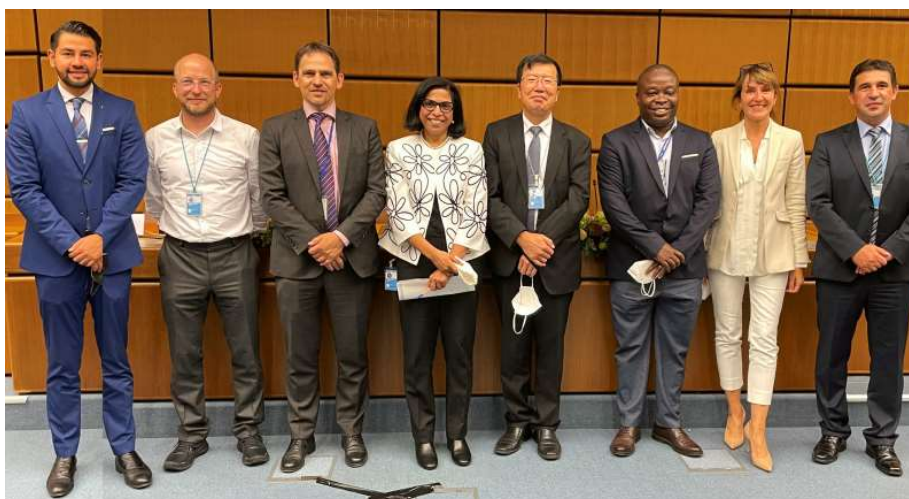
My sincere appreciation for all your support and continued efforts during these difficult times! I look forward to our continuing strong collaborations to deliver important results for global food security and crop adaptation to climate change.

Shoba Sivasankar
Head

Plant Breeding and Genetics Section



Side Event, 20 September 2021.



Side Event, 20 September 2021.

Staff

Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture

Name	Title	Email	Extension	Location
Qu LIANG	Director	Q.Liang@iaea.org	21610	Vienna

Plant Breeding and Genetics Subprogramme

Name	Title	Email	Extension	Location
Shoba SIVASANKAR	Section Head	S.Sivasankar@iaea.org	21626	Vienna
Isaac Kofi BIMPONG	Plant Breeder/Geneticist	I.Bimpong@iaea.org	21617	Vienna
Ljupcho JANKULOSKI	Plant Breeder/Geneticist	L.Jankuloski@iaea.org	21623	Vienna
Cinthy ZORRILLA	Plant Breeder/Geneticist	C.Zorrilla@iaea.org	21618	Vienna
Katayoun ENTEKHABI	Programme Assistant	K.Entekhabi@iaea.org	21621	Vienna
Luis Mauricio ALFONZO GODOY	Team Assistant	L.M.Alfonzo-Godoy@iaea.org	21620	Vienna
Ivan INGELBRECHT	Laboratory Head	I.Ingelbrecht@iaea.org	28285	Seibersdorf
Norman WARTHMAN	Molecular Geneticist	N.Warthmann@iaea.org	28260	Seibersdorf
Anupama HINGANE	Plant Breeder/Geneticist	A.Hingane@iaea.org	28628	Seibersdorf
Abdelbagi MUKHTAR ALI GHANIM	Consultant	A.Mukhtar-Ali-Ghanim@iaea.org	28268	Seibersdorf
Samira TAJEDINI	Consultant	S.Tajedini@iaea.org		Seibersdorf
Hassan MDUMA	Consultant	H.Mduma@iaea.org		Seibersdorf
Mirta MATIJEVIC	Technician	M.Matijevic@iaea.org	28317	Seibersdorf
Joanna Beata JANKOWICZ-CIESLAK	Technician	J.Jankowicz@iaea.org	28275	Seibersdorf
Florian GOESSNITZER	Technician	F.Goessnitzer@iaea.org	28279	Seibersdorf
Adel ALI	Technician	A.Ali@iaea.org	28427	Seibersdorf
Ksenija AJVAZI	Team Assistant	K.Ajvazi@iaea.org	28750	Seibersdorf
Michael HALL	Intern	M.Hall@iaea.org		Seibersdorf

Plant Breeding and Genetics Section

Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture
Wagramer Strasse 5, P.O. Box 100, 1400 Vienna, Austria
Phone: +431 2600 + extension; Fax: +431 26007

Plant Breeding and Genetics Laboratory

FAO/IAEA Agriculture & Biotechnology Laboratories, 2444 Seibersdorf, Austria
Phone: +431 2600 + extension; Fax: +431 26007

Staff News

Welcome



Ms Anupama J. Hingane (India) has joined as Plant Breeder/Geneticist in the Plant Breeding and Genetics Laboratory (PBGL) in November 2021. She has obtained a Ph.D in Genetics and Plant Breeding from Mahatma Phule Krishi Vidyapeeth, Rahuri, India. She has over 12 years of experience in various national and international organizations

and worked on crops like cluster-bean, cotton, wheat and pigeonpea.

Before joining IAEA, she was leading Pigeonpea Breeding Programme at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) for Asia, based at Hyderabad, India. In this role, she worked on enhancing genetic gains while modernizing the breeding programme in the areas of breeding methodology, phenotyping, application of molecular tools, and deploying the Digital Breeding Databases to make data-driven decisions and has also contributed in pigeonpea breeding activities at the Eastern and Southern Africa (ESA) as well.

She has contributed to the development and release of medium-duration pigeonpea hybrids ICPH 3762 and ICPH 2740 in India. During her assignment with ICRISAT, she has facilitated in sharing of more than 3000 pigeonpea breeding lines to researchers in Asia, Africa, Australia, USA and National Agricultural Research System (NARS) from India.

She has also gained expertise in speed breeding technologies and contributed to standardising upscaling protocols for sorghum, pearl millet, groundnut and chickpea.

Anupama has also attracted several funding projects in collaboration with reputed institutions and donors. She organized several national and international training courses and workshops for NARS, private companies, and farmers. She has also guided one PhD, three postgraduates, and four interns in pigeonpea breeding research, and has 30 research articles to her credit.



Ms Cinthya Zorrilla (Peru) joined PBGL in November 2021. She obtained her BSc degree in Biology from Universidad Nacional Agraria La Molina (UNALM) in Lima, Peru. After obtaining her BSc, she started her career with the International Potato Center where she managed the molecular characterization and genetic

diversity analysis of wild and cultivated potato accessions as well as other Andean root and tuber crops such as oca, ulluco, arracacha and yacon for four years.

She obtained her PhD Degree in Plant Breeding and Plant Genetics at the University of Wisconsin, Madison where she was also a graduate research assistant in the Potato Breeding Programme assisting in the valuation of field trials, as well as phenotypic and genotypic data analysis. Her PhD research was on understanding the genetics of potato tuber calcium and its implications in breeding for improved quality where she applied QTL mapping, identification of markers associated to QTL, genetic transformation, gene expression and field/greenhouse/*in vitro*/microscopic evaluations.

Cinthya worked at the Instituto Nacional de Innovacion Agraria (INIA) for four years where she was the Director of the Subdivision of Genetic Resources. At this position, she was also the head of the Peruvian National Genebank that conserves more than 250 species of plants, including medicinal plants, crops, and crop wild relatives; they are conserved in the form of seeds, *in vitro* culture, and field conditions. This genebank also conserves DNA from native and introduced animal genetic resources, as well as pathogenic and beneficial microorganisms associated to plant genetic resources. She commanded the design of an institutional database to store information related to passport, phenotypic and molecular data. She led a CIP and INIA partnership to collect potato crop wild relatives for the global project 'Towards a more complete coverage of the diversity of crop wild relatives' funded by the Crop Diversity Trust. She was principal investigator (PI) in several pre-breeding projects to identify interesting traits that could be transferred from the genebank to the breeding programmes. She was the Peruvian national coordinator for plant genetic resources, animal genetic resources and biodiversity for food and agriculture for the FAO's Commission of Genetic Resources for Food and Agriculture.

Cinthya has worked as a visiting professor at UNALM for four years teaching plant genetics, plant breeding, biology and microbiology to undergrad and grad students.

Cinthya's research work has led to the identification of several germplasm accessions with potential to be used in breeding programmes. She has six peer-reviewed publications and two book chapters. She has trained four BSc and three MSc students from Latin America.



Ms Samira Tajedini (Iran) joined the PBGL Laboratory (PBGL) in June 2021 as a consultant.

Samira has an MSc degree in Plant Breeding and Biotechnology on 'Evaluation of genotype \times environment interactions and stability analysis in barley' where she evaluated the stability of high yielding, adapted varieties in five locations of Iran during 2011–2012 growing season. In May 2018 she joined the PBGL as an intern as part of her

PhD ‘Study of haploidy system in rice and sorghum via androgenesis’ in the context of the CRP D25005 on ‘Mutation breeding for resistance to *Striga* parasitic weeds in cereals for food security’ where she successfully established protocols for *in vitro* microspore and/or anther culture used to develop mutant doubled haploid populations in rice. Samira has experience in *in vitro* plant cell and tissue culture, ploidy analysis and statistics. In her current role, Samira is mainly working on *in vitro* regeneration of coffee and single-cell mutagenesis with partial support from the PUI ‘Establishing climate-smart coffee-banana production systems in Eastern Africa’ (funded by Belgium). Welcome back Samira!



Mr Michael Hall (Texas, USA) joined the PBGL in October 2021 as an intern.

Before this internship Michael was working as a Teaching Assistant in the Department of Management Science and Statistics in the College of Business at University of Texas, San Antonio, USA supporting undergraduate courses. Michael holds a MSc degree in Statistics and Data Science from the College of Business, University of Texas, San Antonio, a BSc in Applied Statistics with a Minor in Mathematics from the University of Houston Downtown, and a BBA in Economics from the Sam Houston State University. Michael considers himself a statistician who enjoys the art and science of data analysis, particularly visualisation. He is interested in solving real world problems using data science, mathematics, and statistics. He is passionate about the environment, the planet, nuclear science applications, linguistics, computer languages, and international relations. Michael hopes to learn data science techniques and methodologies in plant breeding and genetics and looks forward to contributing to PBGLs research efforts.



Mr Hassan Mduma (United Republic of Tanzania) joined the PBGL Laboratory in October 2021 as a PhD consultant.

Hassan obtained a BSc in Horticultural Sciences at Sokoine University, Tanzania and MSc in Life Science (Sustainable Agriculture) at Nelson Mandela African Institution of Science and Technology, Tanzania. Funded by the PUI on Establishing climate-smart coffee-banana production systems in Eastern Africa (Belgium), Hassan is currently taking his PhD in Plant Pathology from Stellenbosch University, South Africa working with the banana breeding programme of the International Institute of Tropical Agriculture, Arusha Tanzania. For his PhD, Hassan wants to develop East African cooking bananas, called Mchare, with resistance to Fusarium wilt race 1 and TR4 through mutation breeding. He will also be applying modern biotechnology

and molecular tools related to plant pathology to screen the mutant population for mutations in pre-selected genes underlying traits of interest for Mchare breeding as part of PBGL’s overall efforts to establish practical methods for molecular-based, predictive mutation breeding at population-level. Welcome Hassan!



Ms Abigail Tweneboah Asare (Ghana) is a researcher working at the Biotechnology & Nuclear Agriculture Research Institute (BNARI)/GAEC, Ghana. Since November 2021 she is on an IAEA Fellowship for her PhD study programme in Plant Breeding at the West Africa Centre for Crop

Improvement (WACCI)/University of Ghana. Part of her research will be conducted at the Plant Breeding and Genetics Laboratory (PBGL) and part at the Applied *In Vitro* Plant Biotechnology Laboratory, UGent, Belgium. She holds an MPhil in Nuclear Agriculture (Biotechnology and Mutation) and a BSc in Agriculture from the School of Nuclear and Allied Sciences/University of Ghana and University of Cape Coast, Ghana respectively. Her PhD research focuses on integrating mutagenesis with modern *in vitro* techniques to improve orchids/roses. She will also employ molecular tools for mutation detection and screening of the mutants. She realizes the economic importance of ornamentals on the global market, to Ghana and the livelihood it provides for the many growers and traders. She intends to strengthen research and development studies in ornamentals in Ghana, which is currently lacking in this sector, to facilitate informed decision making by stakeholders and policy makers, and, ultimately, to boost the flower industry in Ghana.

Farewell



Mr Anibal E. Morales (Puerto Rico, USA)

Funded by Argonne National labs (USA), Anibal joined the PBGL as data science intern for one year. Anibal came with a background in medical and electrical engineering with several previous internships, including at NASA, already under his belt. At PBGL he learned the ins and outs of plant biology, genetics, bioinformatics, and not least about food security in all its challenges. He mainly spent his time computer programming to develop reproducible workflows to analyze genomic datasets. This exposed him to Linux, Conda virtual environments, git, Python, R, and Snakemake. He was instrumental in developing the documentation for most of PBGL’s software tools. We will refer to his documentation in the near future! During lockdown restrictions, Anibal kept up his spirits on long walks experiencing Vienna and the Austrian Alps. He brought those good spirit back to the lab

and brightened everyone's days. Anibal's excellence was noted by other departments and Insect Pest Control Laboratory (IPCL) hired him as Junior Professional Officer. Congratulations and good luck for the future, Anibal, it was a real pleasure having you!



Ms Susu Alkiers (Austria) joined the PBG Laboratory in October 2020 as an intern. Susu obtained a BSc in Agricultural Sciences at BOKU University, Vienna and is currently finalizing her MSc in Agricultural and Food Economy at the same university. Her MSc project simulates a public payment to Austrian farmers that aims to incentivize low N₂O-emission farming practices. Through this internship, Susu wants to strengthen her practical skills and knowledge in plant breeding and genetics. Her internship programme combines field, glasshouse and laboratory experiments for phenotyping, mutant characterization, and marker development for agronomically useful mutants in cereals. We welcome Susu to the PBG team!



Ms Faith Luvai (Kenya) joined the PBG Laboratory in December 2020 as an Intern and stayed with the lab for a full year until 30 November 2021. She joined the lab with a BSc in Molecular and Cellular Biology and experience in malaria research and parasitology. Faith very quickly transitioned to the new environment working with plants and a plant pathogen (*Fusarium*). She was initially trained in plant molecular biology in the context of

the barley Marker-Assisted Selection project for feed quality improvement. However, she was mainly involved in *in vitro* technologies in banana, both cooking and dessert banana, and in banana phytopathology in the context of the *Fusarium* TR4 project and the banana *Fusarium* wilt screening protocol. Her plan is to continue her education and pursue a master's degree in Austria. Faith, it was a pleasure to have you at the PBGL and we wish you all the best in your future endeavors. Always welcome!



Ms Ayca Eda Akgun (Turkey) joined the PBGL for about four months filling a Development Reassignment opening. Eda was no stranger to PBGL, having successfully completed an internship here before. She was quickly up to speed. Eda was mainly involved in the sorghum projects. She initiated the development of a low-cost marker assay for the semi-dwarf trait that was previously mapped to the centromere region on chromosome 4. She also contributed to further mutagenesis and population development for predictive mutation breeding. From PBGL, Eda moved to the IPCL where she plans to pursue a PhD. Very pleased to have had Eda on board again. We wish her the very best for her PhD and beyond, it's well deserved!

Forthcoming Events

Research Coordination Meetings (RCMs) of FAO/IAEA Coordinated Research Projects (CRPs)

First Research Coordination Meeting (RCM) on Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development, D24015, (*Virtual Meeting*), March 2022. (More information on page 11)

Third Research Coordination Meeting (RCM) on Disease Resistance in Rice and Wheat for Better Adaptation to Climate Change, D23032, Sanya, China, 4–8 April 2022. (More information on page 11)

Other Meeting

Workshop on Plant Mutation Breeding at the International Plant and Animal Genome Conference (PAG XXIX), San Diego, USA, 11 January 2022. (More information on page 13)

Regional Training Course on Mutation Breeding and Efficiency Enhancing Techniques for Resistance to Banana Fusarium Wilt Race TR4 in Latin America, RLA0066, Seibersdorf, Austria, 14–25 February 2022 (More information on page 17)

Past Events

Research Coordination Meetings (RCMs) of FAO/IAEA Coordinated Research Projects (CRPs)

First Research Coordination Meeting (RCM) on Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops, D24014, (*Virtual Meeting*), 16–20 August 2021. (More information on page 11)

Second Research Coordination Meeting (RCM) on Enhanced Biotic-stress Tolerance of Pulses Towards Sustainable Intensification of Cropping Systems for Climate Change Adaptation, D22006, (*Virtual Meeting*), 6–10 September 2021. (More information on page 12)

Consultants Meeting

Consultants Meeting on Radiation-induced Crop Genetic Diversity and Functional Genomics to Accelerate Variety Development for Tolerance to Climate Extremes, (*Virtual Meeting*), 2–6 August 2021. (More information on page 12)

Other Meetings

National Training Course on Marker-Assisted Mutation Breeding and Basic Bioinformatics for Improvement of Food Crops in Indonesia, INS5044, (*Virtual Meeting*), 2–13 August 2021. (More information on page 17)

Regional Training Course on Improving Crops Resilience to Climate Change through Mutation Breeding in Pacific Islands, RAS5079, (*Virtual Meeting*), 14–18 October 2021. (More information on page 17)

Workshop to Finalize Banana Fusarium Wilt TR4 Combat Strategy in the Andean Region, RLA0066, La Molina, Peru, 25–28 October 2021. (More information on page 18)

Final Coordination Meeting on Improving Crops Resilience to Climate Change through Mutation Breeding in Pacific Islands, RAS5079, (*Virtual Meeting*), 22–23 November 2021. (More information on page 18)

Advanced Regional Training Course on Digital Breeding Management Systems and Field Experimental Design/Analysis, RAS5088, (*Virtual Meeting*), 22 November–3 December 2021. (More information on page 19)

National Training Course on *Hemileia vastatrix* Diagnosis and Screening, JAM5014, (*Virtual Meeting*), 29 November–7 December 2021. (More information on page 19)

Regional Training Course on Enhancing Productivity and Resilience to Climate Change of Major Food Crops in Europe and Central Asia, RER5024, (*Virtual Meeting*), 6–10 December 2021. (More information on page 19)

Final Project Review Meeting on Promoting the Application of Mutation Techniques and Related Biotechnologies for the Development of Green Crop Varieties, RAS5077, (*Virtual Meeting*), 7–9 December 2021. (More information on page 20)

National Training Course on Using Nuclear Techniques to Improve the Adaptation and Productivity of Forest Species Facing Climate Change, CHI5052. (*Virtual Meeting*), 13–17 December 2021. (More information on page 20)

Coordinated Research Projects (CRPs)

Project Number	Ongoing CRPs	Project Officers
D20003	Impact Assessment of Mutant Crop Varieties Developed by BINA, Bangladesh (Single-contract project) (2019–2021)	S. Sivasankar
D20004	Impact Assessment of Cotton Mutant Varieties Developed by NIAB, Pakistan (Single-contract project) (2020–2022)	L. Jankuloski
D23032	Disease Resistance in Rice and Wheat for Better Adaptation to Climate Change (2018–2023)	L. Jankuloski
D22006	Enhanced Biotic-stress Tolerance of Pulses Towards Sustainable Intensification of Cropping Systems for Climate-change Adaptation (2019–2024)	S. Sivasankar
D24014	Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops (2021–2025)	I.K. Bimpong
D24015 (New)	Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development (For more information, see announcement on page 25)	S. Sivasankar

Impact Assessment of Mutant Crop Varieties Developed by BINA, Bangladesh, D20003

Project Officer: S. Sivasankar

This is a single-contract CRP with the overall objective of estimating the economic impacts of promising mutant rice varieties developed by the Bangladesh Institute of Nuclear Agriculture (BINA).

The specific objectives are (1) to estimate the aggregate economic benefits associated with BINA-developed mutant rice varieties; (2) to determine the annual production and profitability trends of BINA-developed mutant rice varieties by location and variety; (3) to assess the adoption level of BINA-developed mutant rice varieties in all areas; (4) to identify farmers' preferences and constraints for cultivation of mutant rice varieties; and (5) to suggest policy guidelines/recommendations.

This CRP successfully completed in 2021, identifying strong impact from the cultivation of mutant rice varieties in the country. Ex-post economic impact analysis utilizing an economic surplus approach was applied to measure aggregate economic benefits of the short duration high yielding *aman* mutant varieties developed by BINA. Both tabular and statistical analyses were used. Secondary data were collected from several relevant national sources, and statistical analysis was done using the economic surplus approach based on primary data from 14 agricultural regions of Bangladesh. Adoption level of *aman* mutant rice varieties (which were developed at least 12 years ago) and constraints to cultivation were assessed based on field survey data from 64 districts that were classified into the 14 agricultural

regions. This data from a total of 560 farmers selected randomly from the 14 agricultural regions was also used to compare the profitability of the mutant rice variety 'Binadhan-7' against the cultivation of other non-mutant varieties. The livelihood asset pentagon approach was used based on different capitals (namely, human capital, social capital, natural capital, physical capital and financial capital) of farm households to determine the impact of cultivation of *aman* mutant rice varieties on farmer livelihoods in the study areas.

A first paper, *Comparative Profitability and Impact of BINA Developed Aman Mutant Rice 'Binadhan-7' with Non-Mutant in Bangladesh* has been published based on the results. On average, the total cost of production was US \$696 per hectare, with 29 percent for fixed costs and 71 percent for variable cost. The average net return for the cultivation specifically of the mutant rice variety, 'Binadhan-7', ranged from US \$394 per hectare in the Jashore region to US \$828 in the Dinajpur region. The average benefit cost ratio for Binadhan-7 production on total cost basis was 1.90 relative to 1.43 for farmers growing other varieties in the study region. Short duration was ranked as the highest preferred trait by farmers and high yield was ranked fifth among the five trait options in the survey. High cost of labour was identified as the main constraint in cultivation. The study also revealed that the short duration, high yielding rice variety, 'Binadhan-7', plays a vital role in hunger mitigation of the northern areas of Bangladesh.

A second publication with more information on the impact assessment is in draft.

Impact Assessment of Cotton Mutant Varieties Developed by NIAB, Pakistan, D20004

Project Officer: L. Jankuloski

An individual CRP on Impact Assessment of Cotton Mutant Varieties Developed by NIAB, Pakistan, was initiated in 2020.

The overall objective of this single-contract CRP is to evaluate the economic impact of the cotton mutant varieties developed by Nuclear Institute for Agriculture and Biology (NIAB).

The specific objectives of this CRP are (1) to evaluate economic returns from mutant cotton varieties; (2) to assess adoption of mutant cotton varieties in different cotton growing areas of the country; (3) to identify the constraints to adoption of mutant cotton varieties in Pakistan; (4) to assess and determine annual production of NIAB cotton mutant varieties; (5) to evaluate the total area covered with cotton mutant varieties, their yield and economic benefits in total and of each mutant variety; and (6) to provide policy recommendations for promotion of mutant cotton varieties.

The CRP is extended for one more year and planned to be completed by the end of 2022.

Disease Resistance in Rice and Wheat for Better Adaptation to Climate Change, D23032

Project Officer: L. Jankuloski

A range of diseases are responsible for hindering yield improvements in both rice and wheat. Changing climatic conditions are helping diseases to spread to new localities and exacerbating their impact. In addition to the already widespread diseases of rice, such as blast, sheath blight, false smut and bacterial leaf blight, emerging diseases like wheat blast are increasingly becoming serious threats. To minimize the impact of such diseases, environmentally friendly and cost-effective technologies are needed to help prevent and manage them. The use of mutation breeding techniques is a viable tool in the development of disease resistant germplasm and varieties. Mutations are a primary source of genetic variation in any organism, including plants. The use of mutation induction in generating new germplasm and developing new disease resistant varieties in rice and wheat is an efficient and valuable approach in crop improvement and has been very successful in rice and wheat breeding. More than 820 rice varieties and 255 wheat varieties have been developed by mutation breeding using mostly physical mutagens (<https://mvd.iaea.org/#!Home>).

Progress made on planned activities since 2018 is satisfactory and even excellent in certain projects, towards the goals set during the first RCM and according to individual workplans.

Some important achievements are (1) the development of specific primers for *Magnaporthe oryzae* Triticum isolates

and Recombinase Polymerase Amplification (RPA) rapid detection method of wheat blast pathogen, and (2) the identification of five blast resistant wheat mutant lines in M₃ generation. In addition, six wheat orthologs of rice blast susceptible genes were identified uncovering a total of 171 SNPs in M₃ wheat population.

In rice, three highly resistant and two moderately resistant mutant lines to Bacterial Leaf Blight (BLB) were identified in M₃ generation. The development of F₂ generation for phenotyping is in progress. Additionally, two mutant lines showing significantly lower infection of false smut disease in field hotspot (plus artificial inoculation) were identified and four rice mutant lines as putative mutants resistant to bakanae disease (*Gibberella fujikuroi*) were selected.

The network and collaboration among CRP participants are strong, and seed materials from wheat mutant populations and lines were already exchanged for wheat blast phenotyping in Bangladesh. The further collaboration will be established for genotyping of mutant lines as well as F₂ generations.

The CRP officially started in September 2018 and had its first Research Coordination Meeting (RCM) from 10–14 December 2018 in Vienna, Austria. The second RCM was held virtually from 26–30 April 2021. The third RCM will be held in April 2022 in China where the progress will be reviewed, and future activities will be discussed among participants.

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

Project Officer: S. Sivasankar

In this CRP, induced genetic variation and genomics technologies will be used for productivity improvement of three pulses, namely, chickpea, cowpea and lentil, which together account for 40% of global pulses' production. The research focus is on enhancing the tolerance of (1) chickpea to the pod borer, *Helicoverpa armigera*; (2) cowpea to the bod borer, *Maruca vitrata*, and (3) lentil to the disease, *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.

The CRP which started in 2019 had its first RCM in September 2019 in Vienna, Austria. The second RCM took place virtually from 6 to 10 September 2021 (More information on page 12), and the third RCM is planned to be held in November 2022.

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

Project Officer: I.K. Bimpong

The CRP will provide outcomes that can guide National Agricultural Research Systems (NARS) in Member States to accelerate the development of new varieties of vegetatively propagated crops (VPCs) and horticultural tree crops (HTCs) through the use of efficient state-of-the-art technology packages.

The CRP will comprise 13 participating countries from Member States where the crops are grown extensively, some advanced institutions and the CGIAR research centres with the respective mandates. Each country will bring together researchers covering the fields of micropropagation, advanced functional genomics for variant discovery and the use of nuclear techniques to induce genetic diversity at the cell or tissue level in selected VPCs and HTCs to address the research objectives.

The CRP aims to develop new genetic resources and technologies for accelerated breeding in VPCs and HTCs through induced genetic diversity, chimera-free regeneration, and functional genomics.

The CRP will lead to the generation of (a) stable mutant clones that are free-of-chimeras and characterized at the genetic and molecular levels for traits of interest; and (b) publication of protocols for phenotyping and genomic analyses for Member States.

Forthcoming Events

First Research Coordination Meeting (RCM) **Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development, D24015**

Virtual Meeting. March 2022

Project Officer: S. Sivasankar

CRP D24015 was approved in October 2021 and has opened calls for proposals from mid-October to mid-December. It is expected to launch in March 2022 with its first Research Coordination Meeting, likely in virtual mode.

Breeding with induced genetic diversity has remained a highly effective avenue for the improvement of both simple and complex crop traits in developing Member States of the FAO/IAEA. Mutation breeding has mainly relied on gamma rays, but most recently the ion beam, electron beam, proton beam and space irradiation (cosmic rays) are coming into increasing use at least in some Member States, though the effect of these different sources on the plant genome remain to be assessed systematically. Newer genomic technologies that establish genetic associations for marker and candidate gene discovery also remain yet to be applied to mutation

breeding for increased precision and breeding efficiency. Mutant populations generated from induced genetic variation are traditionally used directly as source germplasm for breeding and variety development. However, they can also render themselves to the establishment of genetic associations for marker-assisted breeding and gene editing. Theoretically, mutant populations can also be used for genomic predictions for increased efficiency of the breeding process.

The overall objective of this CRP is to strengthen the ability of the Agency 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.

Third Research Coordination Meeting (RCM) **Disease Resistance in Rice and Wheat for Better Adaptation to Climate Change, D23032**

Sanya, China. 4–8 April 2022

Project Officer: L. Jankuloski

This CRP aims to improve disease resistance in rice and wheat through induced genetic variation and mutation breeding and the development of screening techniques for disease resistance. Specific research objectives are (1) to generate genetic diversity and develop rice lines resistant to important diseases (blast, sheath blight, bacterial blight, and false smut); (2) to develop protocols for the screening of rice mutants resistant to the target diseases; (3) to develop molecular markers for disease resistance using available mutant germplasm; and (4) to generate mutant wheat populations and develop screening methods for resistance to wheat blast.

The CRP officially started in September 2018 and had its first RCM in December 2018 in Vienna, Austria. The second RCM was held virtually in April 2021 and the third RCM is planned to be held in April 2022 in China.

For detailed information on the project achievements, see Coordinated Research Projects (CRPs) on page 10.

Past Events

First Research Coordination Meeting (RCM) **Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops, D24014**

Virtual Meeting. 16–20 August 2021

Project Officer: I.K. Bimpong

This CRP addresses the constraints associated with vegetatively propagated and horticultural tree crops through mutation breeding. It is intended to build on the development of new genetic resources and technologies for accelerated breeding in cassava, potato/sweet potato, and olive crops through induced genetic diversity, chimera-free regeneration, and functional genomics. The CRP also

focuses on development of disease-tolerant and stable clones of mutant for cassava brown streak disease (CBSD), olive quick decline syndrome (OQDS) and any important diseases in potato/sweet potato.

The project has 13 participants including three researchers from Austria, Belgium and Spain as technical contract holders with olive crops as their focus, four researchers from Ghana, Kenya, Malaysia and Uganda as research contracts holders with cassava as their target crop, three researchers from Chile, Colombia and Ethiopia also as research contracts holders with potato/sweet potato as their focus crop, and three researchers from India, Sweden and USA as research agreements holders serving as advisors for the CRP. Technical Officers from the Plant Breeding and Genetics Subprogramme also participated in the meeting. Ms Sivasankar, Head, Plant Breeding and Genetics Section delivered the opening remarks and gave a presentation on the Plant Breeding and Genetics Subprogramme. The following three groups were established among participants:

- (1) *Olive group*: with the aim to use both somatic embryogenesis prepared under axenic tissue cultures conditions as explants and new regeneration tools that will result in single-cell origin, non-chimeric, uniform mutants;
- (2) *Cassava group*: With the aim to use organized embryogenic callus (OES), friable embryogenic callus (FEC) and shoot apical meristem (SAM) which originate from single cells as explants for mutation induction;
- (3) *Potato/sweet potato group*: With the aim to use new regeneration tools that will result in single-cell origin, non-chimeric, uniform mutants in addition to somatic embryogenesis/single cell as explants and use both proton and neutron beam for irradiation.

The second RCM has been proposed to be held in November 2022 subject to the availability of funds.

Second Research Coordination Meeting (RCM) Enhanced Biotic-stress Tolerance of Pulses Towards Sustainable Intensification of Cropping Systems for Climate-change Adaptation, D22006

Virtual Meeting. 6–10 September 2021

Project Officer: S. Sivasankar

The CRP D22006 held its second RCM during 6–10 September 2021 with primary focus on presenting and discussing research results to date, trouble-shooting technical issues in implementation, and planning the next steps including course corrections in research implementation where necessary. This RCM allowed the three separate crop teams (cowpea, chickpea and lentil) to come together immediately after three informal crop meetings in August to ensure effective implementation, with finer coordination where necessary, to achieve intended objectives during the subsequent duration of the CRP.

The CRP which was launched in September 2019 has completed two years now. It aims to develop genetic

resources through induced mutations and associated genomic tools for accelerated adaptation of pulses-based cropping systems to climate change. It is specifically focused on (1) the generation of genetic diversity in chickpea, cowpea and lentil through mutagenesis for resistance to *Helicoverpa armigera*, *Maruca vitrata* and *Stemphylium botryosum*, respectively; (2) the development and/or refinement of phenotyping tools to facilitate precise (confident) and efficient selection of biotic-stress resistance in the selected pulse crops; and (3) the development of genomic tools for accelerated variety development for the selected pulse crops and associated traits of interest.

The second RCM reported good results after two years since the start of the CRP from most participating research groups although some setbacks were experienced mostly for field experimentation as a consequence of the pandemic. In chickpea, one research group has succeeded in the identification of three mutants with resistance to the podborer, *Helicoverpa armigera*, confirmed in two years of lab and field assays. Further, as part of related projects, one research group has identified nine main-effect QTLs for up to 42.49% of the phenotypic variability explained for component traits for podborer resistance in chickpea. Five research groups are focused on developing pod borer (*Maruca vitrata*) resistance in cowpea, of which one group is fairly advanced and has identified three mutants with varying degrees of resistance to infestation when screened under very high pressure of field infestation at M₂. In the case of lentil, the three research groups involved have established the inoculum for *Stemphylium botryosum*, developed/adapted multiplication and inoculation conditions, and M₂ populations are under screening.

The next RCM is planned to be in November 2022.

Consultants Meeting

Radiation-induced Crop Genetic Diversity and Functional Genomics to Accelerate Variety Development for Tolerance to Climate Extremes

Virtual Meeting. 2–6 August 2021

Project Officer: S. Sivasankar

A Consultants Meeting was held virtually during 2–6 August 2021 for the development of the next Coordinated Research Project at PBG. The meeting brought together five experts and one FAO observer with the general objective to strengthen the ability of the Agency and its Member States to develop and test emerging technologies in mutation induction, genomics and big data within the framework of the Mutation Breeding Network to facilitate the accelerated development of crop varieties resilient to the impact of climate change. The Consultants Meeting resulted in the development of the concept note for a new CRP with the title, Radiation-induced crop diversity and genetic associations for accelerating variety development, that has since been approved for start in 2022.

Induced mutations fortify plant germplasm pools and enable faster genetic gain, especially where the genetic base is narrow. Mutation breeding thus has the potential to facilitate larger genetic gain than conventional breeding. This advantage, coupled with emerging front-end technologies for efficient and precise selection, can both accelerate the pace of crop improvement and increase the rate of genetic gain. The new CRP will address: (1) assessment of biological and genomic effects of current and new mutagen sources; (2) development, adaptation and dissemination of computational tool(s) for genetic associations and marker discovery; and (3) piloting of gene editing and genomic prediction. Focus will be on diploid seed crops with good sequence information in the public domain, and simple traits. Genomic prediction will be tested in only one of ten contracts, on a complex trait. Improved mutant lines for targeted traits will be simultaneously generated in the process of implementing the CRP.

The Concept Note from the Consultants Meeting was approved as CRP D24015. A call for proposals opened on 11 October 2021, with a closing date of 15 December 2021, and the CRP is expected to be officially launched in March–April 2022.

News

Workshop

Plant Mutation Breeding

International Plant and Animal Genome Conference, PAG XXIX

San Diego, CA, USA. 11 January 2022

Project Officer: N. Warthmann

PBG will host a workshop on Plant Mutation Breeding at the International Plant and Animal Genome Conference (PAG XXIX, 8–12 January 2022). PAG is the most significant annual conference on the genetics and genomics of plant and animal research and breeding. It brings together over 3000 leading scientists. Our workshop is scheduled for **Tuesday, 11 January 2022, from 1:30 PM to 3:40 PM**, with five slots for 20-minute presentations plus discussion. We will fill the two hours with recent science from modern plant breeding with a particular angle on induced, novel genetic variation; the essence of mutation breeding. We will cover technical aspects such as mutagenesis, phenotyping, genomics, speed breeding, as well as the utility of mutation breeding in generating important crop traits towards reaching the millennium development goals, achieving food security and planetary health, and securing and improving the livelihoods of farmers. We are hoping to establish this workshop at PAG as a yearly activity and networking hub to support our capacity building for Member States.

Technical Cooperation Field Projects

Project Number	Country/Region	Title	Technical Officer(s)
BKF5019	Burkina Faso	Improving Food Crop Genotypes for Enhancing Yield and Adaptation to Climate Change Using Mutation Breeding and Isotopic Techniques	L. Jankuloski (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
BOT5019	Botswana	Improving Selected Legumes and Cereals against Biotic and Abiotic Stresses to Improve Food Production and Security	I.K. Bimpong
BUL5016	Bulgaria	Improving the Productivity and Quality of Economically Important Crops through Mutation Breeding and Biotechnology	C. Zorrilla
CAF5013	Central African Republic	Improving Productivity of Maize and Developing Resistant Armyworm Maize Varieties Using Radio-Mutagenesis Techniques	S. Sivasankar
CHI5052	Chile	Using Nuclear Techniques to Improve the Adaptation and Productivity of Forest Species Facing Climate Change	S. Sivasankar
COL5026	Colombia	Enhancing Crop Productivity of Creole Potato Using Nuclear and Related Techniques	I.K. Bimpong (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
CPR5024	China, People's Republic of	Enhancing the Accelerated Application of Mutant Germplasm and High-Efficiency Breeding in Crops	N. Warthmann
CUB5023	Cuba	Strengthening National Capacities for the Development of New Varieties of Crops through Induced Mutation to Improve Food Security While Minimizing the Environmental Footprint	C. Zorrilla (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
ERI5011	Eritrea	Developing Improved Banana and Maize Varieties through Mutagenic Nuclear Techniques	I.K. Bimpong
GHA5038	Ghana	Using Irradiated Pollen for the Development of Provitamin A Rich, Drought Tolerant and Cassava Mosaic Disease Resistant Cassava Mutants	C. Zorrilla
HON5009	Honduras	Improving Genetic Resistance of Coffee to Coffee Leaf Rust through Mutation Breeding	L. Jankuloski
INS5044	Indonesia	Using Nuclear Technology to Support the National Food Security Programme	S. Sivasankar (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
IRA5015	Iran, Islamic Republic of	Enhancing Capacity of National Producers to Achieve Higher Levels of Self-Sufficiency in Key Staple Crops	L. Jankuloski (<i>Participating</i>) in collaboration with FEP (<i>Leading</i>) and SWMCN (<i>Participating</i>)
IRQ5023	Iraq	Utilizing Nuclear Technology to Improve Key Legume Crops for Climate Change Adaptation	I.K. Bimpong
IVC5040	Cote d'Ivoire	Improving Agricultural Production of Maize, Rice and Cassava through Cultivation of Induced Mutant Adaptable to Climatic Changes	I.K. Bimpong
JAM5013	Jamaica	Improving Crops by Using Experimental Mutagenesis and Diagnostic Technologies	S. Sivasankar

Project Number	Country/Region	Title	Technical Officer(s)
JAM5014	Jamaica	Establishing a Self-Contained Gamma Irradiation Facility for the Introduction of Sterile Insect Technique and Experimental Mutagenesis and Diagnostic Technologies	S. Sivasankar (<i>Participating</i>) in collaboration with IPC (<i>Leading</i>)
KEN5038	Kenya	Using Nuclear Techniques to Evaluate and Improve the Impact of Mutated Forages on the Performance of Smallholder Dairy Cows	I.K. Bimpong (<i>Leading</i>) in collaboration with APH (<i>Participating</i>)
KUW5005	Kuwait	Implementing Mutation Induction to Improve Barley Production under Harsh Environmental Conditions – Phase III	L. Jankuloski
MAG5026	Madagascar	Enhancing Rice and Maize Productivity through the Use of Improved Lines and Agricultural Practices to Ensure Food Security and Increase Rural Livelihoods	L. Jankuloski (<i>Participating</i>) in collaboration with SWMCN (<i>Leading</i>) and IHS (<i>Participating</i>)
MAL5032	Malaysia	Strengthening National Capacity in Improving the Production of Rice and Fodder Crops and Authenticity of Local Honey Using Nuclear and Related Technologies	C. Zorrilla (<i>Leading</i>) in collaboration with FEP (<i>Participating</i>) and SWMCN (<i>Participating</i>)
MLW5003	Malawi	Developing Drought Tolerant, High Yielding and Nutritious Crops to Combat the Adverse Effects of Climate Change	C. Zorrilla (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
NAM5017	Namibia	Improving Crops for Drought Resilience and Nutritional Quality	C. Zorrilla (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
NEP5006	Nepal	Enhancing Productivity of Corps and Fruit Employing Nuclear and Molecular Techniques	I.K. Bimpong
NER5024	Niger	Improving Key Staple Crops towards Food Security	S. Sivasankar
NIC5011	Nicaragua	Broadening the Genetic Variation of Vegetative Propagated Crops Using Nuclear Techniques	C. Zorrilla
PAR1005	Paraguay	Establishing National Capabilities in Irradiation Technologies for the Treatment of Patients with Burns and the Introduction of Mutation Breeding for Enhanced Quality and Productivity of Crops	S. Sivasankar (<i>Participating</i>) in collaboration with RPRT (<i>Leading</i>) and ARBR (<i>Participating</i>)
PER5034	Peru	Improving Yellow Potato and Coffee Crops through Mutation Breeding Techniques	L. Jankuloski
PRC5002	Congo, Republic of the	Developing Disease-Resistant Varieties of Cassava and Banana	I.K. Bimpong
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	A. Hingane (<i>Participating</i>) in collaboration with SWMCN (<i>Leading</i>)
RAF5083	Regional Africa	Enhancing Crop Productivity through Climate Smart Crop Varieties with Improved Resource Use Efficiency (AFRA)	S. Sivasankar/I.K. Bimpong

Project Number	Country/Region	Title	Technical Officer(s)
RAS0080	Regional Asia	Promoting Self-Reliance and Sustainability of National Nuclear Institutions	S. Sivasankar (<i>Participating</i>) in collaboration with PCG (<i>Leading</i>), RPRT (<i>Participating</i>) and PHY (<i>Participating</i>)
RAS5077	Regional Asia	Promoting the Application of Mutation Techniques and Related Biotechnologies for the Development of Green Crop Varieties (RCA)	I.K. Bimpong
RAS5079	Regional Asia	Improving Crop Resilience to Climate Change through Mutation Breeding in Pacific Islands	C. Zorrilla
RAS5088	Regional Asia	Enhancing Crop Productivity and Quality through Mutation by Speed Breeding (RCA)	S. Sivasankar/I.K. Bimpong
RER5024	Regional Europe	Enhancing Productivity and Resilience to Climate Change of Major Food Crops in Europe and Central Asia	C. Zorrilla
RLA5084	Regional Latin America	Developing Human Resources and Building Capacity of Member States in the Application of Nuclear Technology to Agriculture	S. Sivasankar (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>) and APH (<i>Participating</i>)
RWA5001	Rwanda	Improving Cassava Resilience to Drought and Waterlogging Stress through Mutation Breeding and Nutrient, Soil and Water Management Techniques	L. Jankuloski (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
SAF5016	South Africa	Promoting Mutation Breeding of Vegetables to Improve Rural Livelihoods — Phase I	N. Warthmann
SIL5021	Sierra Leone	Improving Productivity of Rice and Cassava to Contribute to Food Security	I.K. Bimpong (<i>Leading</i>) in collaboration with SWMCN (<i>Participating</i>)
SRL5050	Sri Lanka	Supporting Genetic Improvement of Tea	S. Sivasankar
SWA5002	Eswatini, Kingdom of	Improving Adaptability of Cowpea to Climate Change through Mutation Breeding	L. Jankuloski
SYR5026	Syrian Arab Republic	Using Accelerated Mutation Breeding of Staple Crops for Enhanced Resilience to Climate Change through Speed Breeding, Phenotyping and Genotyping	L. Jankuloski
TOG5002	Togo	Improving Crop Productivity and Agricultural Practices through Radiation Induced Mutation Techniques	I.K. Bimpong (<i>Participating</i>) in collaboration with SWMCN (<i>Leading</i>)
TUN5029	Tunisia	Developing Barley and Durum Wheat Resilience to Drought and Heat Tolerance through Mutation Breeding	A. Hingane
UGA5041	Uganda	Developing Disease Resistant High Yielding Farmer Preferred Cassava Varieties in Uganda through Induced Mutation Breeding	I.K. Bimpong/L. Jankuloski
URT5037	Tanzania, United Rep. of	Developing Rice Varieties with Resistance to Rice Blast and Salinity Tolerant Using Mutation Breeding and Biotechnology Techniques	L. Jankuloski

Project Number	Country/Region	Title	Technical Officer(s)
YEM5015	Yemen	Enhancing Sorghum and Legume Crop Productivity through Induced Mutations with Supportive Breeding and Biotechnologies	L. Jankuloski
ZAI5029	Congo, Democratic Republic of the	Enhancing Crop Productivity of Soybean and Maize through Improved Mutant Varieties and Lines	I.K. Bimpong

APH: Animal Production and Health, NAFA; FEP: Food and Environmental Protection, NAFA; IPC: Insect Pest Control, NAFA; SWMCN: Soil and Water Management and Crop Nutrition, NAFA; RPRT: Radioisotope Products and Radiation Technology, NAPC; ARBR: Applied Radiation Biology and Radiotherapy, NAHU; PHY: Physics, NAPC; PCG: Programme Coordinator, NA; IHS: Isotope Hydrology Section, NAPC

Forthcoming Events

Regional Training Course

Mutation Breeding and Efficiency Enhancing Techniques for Resistance to Banana Fusarium Wilt Race TR4 in Latin America, RLA0066

Seibersdorf, Austria, 14–25 February 2022

Project Officer: S. Sivasankar

This training course will be implemented under the regional project, RLA0066, to provide basic knowledge and skills in mutation induction and screening methodologies for resistance to the Fusarium wilt disease in banana, tropical race 4 (TR4). It constitutes one part of the immediate support to Member States of the Andean region to combat this most disastrous pathogen of banana that entered the region for the first time in 2019. It is organized in response to the request of representatives of the Andean region Member States who met recently in Peru to discuss immediate needs for a multi-pronged and holistic approach against the disease, that includes detection, containment, management and genetic resistance.

The main themes of the training course include Fusarium wilt TR4 screening protocols and mutation induction including *in vitro* techniques of mass propagation of banana plantlets, optimization of irradiation treatment. The training course will cover lectures, demonstrations, and practical sessions on the various protocols of mutation induction, screening for TR4 resistance and efficacy enhancing techniques to accelerate breeding methodologies. The course is designed for banana breeders, pathologists and tissue culture specialists of Member States embarking on banana mutation breeding programmes.

Past Events

National Training Course

Marker-Assisted Mutation Breeding and Basic Bioinformatics for Improvement of Food Crops in Indonesia, INS5044

Virtual Meeting, 2–13 August 2021

Project Officer: S. Sivasankar

This national training course was delivered virtually in August 2021 as part of the workplan for the TC project, INS5044, Using Nuclear Technology to Support the National Food Security Programme. The first part of the course covered the basics of induced mutagenesis, types and mechanism of action of various mutagens, the concepts and methodology of mutation breeding, and mutation breeding with specific focus on food crops. The second part of the course addressed introductory molecular biology, molecular markers and genome variations, the basics of omics (covering genomics, transcriptomics and proteomics), basics of linkage analysis, QTL mapping, marker-assisted breeding, genome wide association analysis (GWAS), and introductory bioinformatics.

The course was delivered virtually through a combination of lectures, round table discussions of selected topics with each student required to elaborate one specific question pertinent to the discussion, reading and debating specific research articles, and two video sessions. The two videos covered DNA extraction and running a gel.

Regional Training Course

Improving Crops Resilience to Climate Change through Mutation Breeding in Pacific Islands, RAS5079

Virtual Meeting, 14–18 October 2021

Project Officer: L. Jankuloski

The purpose of the training course on Mutation Breeding and Efficiency Enhancing Techniques for Crop Improvement was to provide participants with opportunities to familiarize themselves with crop mutation breeding and to strengthen understanding on screening protocols and biotechnologies.

The training course was attended by 11 participants from the Pacific Community (SPC), Suva, Fiji. Dr Penna Suprasanna (invited lecturer), kept participants engaged and explained them the details needed for mutagenesis and screening techniques.

This training course included lectures on application of induced mutation in crops of relevance (taro, yam, sweet potato), screening protocols for mutants for biotic/abiotic stress in the lab, greenhouse and under field conditions and breeding cycles from irradiation to release of a variety through mutation breeding.

The lectures provided by Dr Penna Suprasanna included: (1) Mutation breeding procedures/methodologies and handling of mutant population in crops, specifically in taro, yam, sweet potato and banana; (2) *In vitro* mutagenesis protocols in taro, yam, sweet potato, and banana; (3) Screening of mutants for biotic/abiotic stress in the lab, greenhouse and under field conditions; (4) Screening protocols for biotic and abiotic stress tolerance, (5) Breeding cycles from irradiation to release a variety through mutation breeding; (6) Introduction to protocols in the lab, greenhouse and under field conditions to conduct a successful breeding programme; and (7) Molecular and conventional breeding methods.

The five-day virtual training course is part of the TC project on Plant Mutation Breeding to Improve Crop Resilience to Climate Change in the Pacific Islands (RAS5079). The course was very well received by all participants from SPC and they were motivated to undertake the work related to screening protocols acquired through this training course.

Workshop

To finalize Banana Fusarium Wilt TR4 Combat Strategy in the Andean Region, RLA0066
La Molina, Peru. 25–28 October 2021

Project Officer: S. Sivasankar

This workshop was implemented as a rapid response to request from Member States of the Andean Region to combat the banana fusarium wilt, TR4, which was first reported in Latin America in 2019 in Colombia and was recently reported in April of 2021 in Peru. The expert mission was held in Peru from 25 to 28 October 2021 under the Technical Cooperation Project RLA0066, to strengthen the application of the peaceful uses of nuclear technology in participating Member States in Latin America and the Caribbean and contribute to the achievement of Sustainable Development Goal (SDG) 17 Partnership for the goals. It was hosted by the Universidad Nacional Agraria La Molina of Peru, which had recently signed a Collaborating Centre agreement with the IAEA on Plant Mutation Breeding and Associate Biotechnologies.

In order to discuss and develop a holistic strategy to combat the disease, the workshop brought together experts from

the fields of plant breeding, phytopathology and phytosanitary from four countries of the Andean region, namely, Bolivia, Colombia, Ecuador and Peru, where Colombia participated virtually. Discussions centred on immediate needs in terms of human and infrastructure capacity building through training and procurements, and well as the design of a new TC project for the upcoming biennium that is specifically focused on the detection, containment, management and genetic resistance pertinent to the disease.



The IAEA-led Expert Mission at the Universidad Nacional Agraria La Molina, Peru, that deliberated immediate and medium-term actions for the management of banana Fusarium wilt, TR4, in the Andean region.

Final Coordination Meeting

Improving Crops Resilience to Climate Change through Mutation Breeding in Pacific Islands, RAS5079

Virtual Meeting. 22–23 November 2021

Project Officers: L. Jankuloski, C. Zorrilla

The regional TC project is addressing the improvement of main crops for the Pacific Islands (yam, sweet potato, banana and chili) with support from the Joint FAO/IAEA Centre. The main objective of this project was to contribute to food security in the region by using new mutant varieties with increased productivity and better adaptation to biotic/abiotic stress. Nuclear technology is an old technology that has proved efficient for genetic enhancement and it has been recently introduced to the Pacific Islands including Fiji, Marshall Islands, New Guinea, Palau, Papua, and Vanuatu.

This meeting was open to designated counterparts of the project RAS5079. The meeting objective was to identify the most important outputs, recommendations, and points of improvement of the current project in preparation for the phase II project RAS5098 on Improving the Resilience of

Crops to Climate Change through Mutation Breeding — Phase II (SAPI) that will start on 2022.

The Pacific Community Centre for Pacific Crops and Trees (SPC CePaCT) was a highly active regional partner in this project. The national project coordinators presented their outcomes. Capacity building activities implemented included three regional training courses, two virtual courses and one fellowship. Mutant genetic material was obtained for sweet potato, yam, and chili using gamma irradiation at IAEA Seibersdorf Laboratories. In addition, protocols for banana, sweet potato and yam *in vitro* culture were implemented. The outputs obtained will be expanded in the RAS5098 project.

Advanced Regional Training Course **Digital Breeding Management Systems and Field Experimental Design/Analysis, RAS5088**

Virtual Meeting. 22 November–3 December 2021

Project Officer: S. Sivasankar

This training course constitutes the first effort in the plant mutation breeding community supported by the Joint FAO/IAEA Centre to digitise breeding programmes and mainstream advanced statistical tools to facilitate seamless experimental design and analysis for the confident selection of distinctive mutants. The Breeding Management System (BMS) was developed within the last decade by the Consultative Group of International Agricultural Research (CGIAR) with the support of the Bill and Melinda Gates Foundation, and was integrated into plant breeding programmes of the CGIAR and to some extent its partners in National Agricultural Research Systems. The mutation breeding research community supported by the Joint Centre in many Member States remain separate from national agricultural ministries and institutions, as a consequence of which such tools available to agricultural researchers in developing countries are not available or used by the mutation breeding research community.

Thus, this regional training course was developed and offered as part of the ongoing technical guidance efforts of PBG for the digitization of breeding management and incorporation of advanced statistical software for experimental design and analysis as part of all mutation breeding programmes supported by the Joint FAO/IAEA Centre in IAEA Member States. The training course was delivered as part of the regional TC project, RAS5088 on Enhancing Crop Productivity and Quality through Mutation by Speed Breeding.

Course curriculum included breeding informatics in plant breeding, statistics refresher, use of the Breeding Management System (BMS), basics of experimental design and early generation testing, digital data recording, introduction to R language, single-site and multi-site analysis in BMS, Genetics X Environment interactions, and the concept of mega environments and representative

testing. The course was attended by 30 participants across 10 countries and was very well received.

As follow up to this training course, and based on the appreciation and demand from participants, PBG plans to discuss with CGIAR's BMS team the availability and use of the system by the plant mutation breeding community on a routine basis. We also aim to streamline BMS in other national and regional projects where there is demand for the system for digital experimentation, pedigree management, experimental design and analysis with sophisticated statistical software for confident conclusions.

National Training Course **Hemileia vastatrix Diagnosis and Screening, JAM5014**

Virtual. 29 November to 07 December 2021

Virtual Meeting. 29 November–7 December 2021

Project Officer: S. Sivasankar

This training course was implemented in virtual mode as part of the TC project, JAM5014 on Establishing a Self-Contained Gamma Irradiation Facility for the Introduction of Sterile Insect Technique and Experimental Mutagenesis and Diagnostic Technologies.

The training course started with an introduction to the Coffee Institute of Costa Rica and covered specific training topics on the genetics of coffee, mutation induction in coffee, coffee propagation methods, tissue culture methods and micropropagation in coffee, experience and results obtained at ICAFE on induced mutation with gamma irradiation in coffee, introduction to coffee leaf rust, and the characterization, detection, evaluation and severity of coffee leaf rust. The course was attended by a small group of 20 researchers and was delivered over four days over the indicated timeframe, with sessions being delivered over four hours during each training day.

Regional Training Course **Plant Mutation Breeding and Associated Biotechnologies, RER5024**

Virtual Meeting. 6–10 December 2021

Project Officers: S. Sivasankar, C. Zorrilla

This regional training course was delivered virtually to four of the Member States participating in the Regional TC project, RER5024 on Enhancing Productivity and Resilience to Climate Change of Major Food Crops in Europe and Central Asia. Member States that participated in the training course include North Macedonia, Serbia, and Bosnia & Herzegovina.

Course curriculum included an introduction to nuclear techniques in food and agriculture, mutation induction and induced genetic variation, mutation induction in plants by ionizing radiation, the development of mutant population, screening and the impact of mutation breeding, preparation of radiosensitivity curves, *in vitro* mutagenesis in

vegetatively propagated plants, plant tissue culture with specific focus on banana, doubled haploids and their use in mutation breeding, transposable elements, marker-assisted backcrossing, and rapid generation advance. The course was attended by a total of 15 participants (two male and 13 female) from the three countries, including four from Bosnia & Herzegovina, one from North Macedonia and 10 from Serbia.

Final Project Review Meeting

Promoting the Application of Mutation Techniques and Related Biotechnologies for the Development of Green Crop Varieties, RAS5077

Virtual Meeting. 7–9 December 2021

Project Officer: I.K. Bimpong

The Regional Cooperative Agreement's (RCA) mutation breeding programme works to increase environmental-friendly crop productivity through the application of mutation techniques and related biotechnologies with enhanced capability of the RCA Government Parties (GPs) in the effective use of mutation techniques for the development of green crop varieties. The meeting (1) reviewed results that have been achieved regarding the implementation of the individual country workplans, regional project outcomes and outputs from the beginning of the project in 2017; and (2) finalized workplans for end of the project in terms of key achievements (number of mutant varieties released, mutant lines and protocols with improvement of target green traits).

Seventeen National Project Coordinators (NPCs), GPs in Asian and Pacific countries from Australia, Bangladesh, Cambodia, China, India, Japan, Lao P.D.R., Malaysia, Mongolia, Myanmar, Nepal, Pakistan, the Philippines, Republic of Korea, Sri Lanka, Thailand, and Viet Nam) and the IAEA staff participated in the meeting.

National Training Course

Using Nuclear Techniques to Improve the Adaptation and Productivity of Forest Species Facing Climate Change, CHI5052

Virtual Meeting. 13–17 December 2021

Project Officers: S. Sivasankar; C. Zorrilla

A Training Course on Molecular Markers Assisted Plant Breeding and Bioinformatics for Forest Species from South America was developed with 24 participants (11 female and 13 male) from different research institutions, universities, and the forest private sector in Chile. The course covered topics such as mutation breeding: concepts and methodologies, linkage mapping, QTL and GWAS mapping, bioinformatics, molecular markers in plant breeding, and mutation induction. Participants acquired knowledge and exchanged experiences/ideas on how mutation breeding can be a powerful tool for forest genetic improvement.

Developments at the Plant Breeding and Genetics Laboratory (PBGL)

The rapid development of DNA sequencing technologies and related data analysis tools are revolutionizing the way plant breeding is being practiced. Likewise, plant mutation breeding stands to benefit tremendously from advances in these fields. For example, sequencing technologies with supporting informatics tools can help solve a bottleneck in mutation breeding, the selection of mutants at population scale. This typically requires advancing and phenotyping mutant population typically up to five or six generations. Generally, advanced DNA sequencing and bioinformatics tools can add precision and fast track plant mutation breeding programs. PBGL strives to enable Member States to fully participate in this genomics revolution and so enhance their mutation breeding projects. Below summarizes some key approaches for DNA sequence generation and presents an overview of recent progress and tools developed at the PBGL in this area with example applications supporting plant mutation breeding.

PBGL Bioinformatic Toolbox

DNA sequencing currently comes in two main flavours: (1) short read sequencing, and (2) long-read sequencing. For plant breeding applications, both techniques complement each other and PBGL is developing tools utilizing both approaches. Frustratingly, the analysis of current generation sequencing data is still more complicated than it needs to be. PBGL is working towards a set of easy-to-use computer tools to lower the barrier of entry for non-experts and enable effective and reproducible analyses. We are also developing molecular biology protocols to introduce long-read sequencing by Oxford Nanopore's hand-held MinION sequencer to support plant mutation breeding applications.

One domain of short-read DNA sequencing is the re-sequencing of genomes in order to cost-effectively detect mutations, mainly SNPs and InDels. The first steps of the analysis involve turning the raw sequence reads as they come off the sequencer into informative output. This step is computationally demanding, and most laboratories will outsource this task. At PBGL we perform this analysis in house with an automated workflow that we developed (see PBG newsletter No 45). The relevant informative outputs of such primary analysis then are merely text files. Of interest are the (induced) mutations. They are listed in so-called variant call files, or vcf/bcf-files. Another set of files are the so-called sam/bam files. They contain the sequence alignments of all reads against the chosen reference genome. SNPs and small InDels are readily detected from those short-read alignment files by off-the-shelf variant callers to produce vcf files. Ultimately, sam and vcf files are text files and they contain the information breeders need to advance their projects. While extracting information from them is relatively straight-forward and can be performed on a standard laptop, it still requires bioinformatics expertise. This is a major obstacle for adoption. At PBGL, we leverage recent advances in computer science and software development to enable non-expert users to interact with such data, allowing them to perform their custom, project-specific downstream analyses.

For example, Figure 1 illustrates the use of the tool CNV-seq to detect and visualise statistically significant sequence coverage differences between samples, indicative of large genome rearrangements.

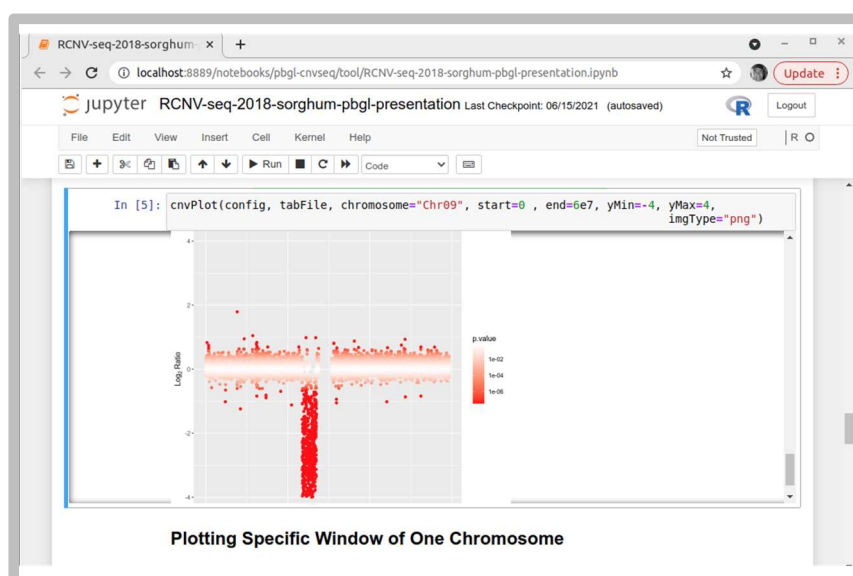


FIG. 1. Detection of a large deletion on chromosome 9 in a *Sorghum* mutant using an R implementation of CNV-seq (Xie, C et al., 2009) in a jupyter notebook.

Most tools in our toolbox use established open-source software and functions. We provide defined conda virtual environments for straight-forward installation of the software along with its dependencies and facilitate interaction with the analysis functions in a web browser through jupyter notebooks. All our tools are hosted on github.org, with detailed documentation on readthedocs.org. This setup allows for efficient capacity building including remote trainings.

A major limitation of short-read sequencing is the difficulty of detecting genome rearrangements; larger regions missing or duplicated, also known as Structural Variants (SVs) and Copy Number Variants (CNVs). They are particularly relevant because physical mutagens, such as ionizing radiation, often lead to such large genomic changes via the DNA strand breaks they induce. CNVseq extracts the coverage information from alignment files (sam/bam) performs a statistical test for coverage differences between samples and plots the significance scores. Our tool provides for easy installation of an R implementation of CNVseq and a jupyter notebook facilitating use through the web browser (Xie, C., Tammi, M.T. CNV-seq, a new method to detect copy number variation using high-throughput sequencing. BMC Bioinformatics 10, 80 (2009). <https://doi.org/10.1186/1471-2105-10-80>).

Software Tools Developed by PBGL This Year

- pbgl-qtI-bSA - Plotting allele frequencies from VCF files (Jupyter/Python);
- pbgl-cnVseq - Identifying copy number variations from BAM files (Jupyter/R);
- pbgl-cnVkit - Identifying copy number variations from BAM files for exome capture data (Jupyter/Python);
- pbgl-gdd - Visualizing INFO and FORMAT attributes from VCF files (Jupyter/Python).

Mutation Detection with a Hand-Held DNA Sequencer

A significant invention of the past decade has been nanopore sequencing: DNA sequence is determined directly as the DNA single-strand molecules are pulled through protein pores across a membrane. This allows for long, up to mega base pair-long sequencing reads. Most importantly, Oxford Nanopore Technologies plc. (ONT) sells a hand-held sequencing device, the 'MinION' (Figure 2). It has the size of a candy bar and can be operated from a laptop via USB. The consumables are ready-to-use, so-called 'flow cells'. The MinION sequencing 'machine' itself is essentially free with negligible delivery cost and zero set-up and maintenance costs. It can, in principle, be operated by anyone, everywhere. It is easy to see how it could become a game

changer in plant breeding, putting genomics at the fingertips of our partners in Member States.

PBGL established MinION technology in house in early 2019. The technology is still evolving with ever decreasing error rates but has now matured to a point where we consider incorporating it in our plant breeding work. Key will be to develop protocols for its cost-effective use at the population-scale, as required in plant (mutation) breeding applications. PBGL identified PCR amplicon sequencing as an important first application. We are modifying existing PCR-amplicon sequencing protocols to enhance fidelity as well as reduce cost.



FIG. 2. The Oxford Nanopore plc MinION DNA Sequencer connected to a laptop through USB and loaded with a Flongle, the sequencing consumable containing the membrane with pores. Flongle costs around 100 Dollars and provides sequencing capacity up to 1.8 Gb.

Detection of Copy Number Variation in Candidate TR4 Resistant Cavendish Banana

Bananas are a staple for over 400 million people. Additionally, more than 16.5 million tons are exported, making it both an important food security and cash crop. Edible bananas are sterile, parthenocarpic and vegetatively propagated rendering them particularly susceptible to diseases. Banana fusarium wilt caused by the soil-borne fungus *Fusarium oxysporum* f. sp. *cubense* (Foc) is one of the most destructive diseases of banana globally. A new, aggressive Foc strain called tropical race 4 (Foc TR4) was identified in the 90's in Southeast Asia that severely affected Cavendish plantations. Recently TR4 has been reported in Latin America thus threatening global banana production. We previously showed that gamma rays can induce large genomic insertions and deletions resulting in Copy Number Variations (CNV) in banana. CNV's have been implicated in several important processes in plants, including disease resistance. To help address the threat of

TR4, the FAO/IAEA and partners set up a mutation breeding program in Cavendish bananas to create new allelic variation and screen for TR4 resistance. A large mutant population of the cultivar Grande Naine was produced and screened for resistance to TR4. To date, a total of eight mutants treated with either 30 or 40 Gy

showed no disease symptoms after artificial inoculation. Of these, four were sequenced and analysed for the presence of CNV's. Twenty-eight deletions ranging between 100kb and 1 Mb were recovered. Example data is shown in Figure 3 and 4 which will also be presented at the upcoming 2022 PAG Conference, San Diego, CA, USA.

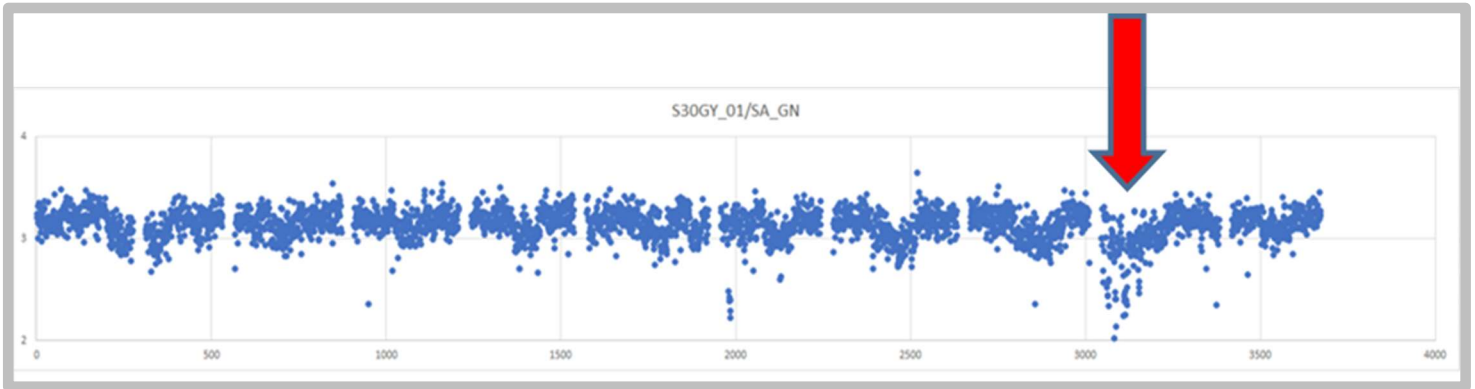


FIG. 3. Relative Sequence Read Coverage (RSRC) along all xx chromosomes of a putatively resistant mutant of Cavendish banana cultivar 'Grand Naine' (gamma-irradiation with 30 Gy). Top of chromosome 10 shows evidence of a copy number variant (red arrow). Software: bin-by-sam. <https://github.com/Comai-Lab/bin-by-sam>

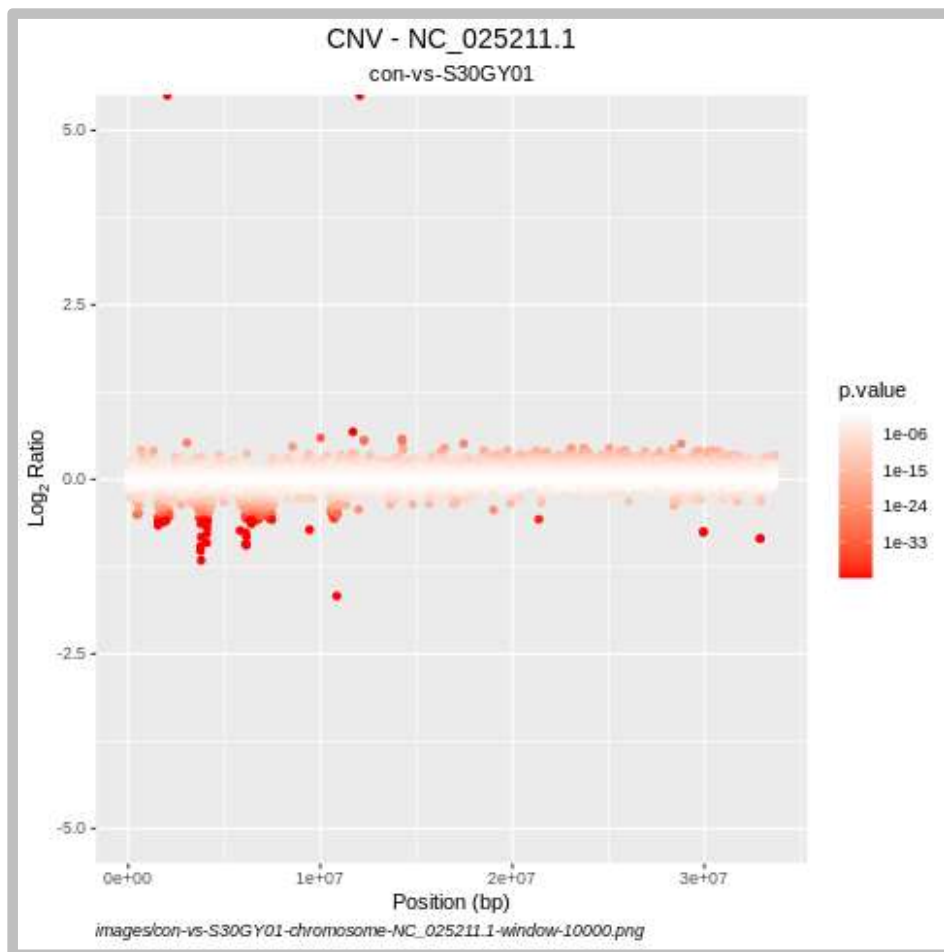


FIG. 4. Statistical analysis of relative sequence read coverage along chromosome 10 of a putatively resistant mutant of Cavendish banana cultivar 'Grand Naine' (gamma-irradiation with 30 Gy). The plot indicates several areas of reduced coverage, indicative of several copy number variants. Software: CNVseq. <https://github.com/pbgl/pbgl-cnvseq>

Crop Irradiation Services Provided to Member States

Table 1 lists the irradiation requests that the PBGL have received so far (15 November) during 2021. The PBGL has received 33 requests from 22 Member States across 24 different plant species covering a total of 297 accessions/varieties.

Table 1. Crop Irradiation Services

Request Number	Country	Request Type	Species
1647	Namibia	TC	Groundnut
1648	Slovakia		Wheat
1649	Central African Republic	TC	Maize
1650	Germany		Ornamental
1651	Hungary		Ornamental
1652	Serbia	TC	Soybean
1653	Kyrgyzstan	TC	Barley, Wheat
1654	Poland		<i>Brassica napus</i>
1655	Croatia	TC	<i>Phaseolus vulgaris</i>
1656	Nigeria		Yam
1657	Greece	TC	Chickpea, Sesame
1658	Germany		Ornamental
1659	Bosnia and Herzegovina	TC	<i>Phaseolus vulgaris</i>
1660	Burkina Faso	TC	<i>Digitaria exilis</i>
1661	Honduras	TC	Coffee
1662	The Netherlands		Ornamental
1663	Germany		Ornamental

Request Number	Country	Request Type	Species
1664	Poland	TC	Buckwheat
1665	Poland	TC	Barley
1666	Germany		Ornamental
1667	PBGL		Sorghum
1668	United Republic of Tanzania	TC	Rice
1669	UK		<i>Euphorbia peplus</i>
1670	Namibia	TC	Groundnut, Maize, Bambara Groundnut
1671	Eritrea	TC	Maize
1672	North Macedonia	TC	Common Bean
1673	Iraq	TC	Peanut, Mungbean
1674	Kenya	CRP	Sorghum
1675	Nigeria		<i>Vigna vexillata</i>
1676	Namibia	TC	Pearl Millet
1677	Slovakia	TC	Wheat
1678	Croatia	TC	Wheat
1679	UK		<i>Papaver somniferum</i>

Individual Training

During 2021 the PBGL hosted four interns, one fellow, one scientific visitor and one PhD student as summarized in Table 2.

Table 2. Individual Training Activities at the PBGL

Name	Country	Status	Topic	Period
Ms Susu ALKIERS	Austria	Intern	Plant breeding and genetics	1 year
Mr Michael OSAE	Ghana	Scientific Visitor	Mutation breeding	2 weeks
Mr Anibal E. MORALES ZAMBRANA	USA	Intern	Data science	1 year
Ms Faith LUVAI	Kenya	Intern	Banana Fusarium wilt screening protocols	1 year
Mr Phillipe NIKIEMA	Burkina Faso	Fellow	Screening protocols for resistance to the parasitic weed <i>Striga</i>	4 months
Mr Michael HALL	USA	Intern	Data science	1 year
Mr Hassan MDUMA	United Republic of Tanzania	PhD-Consultant	Mutation breeding for Fusarium wilt resistance in African cooking banana	3 months

New CRP: Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development (D24015)

Sobhana Sivasankar, IAEA Department of Nuclear Sciences and Applications



The IAEA is launching a new Coordinated Research Project (CRP) on radiation-induced crop diversity and genetic associations, with a time frame of five years from 2022 to 2026.

Induced genetic diversity and breeding with promising mutations for farmer-preferred traits in agronomically sound genetic backgrounds have paved the way for crop improvement across the globe for over seven decades now. Testament to this is the more than 3300 mutant varieties in over 220 plant species from more than 70 countries represented in the [Mutant Variety Database](#) (MVD).

Induced mutations fortify plant germplasm pools and enable faster genetic gain, especially where the genetic base is narrow. Mutation breeding thus has the potential to facilitate larger genetic gain than conventional breeding. This advantage, coupled with emerging front-end technologies for efficient and precise selection, can both accelerate the pace of crop improvement and increase the rate of genetic gain.

Breeding with induced genetic diversity has remained a highly effective avenue for the improvement of both simple and complex crop traits in developing Member States of the Food and Agriculture Organization of the United Nations (FAO) and the IAEA.

‘Mutation breeding has so far mainly relied on gamma rays,’ says Shoba Sivasankar, Head of the IAEA’s Plant Breeding and Genetics Section. ‘Most recently the ion beam, electron beam, proton beam and space irradiation — cosmic rays — are coming into increasing use at least in

some countries, though the effect of these different sources on the plant genome remain to be assessed systematically.’

Newer genomic technologies that establish genetic associations for marker and candidate gene discovery are also yet to be applied to mutation breeding for increased precision and breeding efficiency. Mutant populations generated from induced genetic variation are traditionally used directly as source germplasm for breeding and variety development. However, they can also render themselves to the establishment of genetic associations for marker-assisted breeding and gene editing. Theoretically, mutant populations can also be used for genomic predictions for increased efficiency of the breeding process.

Technical support of the Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture has led to capacity building in crop improvement and the development of improved varieties in more than a hundred Member States since 1964. This technical support has centred on mutation induction, phenotypic selection and variety development, advancing very recently to explore molecular markers for increased precision in selection and efficiency in breeding.

The proposed CRP is aimed at addressing three important emerging trends and needs 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.

CRP Overall Objective

To strengthen the ability of the IAEA 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.

Specific Research Objectives

1. To assess the nature of mutations induced by different mutagen sources, including gamma rays, ion beam, proton beam, electron beam and cosmic radiation.
2. To determine molecular variant(s) underlying mutations for marker-assisted breeding.

3. To confirm at least one mutant phenotype using gene editing. Focus will be on seed crops, diploid genomes and simple traits.
4. To develop a test case to effectively apply genomic selection in mutation breeding.
5. To identify novel mutants for crop-trait combinations included in the project.
6. To develop/adapt reproducible computational tools and platforms to determine genetic associations.

Outputs

1. Mutant population(s) generated from different mutagen sources for discovery research and variety development.
2. Data on effect of different mutagen sources on the genome (i.e. nature and frequency of mutations).
3. Molecular variants underlying mutations determined for use as markers in molecular breeding or as candidate genes in gene editing.
4. Bioinformatic platform(s) developed/adapted for genetic association, genomic prediction.
5. Improved mutant lines identified for traits of interest.
6. Scientific publications in high impact journals.
7. Protocols and training manuals developed and disseminated.

How to join this CRP

Up to three research/technical contracts are expected to be awarded on the study of the effect of mutagen sources on

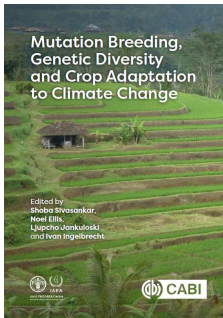
crop genome, five to six research/technical contracts on the study of genetic associations in established, structured plant populations built on clear phenotypes for simple traits (one or few genes expected to be involved), and one research/technical contract addressing genomic selection in mutation breeding. Proposals submitted on the study of genetic associations are encouraged to include data on expression of the phenotype and the status of populations amenable for genetic analysis. Up to five no-cost agreement holders from advanced laboratories are also expected to participate. Research institutes with recognized expertise in the targeted technologies will be invited to share their experience with the contract holders and contribute to the development and validation of the planned technical packages. Coordination and technical management will be handled by the scientific secretary in the IAEA's Plant Breeding and Genetics Section with involvement of the Plant Breeding and Genetics Laboratory.

Please submit your Proposal for Research Contract or Agreement by email to the IAEA's [Research Contracts Administration Section](#), using the appropriate template on the [CRA](#) web portal. Same form can be used for the research contract and the technical contract.

For further information related to this CRP, potential applicants should use the [contact form](#) under the CRP page.

Publications

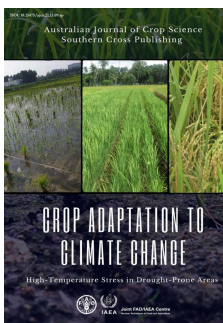
Books



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
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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



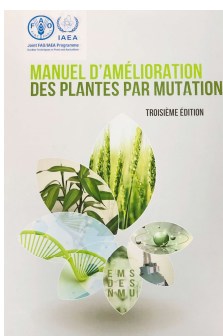
Manual de mejoramiento por mutaciones, Tercera edición

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.

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[Manual de mejoramiento por mutaciones \(fao.org\)](https://www.fao.org/publications/default.asp?lang=es&sk=69232211001_000_0_000)



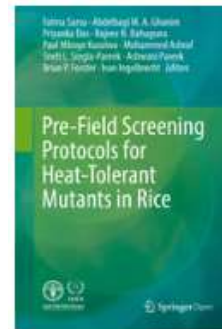
Manuel d'amélioration des plantes par mutation, Troisième édition

Édité par M.M. Spencer-Lopes, B.P. Forster et L. Jankuloski, Sous-programme de Génétique et d'Amélioration des Plantes Division mixte FAO/OIEA des Techniques Nucléaires appliquées à l'Alimentation et à l'Agriculture.

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[Manuel d'amélioration des plantes par mutation \(fao.org\)](https://www.fao.org/publications/default.asp?lang=fr&sk=69232211001_000_0_000)

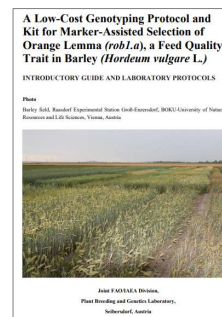


Pre-Field Screening Protocols for Heat-Tolerant Mutants in Rice

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
ISBN 978-3-319-77338-4

[Pre-Field Screening Protocols for Heat-Tolerant Mutants in Rice | Fatma Sarsu | Springer](https://www.springer.com/9783319773384)

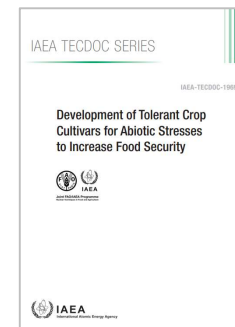


A Low-Cost Genotyping Protocol and Kit for Marker-Assisted Selection of Orange Lemma (*rob1.a*), a Feed Quality Trait in Barley (*Hordeum vulgare* L.).

Introductory guide and laboratory protocols. I. Ingelbrecht *et al.*, May 2021.

[Diagnostic-marker-assay-OL-barleyMay2021.pdf \(iaea.org\)](https://www.iaea.org/publications/2021/05/diagnostic-marker-assay-ol-barley)

Technical Documents



IAEA-TECDOC-1969

Development of Tolerant Crop Cultivars for Abiotic Stresses to Increase Food Security

Contributors: N.K.A. Amoah, B. Manneh and I.K. Bimpong.

Salt stress (both salinity and sodicity) is the second most widespread soil problem after

drought and is a serious constraint in rice production worldwide. Soil is considered saline if the electrical conductivity is above four units of its measurement scale. Rice is most sensitive to salt stress during the early seedling (1–3 weeks) and reproductive stages, when the threshold is as low as an electrical conductivity of three units of its measurement scale. Plant breeding for crop improvement can decrease the grain yield gap in salt-prone soils, thus contributing to food security and alleviating poverty.

This publication provides information on a system for phenotyping problem soils to identify tolerant lines for use in breeding programmes that target salt stress. The standard operating procedures presented here provide comprehensive information on (a) developing a suitable phenotyping system for the two main stages of crop

sensitivity to salt stress, including pre-screening of large sets of test lines in a controlled or semi-controlled environment and evaluation under field conditions, and on (b) reducing experimental error and improving repeatability of the experiment through proper stress management. The present publication is expected to be a valuable resource for plant breeders and field technicians involved in phenotyping of soils.

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ISBN 978-92-0-123221-2 (pdf)

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[IAEA-TECDOC-1969](https://www.iaea.org/publications/iaea-tecdoc-1969)

Peer-reviewed Publications

2021

BOHRA, A., KILIAN, B., SIVASANKAR, S., CACCAMO, M., MBA, C., MCCOUCH, S.R., VARSHNEY, R.K. (2021) Reap the crop wild relatives for breeding future crops. Trends in Biotechnology Oct 8; S0167-7799(21)00197-9.

RAHMAN, M.H., SULTANA, R., SARKAR, M.M.A., ISLAM, S., AZAD, M.A.K., SIVASANKAR, S. (2021) Comparative Profitability and Impact of BINA Developed Aman Mutant Rice Binadhan-7 with Non-Mutant Variety in Bangladesh. Asian Research Journal of Agriculture 14(3): 11-25.

HUSSAIN, M., JANKULOSKI, L., HABIB-UR-RAHMAN, M., MALEK, M., KAMRUL ISLAM, Md., RAHEEMI, M.R., DANA, J., MYAT LWIN, K., AHMAD, F., RIZWAN, M., MOHYUDDIN TALHA, G., ASIF, M., ALI, S. (2021) Improving Sustainable Cotton Production Through Enhanced Resilience to Climate Change Using Mutation Breeding. In: Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change. S. Sivasankar *et al.* (eds.), CABI.

SOFKOVA-BOBCHEVA, S., PANTCHEV, I., KIRYAKOV, I., CHAVDAROV, P., MUHOVSKI, Y., SARSU, F., TOMLEKOVA, N. (2021) Induced Mutagenesis for Improvement of Bean (*Phaseolus vulgaris* L.) Production in Bulgaria. In: Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change. S. Sivasankar *et al.* (eds.), CABI.

JANKULOVSKA, M., IVANOVSKA, S., JANKULOSKI, L., MARKOSKI, M., KUZMANOVSKA, B., BOSHEV, D. (2021) Evaluation of Advanced Wheat Mutant Lines for Food and Feed Quality. In: Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change. S. Sivasankar *et al.* (eds.), CABI.

CÉSPEDES, R., ARRIETA, N., BARQUERO, M., ABDELNOUR, A., NIELEN, S., INGELBRECHT, I. (2021) Determination of Radiosensitivity of *Coffea*

arabica var. Venecia Seeds to Gamma-ray Irradiation. In: Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change. S. Sivasankar *et al.* (eds.), CABI.

RABEFIRAISANA, H.J., GHANIM, A.M.A., ANDRIANJAKA, A., RASOAMAMPIONONA, B., JANKULOSKI, L., RAZAFINDRASOA, M.A., RAVELONJANAHARY, N.H., RAKOTOARISOA, N.V. (2021) Impact of Mulch-Based Cropping Systems Using Green Mulch and Residues on the Performance of Advanced Mutants Lines of Maize (*Zea mays* (L.)) Under Infested Field with the Parasitic Weed *Striga asiatica* (L.) Kuntze in Madagascar. In: Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change. S. Sivasankar *et al.* (eds.), CABI.

JANKOWICZ-CIESLAK, J., GOESSNITZER, F., DATTA, S., VILJOEN, A., INGELBRECHT, I., TILL, B.J. Induced Mutations for Generating Bananas Resistant to Fusarium Wilt Tropical Race 4. In: Mutation Breeding, Genetic Diversity and Crop Adaptation to Climate Change. S. Sivasankar *et al.* (eds.), CABI.

THUDI, M., PALAKURTHI, R. SCHNABLE, J.C., CHITIKINENI, A., DREISIGACKER, S., MACE, E., SRIVASTAVA, R.K., SATYAVATHI, C.T., ODENY, D., TIWARI, V.K., LAM, H.M., HONG, Y.B., SINGH, V.K., LI, G., XU, Y., CHEN, X., KAILA, S., NGUYEN, H., SIVASANKAR, S., JACKSON, S.A., CLOSE, T.J., SHUBO, W., VARSHNEY, R.K. (2021) Genomic Resources in Plant Breeding for Sustainable Agriculture. Journal of Plant Physiology (TSI), 257. pp. 1–18. ISSN 0176-1617.

<https://doi.org/10.1016/j.jplph.2020.153351>

MATOVA, P.M., KAMUTANDO, C.N., SARSU, F., MAGOROKOSHO, C., LABUSCHAGNE, M. (2021) Determining the Optimum Gamma Irradiation Dose for Developing Novel Maize Genotypes. Journal of Crop Improvement.

<https://doi.org/10.1080/15427528.2020.1850591>

SARSU, F., BIMPONG, I.K., JANKULOSKI, L. (2021). Contribution of Induced Mutation in Crops to Global Food Security. ACI Avances en Ciencias e Ingenierías, 12(22), 2–11.

<https://revistas.usfq.edu.ec/index.php/avances/issue/view/153>

JANKOWICZ-CIESLAK, J., GOESSNITZER, F., TILL, B.J., INGELBRECHT, I. Physical Mutagenesis and Population Development in *Musa* spp. In: Efficient Screening Techniques to Identify Mutants with TR 4 Resistance in Banana. Springer Nature. (*in press*)

JANKOWICZ-CIESLAK, J., INGELBRECHT, I., TILL, B.J. Mutation Detection Using Low Coverage Copy Number Variation. In: Efficient Screening Techniques to

Identify Mutants with TR 4 Resistance in Banana. Springer Nature. (*in press*)

AMRI-TILIOUINE, W., JANKOWICZ-CIESLAK, J., TILL, B.J., LAOUAR, M. Generation of Mutant Plants by Gamma Ray Exposure and Development of Low-cost TILLING Population in Chickpea (*Cicer arietinum* L.). In: Plant Gametogenesis: Methods and Protocols. Lambing, C, (eds.) Humana Press. (*in press*)

2020

NIKIÈMA, M.P., OUÉDRAOGO, N., TRAORÉ, H., SAWADOGO, M., JANKULOSKI, L., GHANIM, A.M.A., YONLI, D. (2020). Sorghum Mutation Breeding for Tolerance to Water Deficit Under Climate Change. Journal of Plant Breeding and Crop Science, 12(3), 192–199. <https://doi.org/10.5897/JPBCS2020.0886>

AHUMADA-FLORES, S., GÓMEZ PANDO, L.R., PARRA COTA, F.I., DE LA CRUZTORRES, E., SARSU, F., DE LOS SANTOS VILLALOBOS, S. (2020) Technical Note: Gamma Irradiation Induces Changes of Phenotypic and Agronomic Traits in Wheat (*Triticum turgidum* ssp. durum), Applied Radiation and Isotopes. <https://doi.org/10.1016/j.apradiso.2020.109490>

WANGA, M.A., SHIMELIS, H., HORN, L.N., SARSU, F. (2020) The Effect of Single and Combined Use of Gamma Radiation and Ethylmethane Sulfonate on Early Growth Parameters in Sorghum. Plants 2020, 9, 827. <https://www.mdpi.com/2223-7747/9/7/827>

SIVASANKAR, S., HENG, L.K, KANG, S.-Y. (2020) Agriculture: Improving Crop Production. Elsevier Encyclopedia of Nuclear Energy. <https://doi.org/10.1016/B978-0-12-409548-9.12323-1>

NIKIÈMA, M.P., YONLI, D., RABEFIRAISANA, H.J., ALI, A., OUÉDRAOGO, N., TRAORÉ, H., YANOOGO, H.Y.A., DAO, K., SAWADOGO, M., JANKULOSKI, L., INGELBRECHT, I., GHANIM, A.M.A. Induced Resistance to *Striga hermonthica* in Sorghum by Gamma Irradiation. American Journal of Plant Sciences, 2020, 11, 1545–1561. <https://doi.org/10.4236/ajps.2020.1110112>

GENNETT, A., GOESSNITZER, F., JANKOWICZ-CIESLAK, J., INGELBRECHT, I., GHANIM, A.M.A. Reliable non-destructive phenotyping assay for evaluating Fusarium wilt tropical race 4 resistance screening of Cavendish banana. In: Efficient Screening Techniques to Identify Mutants with TR4 Resistance in Banana. (*submitted*)

HAWLICZEK, A., BOLIBOK, L., TOFIL, K., BORŻĘCKA, E., JANKOWICZ-CIEŚLAK, J., GAWROŃSKI, P., KRAL, A., TILL, B.J. and BOLIBOK-BRĄGOSZEWSKA, H. Deep Sampling and Pooled Amplicon Sequencing Reveals Hidden Genic Variation in

Heterogeneous Rye Accessions. *BMC Genomics* 21: Article number 845 (2020).

<https://bmcbgenomics.biomedcentral.com/articles/10.1186/s12864-020-07240-3>

MBA, C., ABANG, M., DIULGHEROFF, S., HRUSHKA, A., HUGO, W., INGELBRECHT, I., JANKULOSKI, L., LESKIEN, D., LOPEZ, V., MUMINJANOV, H., MULILA MITTI, J., NERSISYAN, A., NOORANI, A., PIAO, Y. and SAGNIA, S. (2020). FAO Supports Countries in the Implementation of the Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture. *Acta Hort.* 1267, 197–208.

<https://doi.org/10.17660/ActaHortic.2020.1267.30>

ROY, S., GHANIM, A.M.A., NUNEKPEKU, W., RASHIDUL ISLAM, MD. RASEL AND MD. MAHMUD AL NOOR (2020). Phenotyping of Lentil Genotypes for Drought Tolerance Using Polyethylene Glycol. *Indian Journal of Natural Sciences* ISSN: 0976–0997; Vol.10, Issue 58, February 2020.

2019

PANTCHEV, I., AZIZ, S., SARSU, F., TOMLEKOVA, N. (2019) Applicability of ISAP, ISSR and SSR Markers in Tomato Breeding Programs. *Vegetable Crops of Russia* (6):24–26.

<https://doi.org/10.18619/2072-9146-2019-6-24-26>

KENZHEBAYEVA, S., ABEKOVA, A., ATABAYEVA, S., YERNAZAROVA, G., OMIRBEKOVA, N., ZHANG, G., TURASHEVA, S., ASRANDINA, S., SARSU, F., WANG, Y. (2019) Mutant Lines of Spring Wheat with Increased Iron, Zinc, and Micronutrients in Grains and Enhanced Bioavailability for Human Health. *Hindawi BioMed Research International* Volume 2019, Article ID 9692053, 10 pages.

<https://doi.org/10.1155/2019/9692053>

WILSON, P.B., STREICH, J.C., MURRAY, K.D., EICHTEN, S.R., CHENG, R., AITKEN, N.C., SPOKAS, K., WARTHMAN, N., GORDON, S.P., VOGEL, J.P., and BOREVITZ, J.O. (2019). Global Diversity of the Brachypodium Species Complex as a Resource for Genome-Wide Association Studies Demonstrated for Agronomic Traits in Response to Climate. *Genetics*, 2019, 211(1), 317–331.

<https://doi.org/10.1534/genetics.118.301589>

OBERHOFER, M., HESS, J., LEUTGEB, M., GÖSSNITZER, F., RATTEI, T., WAWROSCHE, C. and ZOTCHEV, S.B. (2019). Exploring Actinobacteria Associated with Rhizosphere and Endosphere of the Native Alpine Medicinal Plant *Leontopodium nivale* Subspecies alpinum. *Frontiers in Microbiology* 10.

<https://doi.org/10.3389/fmicb.2019.02531>

TRAMONTANO, A., JARC, L., JANKOWICZ-CIESLAK, J., HOFINGER, B.J., GAJEK, K., SZURMAN-ZUBRZYCKA, M., SZAREJKO, I., INGELBRECHT, I.

and TILL, B.J. (2019). Fragmentation of Pooled PCR Products for Highly Multiplexed TILLING. *G3-Genes Genomes Genetics* 9(8): g3.400301.2019. <https://doi.org/10.1534/g3.119.400301>

Conference Abstracts and Posters

2021

SAIF, A.A., AL-SHAMIRI, A., ALSAGIR, M., JANKULOSKI, L. (2021) Evaluation and Selection Disease Resistant Wheat Mutants to Yellow Rust Disease *Puccinia striiformis f. sp. triticii* Using Gamma-Irradiation Technique in Yemen. 15th Arab Conference on the Peaceful Use of Atomic Energy. 12–16 December 2021. Aswan, Egypt.

TILL, B.J., HAWLICZEK, A., JANKOWICZ-CIEŚLAK, J., GUPTA, P., HOWARD-TILL, R., OSORIO, C.E., BOLIBOK-BRĄGOSZEWSKA, H. (2021) High-Throughput Discovery of Induced and Natural Mutations in Plants. Application Genetics of Plants – Challenges of the 21st Century, 22–24 September 2021 at the Warsaw University of Life Sciences (SGGW), Warsaw, Poland.

AZIZ, S., KANTOGLU, Y., TOMLEKOVA, N., STAYKOVA, T., GANEVA, D., SARSU, F. (2021) Molecular Characterization of Tomato Genotypes (*Solanum lycopersicum* L.) by Simple Sequence Repeat (SSR) Markers. Presented at the 5th Balkan Scientific Conference on Biology (BalkanBio'2021), Plovdiv, Bulgaria: Zenodo. <http://doi.org/10.5281/zenodo.4650460>

2020

SARSU, F., SIVASANKAR, S., BIMPONG, I.K., JANKULOSKI, L. 2020. Induced Mutations for Food Security. Presented at the 2nd Latin American Symposium on Nuclear Applications in Agriculture, 5–6 March 2020, Ecuador.

WARTHMAN, N., GHANIM, A.M.A, ALI, A., and INGELBRECHT, I. (2020). Mutation Breeding Creates Desired Traits for African Sorghum –Semi-Dwarf and Early Maturing. PE0810. Plant and Animal Genome XXVIII, 11-15 January 2020, San Diego, USA.

WARTHMAN, N., GHANIM, A.M.A., ALI, A. and INGELBRECHT, I. (2020). Mutation Breeding Creates Desired Traits for African Sorghum – Semi-Dwarf and Early Maturing. International Symposium of the Society for Plant Breeding (GPZ), Digital Breeding, 11–13 February 2020, Tulln – Austria.

2019

RABEFIRAISANA, H.J., GHANIM, A.M.A., ANDRIANJAKA, A., ALI, A., RASOAMAMPIONONA, B., JANKULOSKI, L., INGELBRECHT, I., RAKOTOARISOA, N.V. (2019). Assessing the Reaction of Advanced *Striga asiatica*-resistant Mutants (M₅) of Rice (*Oryza sativa*) to Infestation of *Striga hermonthica*. WCPPP June 2019, Amsterdam, the Netherlands.

News Highlights

- Nuclear Techniques Help Bangladeshi Experts Develop Improved Cotton Varieties in Record Time **(23 November 2021)**
[Bangladesh Develops Improved Cotton in Record Time | IAEA](#)
- Nuclear Science Helps to Adapt to Climate Change, COP26 Participants Hear **(6 November 2021)**
[Nuclear Science Helps to Adapt to Climate Change: COP26 | IAEA](#)
- Director General of Nuklear Malaysia: Committed to Nuclear Science and Helping Others **(20 October 2021)**
[Director General of Nuklear Malaysia: Committed to Nuclear Science and Helping Others | IAEA](#)
- New CRP: Radiation-induced Crop Diversity and Genetic Associations for Accelerating Variety Development (D24015) **(14 October 2021)**
[New CRP: Radiation-induced crop diversity and genetic associations for accelerating variety development \(D24015\) \(iaea.org\)](#)
- Ahead of COP26, IAEA Issues Report on the Role of Nuclear Science and Technology in Climate Change Adaptation **(14 October 2021)**
[Ahead of COP26, IAEA Issues Report on the Role of Nuclear Science and Technology in Climate Change Adaptation | IAEA](#)
- Global Success in Plant Breeding Celebrated with New achievement Awards **(20 September 2021)**
[Achievement Awards Celebrate Global Plant Breeding Success | IAEA](#)
- New Crop Varieties Improve Tomato and Soybean Yields in Cuba **(24 August 2021)**
[Crop Varieties Improve Tomato and Soybean Yields in Cuba | IAEA](#)
- How Do Nuclear Techniques Contribute to Measuring and Adapting to Climate Change? **(5 August 2021)**
[How Do Nuclear Techniques Contribute to Measuring and Adapting to Climate Change? \(iaea.org\)](#)
- Boosting Tea Plant Diversity, Quality and Resilience in Sri Lanka **(16 June 2021)**
[Boosting Tea Plant Diversity, Quality and Resilience in Sri Lanka | IAEA](#)
- IAEA Helps Countries Halt Ecosystems Degradation **(4 June 2021)**
[IAEA Helps Countries Halt Ecosystems Degradation | IAEA](#)
- Nuclear Techniques Help to Revive Ginger Production in Jamaica **(11 May 2021)**
[Nuclear Techniques Help to Revive Ginger Production in Jamaica | IAEA](#)
- Call for Nominations: Recognizing Excellence in Plant Mutation Breeding and Associated Biotechnologies **(15 March 2021)**
[Recognizing Excellence in Plant Mutation Breeding | IAEA](#)
- Cotton in Pakistan: How Nuclear Techniques are Helping the Textile Industry **(22 January 2021)**
[Nuclear Techniques and the Textile Industry | IAEA](#)
- Improved Soil and Nutrient Management Practices Increase Rice Yields in Lao PDR **(20 January 2021)**
[Improved Soil and Nutrient Management Practices Increase Rice Yields in Lao PDR | IAEA](#)
- Climate Change and Coffee: Combatting Coffee Rust through Nuclear Techniques **(21 December 2020)**
[Climate Change and Coffee: Combatting Coffee Rust | IAEA](#)

- New CRP: Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops (D24014) **(16 December 2020)**
[Development of Integrated Techniques for Induced Genetic Diversity and Improvement of Vegetatively Propagated and Horticultural Tree Crops \(D24014\)](https://www.iaea.org/newscenter/news/new-iaea-publications-highlight-technical-cooperation-achievements-in-asia-and-the-pacific)
- New IAEA Publications Highlight Technical Cooperation Achievements in Asia and the Pacific **(2 December 2020)**
<https://www.iaea.org/newscenter/news/new-iaea-publications-highlight-technical-cooperation-achievements-in-asia-and-the-pacific>
- World Food Day 2020: IAEA & FAO's Joint Work Benefits Farmers and Increases Food Security Worldwide **(16 October 2020)**
<https://www.iaea.org/newscenter/news/world-food-day-2020-iaea-faos-joint-work-benefits-farmers-and-increases-food-security-worldwide>
- Homegrown Soybeans are Making a Comeback in Indonesia Thanks to New Varieties Developed Using Irradiation **(5 October 2020)**
<https://www.iaea.org/newscenter/news/homegrown-soybeans-are-making-a-comeback-in-indonesia-thanks-to-new-varieties-developed-using-irradiation>
- Asian Cooperative Agreement Convenes 49th Annual Meeting to Discuss Regional Priorities, Challenges and Solutions **(23 September 2020)**
<https://www.iaea.org/newscenter/news/asian-cooperative-agreement-convenes-49th-annual-meeting-to-discuss-regional-priorities-challenges-and-solutions>
- Double the Yield, Double the Harvest: Zanzibar Improves Rice Production Using Nuclear Techniques **(7 August 2020)**
<https://www.iaea.org/newscenter/multimedia/photoessays/double-the-yield-double-the-harvest-zanzibar-improves-rice-production-using-nuclear-techniques>
- Tastier and More Nutritious Vegetables: Bulgaria Improves Food Quality with IAEA Support **(27 July 2020)**
<https://www.iaea.org/newscenter/news/tastier-and-more-nutritious-vegetables-bulgaria-improves-food-quality-with-iaea-support>
- Nuclear Technology Helps to Develop Heat-Tolerant Tomato Varieties in Mauritius **(15 July 2020)**
<https://www.iaea.org/newscenter/news/nuclear-technology-helps-to-develop-heat-tolerant-tomato-varieties-in-mauritius>
- World Environment Day 2020: How the IAEA Contributes to Soil, Plant and Animal Biodiversity **(4 June 2020)**
<https://www.iaea.org/newscenter/news/world-environment-day-2020-how-the-iaea-contributes-to-soil-plant-and-animal-biodiversity>
- Drought Tolerant Crops: Zambia, IAEA and FAO Help Zambia Improve Production and Farmers' Income **(1 June 2020)**
<https://www.iaea.org/newscenter/news/drought-tolerant-crops-zambia-iaea-and-fao-help-zambia-improve-production-and-farmers-income>
- Malaysia's Nuclear Agency and Partners Bring Improved Rice Variety to Country's Farmers **(6 April 2020)**
<https://www.iaea.org/newscenter/news/malysias-nuclear-agency-and-partners-bring-improved-rice-variety-to-countrys-farmers>
- IAEA and FAO Help Zanzibar Grow More Rice **(12 March 2020)**
<https://www.iaea.org/newscenter/news/iaea-and-fao-help-zanzibar-grow-more-rice>
- Fighting Two Major Cassava Diseases in Burundi with Nuclear Technology **(18 February 2020)**
<https://www.iaea.org/newscenter/news/fighting-two-major-cassava-diseases-in-burundi-with-nuclear-technology>



Awards in Plant Mutation Breeding and Associated Biotechnologies

Vienna, 20 September 2021

AWARDS 2021
PLANT MUTATION BREEDING

Outstanding Achievement

BANGLADESH

Bangladesh Institute of Nuclear Agriculture



The Bangladesh Institute of Nuclear Agriculture (BINA) has been pursuing research in crop improvement through induced mutations for several decades. The institute has developed 37 mutant varieties across 15 different crops using induced mutations. Within just the last decade, BINA has released nine mutant rice varieties developed through ^{60}Co gamma ray and carbon ion beam irradiation techniques. These mutant varieties are popular, widely being cultivated and playing a significant role in Bangladesh agriculture ensuring food security and increasing cropping intensity.

'Binadhan-14' was developed using carbon ion beam from a rice landrace and offers late transplanting potential for irrigated rice. It is a high yielding (6.0 t/ha), short duration (120–130 days), and high-temperature tolerant ($\sim 36^\circ\text{C}$) variety. Due to its special features, farmers can accommodate an extra crop like mustard, lentil, and other vegetables in between rainfed and irrigated rice which facilitates increase of cropping intensity. Two upland rice varieties 'Binadhan-19' and 'Binadhan-21' which were developed from NERICA (New Rice for Africa) cultivar using gamma ray irradiation are suitable for cultivation in rainfed and drought conditions. 'Binadhan-20' is a biofortified rice variety containing 27.5 ppm zinc and 25–31 ppm iron and can supplement zinc and iron for children, and pregnant and lactating women. During the last 10 years, BINA has also developed 11 mutant varieties of pulses including mungbean, chickpea and lentil which are early maturing, high yielding and tolerant to different biotic and abiotic stresses. In Bangladesh pulses are sometimes referred to as poor man's meat. The mungbean varieties 'Binamoog-8', 'Binamoog-9' and 'Binamoog-10' are providing a significant content of protein, iron, and zinc to the daily diet of Bangladeshi people. These varieties are vastly used in the confectionery industries. Cultivating these varieties comes with additional benefits such as self-employment, value addition, income generation, and family care especially for women. The chickpea mutant varieties 'Binasola-7', 'Binasola-9' and 'Binasola-10' are providing a significant amount of protein, fat, essential

amino acids, and a good source of vitamin B to diets in the country. These chickpea varieties have already become an important crop for rural households for both cash income and consumption. Being a rich source of vegetable protein, the lentil mutant varieties 'Binamasur-5', 'Binamasur-6', 'Binamasur-8', 'Binamasur-9', and 'Binamasur-11' contain higher amount of nutrition which helps to improve malnourished people in Bangladesh. Pulse mutant varieties can be grown in residual soil moisture. Among the oilseed crops, BINA has released five groundnut, four mustard, three sesame, and two soybean mutant varieties in the last decade. The groundnut varieties are early maturing, salt tolerant (6–8 dS/m) and high yielding. The mustard varieties are tolerant to some biotic stresses and play an important role in edible oil production in Bangladesh. The sesame and soybean varieties are vastly used in the confectionery and feed processing industries, respectively. Among the spices, BINA developed three mutant varieties of onion and chilli. These varieties are playing a vital role in the country's agriculture by increasing cropping intensity, diversifying the cropping system, increasing the total crop production, nutritional values and also improving the socio-economic conditions of farmers. Thus, BINA crop mutant varieties ensure nutritional food security and are expected to contribute towards fulfilling targets of the SDG by 2030.



Rice experimental fields at BINA.



Early (short duration) rice mutant line in field trials.

CHINA

Wheat Mutation Breeding Team

Institute of Crop Sciences, Chinese Academy of Agricultural Sciences



The Wheat Mutation Breeding Team, from the National Center of Space Mutagenesis for Crop Improvement, Chinese Academy of Agricultural Sciences (CAAS), led by Prof Luxiang Liu, in collaboration with the Joint FAO/IAEA Centre of Nuclear Techniques in Food and Agriculture, has been working on mutation breeding for crop improvement since 1989.

During the last decade, the team has coordinated 18 programmes /projects in China including National Key Research and Development Programmes and seven RCA/TC/CRP projects with the IAEA. Team members have established and optimized technologies and methodologies on mutation induction as well as high-throughput mutant screening and have developed elite mutant germplasm pools in wheat. Using the mutants as parents, they have developed and officially released eight mutant wheat (*Triticum aestivum* L.) varieties within 10 years.

These varieties are adaptable to different wheat cultivation regions in China and have benefited thousands of farmers. The variety, 'Hangmai 247', was released nationally in 2016 at the Northern Winter Wheat Region of China. It is a high yielding, semi-dwarf variety with enhanced tolerance against lodging, drought, and the main diseases across the region. This variety also shows less symptoms against crown rot disease, which has been a recent disease spreading in wheat. It has a yield advantage of 2.4% (3.65 t/ha) in the farmers field without any irrigation over the local variety. The water use efficiency of 'Hangmai 247' is 1.77 kg per m³, which would save about 900 m³ per hectare of water applied for the cultivation of non-drought tolerant wheat varieties.

The variety, 'Luyuan 502', with high-yield-potential and enhanced adaptability and lodging resistance was released nationally in 2011 at the Yellow-Huai River Valley Winter Wheat Region of China. Its average grain yield is 8.2 t/ha with a reported maximum yield of 12.2 t/ha, resulting from more grain numbers per spike and higher thousand-grain-weight. Its cultivation has removed the lodging impediments in wheat production when yield is contributed

by heavier spikes. The variety has been cultivated on more than 5.54 million hectares in China, which has very significant social-economic impacts and benefits thousands of farmers.

The National Center of Space Mutagenesis for Crop Improvement laboratory has been authorized as one of the IAEA Collaborating Centres for Nuclear Techniques in Plant Mutation Breeding since 2019. Under the support of IAEA/RCA projects, the team has established the Asia and Oceania Association of Plant Mutagenesis (AOAPM). Several outstanding scientists and their teams from Member States in the region have participated in the association to promote the development of plant mutation breeding. The team has hosted two technical meetings, four training courses, six scientific visits and two fellows as part of the IAEA Technical Cooperation Projects, with technical support from the Joint FAO/IAEA Centre. The team chief, Prof Luxiang Liu has been a Programme Advisory Committee (PAC) member of IAEA since 2017. In the past 10 years, he has coordinated three RCA projects, RAS5045, RAS5056 and RAS5077, as the Lead Country Coordinator.

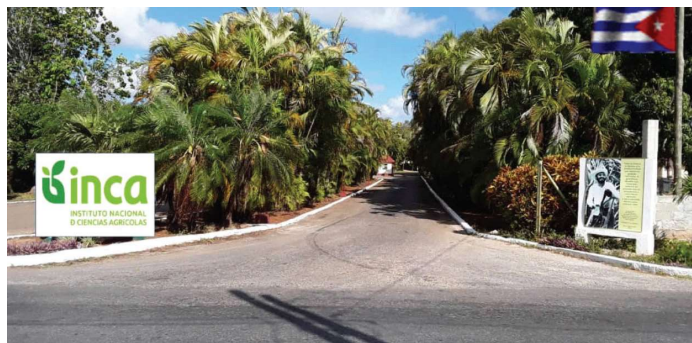


Wheat mutant variety, 'Luyuan 502'.



CAAS-IAEA Collaborating Center.

CUBA
Nuclear Techniques Applied Group
National Institute of Agricultural Science



The Nuclear Techniques Applied at the Genetics and Improvement Department of the National Institute of Agricultural Science (INCA) has been working for the last 33 years on Mutation Breeding Programmes in different crops (rice, tomato, soybean, common bean, *Hibiscus sabdariffa* L. and sesame) in order to obtain new tolerant varieties to abiotic stresses (salinity, drought, high temperature).

The team's effort has led to the registration of three tomato mutants, three mutants of rice and three mutants of roselle (*Hibiscus sabdariffa*), an emergent crop of nutritious and medicinal importance. The mutant varieties of rice are now cultivated in 35% of the national rice area and the mutants of roselle cover 88% of the total cultivated area under this crop.

The drought tolerant tomato mutant, 'Domi', and three varieties of roselle (*Hibiscus sabdariffa*) 'Ana Delia', 'Dogo' and 'Benito', have been released within the last ten years.

Most recently, two new mutant varieties, one in tomato and one in soybean, have been approved as commercial varieties. The tomato mutant variety, 'Giron 50', has high demand as it shows very good performance in farmers' fields. The soybean mutant variety, 'Cuvin-22', is a black-seeded variety. Although these varieties do not yet have the registration certificate due to the pandemic situation in Cuba, they have already been endorsed for cultivation.

'Roselle' has not been a well-known species in Cuba until the research of the group which resulted in the development of new mutant varieties. The group also carried out wide diffusion efforts through workshops, field days, television programmes and two symposia. Currently, there is great demand for its utilization in the production of wines, sodas, tea and medicines. It has been introduced in 24 production areas of seven provinces of the country as well as in Guadalupe and Paraguay. All the varieties of 'Roselle' in Cuba are mutants. These include 'Ana Delia' (released in 2012), 'Dogo' (released in 2013), and 'Benito' (released in 2013).

The soybean mutant varieties developed by the team has significant demand for animal feeding purposes in two provinces in Cuba. The tomato mutant varieties 'Domi' (released in 2015), and 'Giron 50' (approved for cultivation in 2021) are double-purpose varieties with very good quality and high productive potential. These are grown across five provinces in Cuba.



'Ana Delia', a mutant variety of *Hibiscus sabdariffa* developed at INCA.



Tomato mutant variety, 'Giron 50', approved for commercial cultivation in 2021.

INDIA

Mutation Breeding Team

Bhabha Atomic Research Centre



Under the peaceful applications of atomic energy, the Bhabha Atomic Research Centre (BARC), Mumbai, India, initiated mutation breeding for genetic improvement of crops more than six decades ago. Presently, the BARC is focusing on major cereals, pulses, and oilseeds of importance to the country including rice, wheat, sorghum, groundnut, mustard, soybean, sunflower, linseed, pigeonpea, mungbean, blackgram, chickpea and cowpea.

The primary objectives have been to develop high yielding varieties with early maturity, large seed size, tolerance to biotic and abiotic stresses, high oil (oilseed crops) and protein (pulses) contents, and improved seed quality traits. Sustained research involving mutation and conventional breeding has resulted in the release of 49 crop varieties including rice (5), groundnut (15), mustard (4), soybean (2), sunflower (1), linseed (1), mungbean (8), blackgram (5), pigeonpea (5), cowpea (2) and jute (1). In the last decade alone, 11 varieties (direct mutants, inter-mutant, or cultivar-mutant derivatives) have been released for commercial cultivation by the Government of India.

The most prominent contribution by BARC has been in the development of early maturing, confectionery grade, large-seeded (100-seed weight >60g), export and consumption-oriented groundnut varieties ('TG 39' 'TPG-41', 'TLG-45' and 'RARS-T-1'). The large-seeded groundnut mutant variety 'RARS-T-1' ('TG-47') is increasingly being adopted for value addition. More than 1600 tons of breeders' seeds have been supplied to various seed agencies since 2010 for distribution of quality seeds of BARC varieties to farmers. The high yielding ability of Trombay groundnut (TG) varieties can be perceived from the record harvest of various farmers (as high as 10 t/ha and earning a net profit up to US \$2000 per hectare) and the consequent enhancement of groundnut productivities in core states, apart from the benefits reaped by traders and exporters. The recently released linseed variety 'TL-99' with its unique fatty acid composition (very low linolenic acid) has already made inroads covering more than 100 ha within a year and could be a potential alternative for edible oil.

The black gram variety 'TU-40' that is resistant to the yellow mosaic disease (YMD) has uplifted the socio-economic status of farmers by enabling them to cultivate rice-fallow areas thus gaining 'additional income up to US \$350 per hectare. The early maturing pigeonpea varieties 'TT-401' and 'TJT-501' have been important to farmers in Madhya Pradesh as they escape damage from terminal fog, while the medium duration mutant variety 'PKV-TARA' is a reprieve to farmers in Maharashtra from prolonged monsoon. These varieties garner annually about 11% of the national breeder seed indent (peaked 23% during 2017–2018).

To meet the burgeoning demand of 'TJT-501' that occupies nearly 60% of pigeonpea area in Madhya Pradesh, 117 tons of breeder seeds were produced (2015–2018). As estimated, these varieties were cultivated by two million farmers in over 2.5 million hectares with cumulative production of 4.35 million tons (2013–2020). The on-farm income of farmers has increased up to US \$600 per hectare. The four rice mutant varieties ('TCDM-1', 'Vikram-TCR', 'CGJT' and 'TKR-Kolam') with semi-dwarf characteristic and tolerance to lodging have offset the economic losses due to cultivation of traditional lodging susceptible and tall parent varieties in the States of Chhattisgarh and Maharashtra. The mustard mutant variety 'TBM204' has opened avenues to increase production by capturing non-conventional areas in West Bengal. The BARC has thus made outstanding contributions in developing and deploying mutant varieties with significant societal impacts across India.



Breeder seed multiplication of Trombay groundnut variety 'TG 38' in Karnataka, India.



Cluster demonstration of Trombay mutant pigeonpea variety 'TJT-501'.

INDONESIA

Plant Breeding Group, Agriculture Division
Centre for Isotopes and Radiation Application,
National Nuclear Energy Agency



Plant mutation breeding plays a very important role in varietal improvement of food crops and has contributed to significant increases in food production and has maintained self-sufficiency of food in Indonesia. Research on plant mutation breeding is mainly conducted at the Center for Isotopes and Radiation Application (CIRA) under the National Nuclear Energy Agency of Indonesia (BATAN).

The available infrastructure and facilities include the office building, gamma irradiators, laboratories for plant breeding, tissue culture and biotechnology, storage room for mutant seed germplasm, greenhouse and mutant nursery facilities, experimental field, processing unit and other supporting equipment.

In addition, the manpower capability working on mutation breeding makes it possible for Indonesia to release more and more superior crop mutant varieties with improved desirable traits. BATAN has also been recognized as an IAEA Collaborating Centre for Plant Mutation Breeding since 2017, meaning that Indonesia participates and helps other countries improve their capability of doing effective research on mutation breeding to support food security. Indonesia has been very closely collaborating with the IAEA in handling many mutation breeding activities including research, conducting scientific visits, hosting training courses and workshops, and providing experts to some recipient countries in the Asia-Pacific and Africa regions.

During the 10-year period from 2010 until present, BATAN, Indonesia has released many mutant varieties of important food crops including rice (18), soybean (9), sorghum (3), mung bean (1), groundnut (1) and banana (1). All these mutant varieties have been grown and developed further by stakeholders including farmers throughout Indonesia. In rice, for example, average growing areas of mutant varieties are recorded at 3 892 250 hectares (3.53% of the total rice growing area in Indonesia), contributing to 4.72% of the total rice production in Indonesia. Among the rice mutant varieties, Sidenuk is the most popular variety grown by farmers. In the case of soybean, mutant varieties

contribute to 15.54% of the total soybean production in Indonesia.

This has reduced the import of soybean by about 7%. In addition to supporting food security in Indonesia, sorghum mutant varieties have also been developed and released, and are now showing significant potential for increasing Indonesia's food security, improving farmer incomes, and supporting more sustainable agriculture practices.

In conducting research and development in plant mutation breeding, BATAN collaborates with both national and international partners. National partners include the Ministry of Agriculture, universities and research institutions and private companies. International partners include the Joint FAO/IAEA Centre, Forum for Nuclear Cooperation in Asia (FNCA), the Japan Society for the Promotion of Science (JSPS) and the Asia-Pacific Economic Cooperation (APEC). In collaboration with the Joint FAO/IAEA Centre, BATAN has been involved in many projects including Coordinated Research Projects (CRP-16947, CRP-20416, CRP-22433 and CRP-23032), National Technical Cooperation Projects (INS5030, INS5039), and Regional Technical Cooperation Projects (RAS5040, RS5045, RAS5056, RAS5070, RAS5073 and RAS5077).



Rice mutant evaluation in the nursery at CIRA, BATAN.



Maintenance of soybean mutants at CIRA, BATAN.

IRAN

Plant Breeding Department

Nuclear Agricultural Research School, Nuclear Science and Technology Institute



Crop improvement using induced mutation with gamma ray started in 1986 at the Nuclear Agriculture Research School in Iran. The plant breeding group at the institute has laboratories in tissue culture, genetics, and plant physiology.

These labs have helped in the detection and selection of mutant genotypes. Seed or other plant material from a variety of food crops including rice, wheat, barley, canola, beans, cotton, tangerine, pomegranate, apricots, and bananas, and of ornamental plants including roses, pothos, anthurium, etc. were subjected to induced genetic variation by gamma ray.

Plant materials were irradiated at the gamma cell of the Nuclear Agricultural Research School. Mutants in these plants were selected for traits of interest, and several significantly improved mutants have been released as mutant cultivars. Dwarf wheat mutants, salinity-tolerant, and drought-tolerant mutant lines in wheat, barley, and rice currently have advanced promising lines. In addition, banana mutants resistant to the disease Fusarium wilt TR4, bean mutant lines with different seed color, pomegranate with frost tolerance and apricot with late spring frost tolerance are in the pipeline for registration as new varieties in the coming years.

Since 2009, eight new and improved mutant varieties in five different crop species have been officially released and provided to farmers for cultivation. These include two new rice varieties, namely, 'Roshan' and 'Shahriyar', both released in 2014. Specific characteristics include dwarfism

and earliness, with earlier maturity of 25 days and 15 days, respectively, for the two. In cotton, two improved varieties, namely, 'Parto' and 'Tavan', were released in 2019. 'Parto' is a variety suitable for hot and dry areas and has an average yield of 3400 kg/ha and a maturity of 135 to 140 days. 'Tavan' has the same maturity range and an average yield of 3600 kg/ha. It is a variety suitable for temperate regions.

Both 'Tavan' and 'Parto' are resistant to salinity in the soil and water (8–12 ds/m). These cultivars are derived by gamma irradiation of existing Iranian cultivars. A gamma ray dose of 215 Gy was used in these mutation breeding programmes. The last decade also saw the development and release of two tangerine varieties, 'Zarrin' and 'Narin', that were introduced for cultivation in 2019. 'Zarrin' is a variety suitable for the temperate regions in northern Iran and has large fruits. 'Narin' is suitable for the southern regions and also has larger sized fruit.

The Institute has released one soybean variety during the last decade, namely, 'Kowsar', that was introduced for cultivation in 2015. The maturity of this cultivar is 15 days earlier than existing varieties. It is resistant to Phytophthora and is suitable for cold climates. Most recently, in 2020, a rapeseed variety, 'Roshna', was released with high productivity (400 kg more than the parental variety) lodging resistance, and tolerance to salinity stress in the range of EC 6–8 ds/m. It also has 28.6% higher oil yield.



Planted M₂ rice generation of rice.

MALAYSIA

Malaysian Nuclear Agency



The Malaysian Nuclear Agency (Nuklear Malaysia) is the leading research institute for plant mutation breeding in Malaysia where both acute and chronic gamma rays are used to induce mutations for crop improvement. At present, more than 35 new plant varieties have been successfully developed by Nuklear Malaysia. The projects in mutation breeding were formulated to address the national agenda and policy to generate new crop varieties that will lead to national self-sufficiency in staple foods, and subsequently help increase livelihoods and well-being of farmers. In addition to developing new and improved mutant crop varieties, Nuklear Malaysia has also established various research facilities to support mutation breeding activities including an acute gamma irradiation facility, the Gamma Greenhouse, screening glasshouses, molecular biology lab, plant physiology lab, stable isotope lab and others. In 2019, the Gamma Greenhouse was designated as an IAEA Collaborating Centre for research, training and development in plant mutation breeding using chronic gamma irradiation.

One of the recent most important achievements is the commercialization of new mutant rice varieties. These mutants were successfully granted with Certificate of Registration of New Plant Variety and Grant of Breeder's Right by the Department of Agriculture Malaysia in February 2020 with registration numbers PBR 0156 (for 'NMR 152') and PBR 0159 (for 'NMR 151'). In addition, the 'NMR 152' mutant was certified as a new national rice variety by the Ministry of Agriculture and Food Industries, Malaysia (MAFI).

These rice mutants have consistently recorded yield between 7–11 t/ha depending on the planting region and field management, a value that is significantly higher than the national average yield of 4.2 t/ha. In 2019, Nuklear Malaysia successfully signed a Memorandum of Understanding (MoU) with two authorized seed producers. This collaboration has added more value to the seeds of 'NMR 151', 'NMR 152' mutant varieties, and other advanced mutant lines, ultimately resulting in more improved varieties available in the market. Due to the consistency in producing high yield, in 2021 the planting of mutant rice variety 'NMR 152' was expanded to various

regions in Malaysia covering approximately 24 600 hectares of paddy fields in peninsular Malaysia. In recent years, farmers, private growers, and the general public in Malaysia have become more receptive to new varieties generated through mutation breeding and of the technology itself. Since 2016, about 20 000 rice farmers have planted mutant rice varieties developed by Nuklear Malaysia.

Nuklear Malaysia also received requests from several other agencies for new strategic collaborations to improve various crops such as rice, banana, pineapples, sweet potato, kenaf, taro, vanilla, fodder grass, sago, and ornamentals (orchid, chrysanthemum, canna, hibiscus, etc). In 2017, 22 potential growers from the Sabah rural areas were trained to produce chrysanthemum and orchid mutants commercially. At present, Nuklear Malaysia also collaborates with a private company for field evaluation of pineapple and stevia mutant lines, and with the National Kenaf and Tobacco Board for improvement of kenaf.



Sorghum in gamma greenhouse.



Aerial view of the gamma greenhouse.

MALI

Mr Fousseyni Cisse
Institut d'Economie Rurale



Mr Fousseyni Cisse is an employee of Institut d'Economie Rurale (IER) which is a financially autonomous public scientific, technical, and cultural establishment with a mandate to conduct agricultural research in order to ensure food security and biodiversity in Mali. The IER has 17 research programmes (millet, sorghum, lowland rice, irrigated rice, maize, cowpea, groundnut, cotton, fruit and vegetables, cattle, small ruminants, poultry, forest resources, fishery resources, natural resource production and management systems, supply chain economics, and agricultural machinery) at six Regional Agricultural Research Centres (CRRAs), with regional scientific portfolios depending on local potentials.

Mr Cisse has been actively involved in rice research for the past 30 years and has conducted research across the entire rice value chain and is therefore highly knowledgeable in the field of rice research and development. His research on rice has been focusing on improving the wild relatives of domesticated rice such as *Oryza glaberrima* and *Oryza longistaminata* which are endemic to Sub-Saharan Africa (SSA) for special traits such as high yield potential, tolerance to major pests and diseases, climate adaptability and, quality traits including taste and acceptable grain colour.

Since 1988, Mr Cisse and his team have been using mutation induction techniques with the support from IAEA through a Coordinated Research Project (CRP) to improve some traits in African rice (*O. glaberrima*) and wild rice (*O. longistaminata*) leading to the release and dissemination of mutant varieties such as 'MUT93-2-2-1-4', 'SIK350-A 150' and 'SIK353-A 10' which have high yield potential, are non-lodging and have tolerance to grain shattering.

Mr Cisse has also developed and released several new mutant varieties including 'DKA-M7' and 'DKA-M8' (which is currently under field demonstration for its wide adoption under rainfed lowland and deep-water ecologies). The most appealing points for these varieties are their improved grain quality (from red caryopsis to white caryopses). Both mutants are best suited for flood-prone and submerged environments and have an average yield of 5–6 t/ha. Research is currently underway to confirm if the mutants developed since 2019 have the potential to be used as a source for bidirectional hybrids (Environment-sensitive genic male sterility (EGMS) in hybrid rice production). In addition, he has continued to develop several other mutant populations which are in different stages, including ninety-nine upland M₄ lines and two M₂ populations from *O. longistaminata*, which are in the pipeline for release and targeting diverse traits of importance across all the rice growing environments.



Rice field experiments at Longorola station, Mali.



Mutant rice under evaluation in the field.

PAKISTAN

Nuclear Institute for Agriculture and Biology
Pakistan Atomic Energy Commission



The Nuclear Institute for Agriculture and Biology (NIAB) has a long track record in the successful use of nuclear technologies for crop improvement. NIAB is widely recognized as a premier institute at the national and international levels for introducing new crop varieties and technologies in the agriculture sector since 1972. Since the 1970's, the Joint FAO/IAEA Centre has been collaborating and supporting NIAB scientists by providing technology packages and equipment for mutation breeding, and organizing staff trainings through fellowships, national and regional training courses.

The food security of an ever-increasing population is an important focus for the country. Therefore, NIAB has a special focus on related research disciplines, especially, plant breeding and genetics.

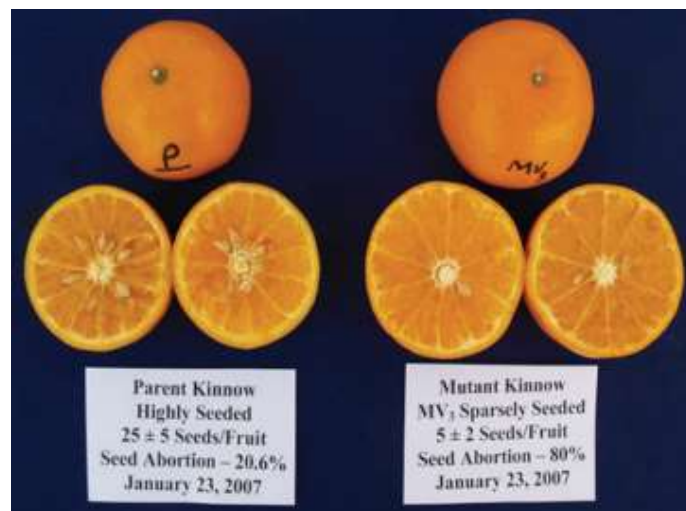
The research endeavours of Plant Breeding and Genetics Division have so far culminated in the release of a total of 52 crop varieties, including cotton (17), rice (5), chickpea (7), mung bean (14), tomato (2), lentil (3), sesame (2), citrus (1) and castor (1). Out of these, 24 varieties (cotton (8), rice (3), chickpea (2), mung bean (4), tomato (2), sesame (2), lentil (1), citrus (1), and castor (1)) were released during the last decade, between 2010 and 2020. These varieties have been developed using induced mutations and related breeding approaches. They are high yielding and possess different traits of economic importance and acceptability to the farmer community in the country.

Cotton mutant varieties from NIAB cover a significant area in Pakistan. The variety 'NIAB KIRAN' covers about 65% of the cotton area in the Sindh province, and 'NIAB-878/B'

covers about 40% of the cotton area in the Punjab province. The mung bean varieties, 'MUNG 2011' and 'NIAB MUNG 2016', released in 2011 and 2016, respectively, are popular among farmers and have seen peak annual area of about 90 000 hectares. Of the total sesame area in Pakistan, the mutant varieties 'NIAB Pearl' and 'NIAB Sesame' 2016 cover 30% (30 000 hectares) and 20% (20 000 hectares) respectively. 'NIAB Kinnow' released in 2017 is a high yielding citrus mutant variety which has fewer seeds and a yield of 31.2 t/ha. Further, the castor mutant variety, 'NIAB Gold', is noted for its high oil content and early maturity and is one of the most popular castor varieties in Pakistan covering 80% of the cultivated area under the crop.



Rice experimental fields at NIAB.



Improved mutant citrus from NIAB.

PAKISTAN

Cotton Mutation Breeding Team
Pakistan Atomic Energy Commission

The Cotton Mutation Breeding Team (Mr Manzoor Hussain, Mr Muhammad Kashif, Riaz Khan, Mr Sajjad Haidar, Mr Hafiz Mumtaz, Hassan, Mr Allah Ditta) at the Nuclear Institute for Agriculture and Biology (NIAB) has cogent R&D and teaching experience in the field of mutation breeding coupled with molecular genetics and genomics in cotton. They have made tremendous contributions in innovation of nine high yielding cotton varieties during the period of 2010 to 2020. These evolved varieties not only sustained the productivity of cotton crop under the changing climate scenario of Pakistan but also upheld the profitability of cotton growers.

The first virus-tolerant coupled with longer and fine fibre variety 'NIAB-111' evolved in 2004, covered an area of 304 728 hectares in Punjab province since its inception in 2014–2015 with an impact of billion rupees on country's economy. The recently evolved cotton varieties i.e., 'NIAB-878/B' (2017), 'NIAB KIRAN' (2013 and 2016), 'NIAB-545' (2018), and 'NIAB-1048' (2018) has demonstrated their excellent ability to 'unlock yield potential under prevailing climate change' of Pakistan with contribution of more than 50% share in seed production system and same proportionate of area covered in Punjab (2018–2019 and 2019–2020) with billions of rupees impact on country's economy.

'NIAB KIRAN' covered about 67% area against NON-GMO varieties in Sindh during 2017–2018 and proved to be the best cotton variety in Baluchistan province (2019–2020) for organic cotton production. In addition to the above, the cotton group remained involved in the evaluation and maintenance of internationally recognized and revolutionary cotton variety 'NIAB-78', that covered more than 80% area in Pakistan. The impact of mutant background varieties of Pakistan can be envisaged from IAEA success stories.



Seed multiplication of cotton mutant variety 'NIAB KIRAN'.



Seed multiplication of cotton mutant variety 'NIAB-878/B'.

SOUTH AFRICA

Mutation Breeding Team

Council for Scientific and Industrial Research



The Mutation Breeding Team at the Council for Scientific and Industrial Research (CSIR), Pretoria, South Africa, tackles a variety of traits in a variety of crops with mutation breeding and has made significant progress on many of them.

The team consists of the researchers, Mr Luke Mehlo, Ms Zodwa Mbambo, Ms Priscilla Dikiso, Mr Moses Mokoena, Mr Darius Moeletsi, and Mr Oupa Makgetwa. The team not only successfully breeds and releases new mutant varieties, but they also contribute to science through publications in peer-reviewed journals and often take the next step of facilitating industrial uses of their products.

Mutant varieties of sorghum with suppressed storage kafirin proteins in the endosperm were obtained through gamma irradiation. Kafirins are associated with poor nutrition in sorghum. They are deficient in major essential amino acids; they restrict digestion of the proteins when sorghum is cooked, and they also interfere with the availability of other nutrients in diet. Suppression of the kafirins resulted in sorghum with high content of essential amino acids such as lysine, methionine and tryptophan and digestible protein and starch (through changes in surface structure of protein and starch bodies).

Additional support from the Department of Rural Development and Land Reform and the U.S. Agency for International Development (USAID) allowed the new sorghum varieties to be grown and be adopted in three provinces of Gauteng, Limpopo, and Mpumalanga. The villagers recommended that the varieties should not be registered since they would not be able to purchase the seed. Rather, and because they are inbred lines, they continue producing them and distributing seed amongst other farmers at no cost. The varieties will soon be grown also in Mozambique with support from the company, Moza Agro Business.

In sunflower, a purple hull mutant was developed using chemical mutagenesis. The mutant sunflower synthesizes and accumulates health-benefiting colouring anthocyanins

in seed hulls and in petals. An additional value chain to the normal use of the sunflower to produce oil was developed in which a natural colouring dye is manufactured from the normally discarded seed hulls. The colourant can be used as a safe replacement of toxic synthetic dyes in food, beverages, cosmetics, and medical products. Currently a private company called Pharmakine (Pty) Ltd (www.pharmakyne.com) is assisting select community groups to set up a small start-up company that would manufacture the colourant and supply Pharmakine.

The team has also worked on mutagenizing and developing novel strains of mutant microalgae using chemical mutagenesis. The microalgae accumulate elevated levels of omega-6 and omega-3 fatty acids together with many other fatty acids of industrial importance. Current efforts are aimed at using the microalgae as feed for fish and as a feedstock for biodiesel production. Research towards combining the microalgae and industrially reared mealworm insects for commercial feed formulations for Tilapia and Catfish are at advanced stage, the efforts being supported by USAID and the Department of Rural Development and Land Reform.



Mutant sunflower developed by the Mutation Breeding Team at CSIR.



Mutant sorghum in the field.



Joint FAO/IAEA Centre
Nuclear Techniques in Food and Agriculture

Women in Plant Mutation Breeding Award

AWARDS 2021
PLANT MUTATION BREEDING

BANGLADESH

Ms Shamsun Nahar Begum

Bangladesh Institute of Nuclear Agriculture



Ms Shamsun Nahar Begum specializes in plant mutation breeding and has been doing research on mutation breeding since 1994. This was later combined with research in molecular plant breeding, marker-aided selection and plant biotechnology. From the very beginning of her service, Ms Begum has been focusing on varietal improvement of rice, mungbean, chickpea and grasspea through induced mutations.

She has developed 20 varieties of different crops. Among these seven are mutant varieties viz., Rice 'Binadhan-21', Mungbean 'Binamoog-8', 'Binamoog-9', 'Binamoog-10', Chickpea 'Binasola-7', 'Binasola-9', 'Binasola-10' which were developed by Ms Begum during the last ten years (since 2010). Besides this, she has also been working on varietal improvement of pigeon pea and garden pea.

Ms Begum did her PhD research on marker assisted pyramiding of bacterial blight resistance genes in Basmati derived rice lines at the International Rice Research Institute (IRRI), Philippines. Germplasm of rice, mungbean, pigeonpea and gardenpea have been irradiated with ⁶⁰Co or with other mutagens for developing mutant populations. Advanced mutant lines of different crops have been identified using mutation breeding for the development of varieties with tolerance to salinity, drought, submergence; with resistance to diseases and insects; and with fine grain quality, aroma and acceptable yield. She was involved in different International Atomic Energy Agency (IAEA) projects as an Associate Investigator and is a resource person for mutation breeding techniques to the young scientists and staff.

The released upland rice variety, 'Binadhan 21', derived from NERICA (New Rice for Africa) is a short-duration, drought-tolerant and high yielding variety with medium fine grain. It has received wide acceptance among farmers. The mungbean mutant variety, 'Binamoog-8' is a high yielding and high-protein variety with tolerance to *Cercospora* leaf spot and yellow mosaic virus (YMV)

diseases. It has an average yield that is 35–45% higher compared to other existing mungbean varieties in Bangladesh. It covers 32% of the dedicated area currently cultivated under this crop. 'Binamoog-9' and 'Binamoog-10' are short-duration and high yielding varieties, which allow farmers to raise 3–4 crops annually in their fields. These varieties thus play a vital role in Bangladesh agriculture by increasing the cropping intensity. They also facilitate employment of rural poor women farmers in the harvesting of mungbean pods. The chickpea mutant varieties, 'Binasola-7' (high-yield with bright seed coat color), and 'Binasola-9' (kabuli type with cream seed coat colour and tolerant to root rot and grey mould diseases) are widely accepted by farmers. The newly released chickpea variety 'Binasola-10' is a high yielding variety with bolder seed size.

These varieties released by Ms Begum are being widely cultivated in farmers' fields and are contributing to Bangladesh agriculture through higher income for farmers and the improvement of socio-economic conditions.



Field evaluation of rice mutant variety 'Binadhan-21' grown in farmer's field at Nalitabari village of Sherpur district, Bangladesh, during Aus (upland) season, 2019.



Field visit of mungbean mutant variety 'Binamoog-8' grown in farmer's field at Haibatpur village of Natore district, Bangladesh, during summer, 2020.

CHINA

Ms Huijun Guo

Institute of Crop Sciences, Chinese Academy of Agricultural Sciences



Ms Huijun Guo, a wheat mutation breeder, joined the Wheat Mutation Breeding Team of the Institute of Crop Sciences at the Chinese Academy of Agricultural Sciences in 2002. She has been an associate professor since 2012 and the supervisor of master's degree candidates since 2018.

Ms Guo is the Leading Country Coordinator (LCC) of the IAEA/Regional Cooperative Agreement (RCA) project on plant mutation breeding, Associate Editor of the Journal of Nuclear Agricultural Sciences, Council Member of the Chinese Society of Nuclear Agricultural Sciences, and Standing Council Member of the Beijing Nuclear Society.

In the past ten years, she has hosted three national projects and three IAEA projects on plant mutation breeding as a Chief Scientific Investigator (CSI)/LCC /Counterpart (CP). She has established four technologies on mutation induction and high-throughput mutant screening as the main executive and authorized three patents and two software copyrights.

Ms Guo developed a wheat mutant library with broad spectrum traits, officially released seven new mutant wheat varieties in China, and published 45 peer-reviewed scientific research papers. The released mutant wheat varieties are cultivated by farmers in China. New mutagens including heavy ion beams and space simulated environment have been developed and utilized in breeding, thus contributing to the sustainable development of mutation induction. Protocols for heavy ion beam irradiation in wheat and other crops have been established and used to develop wheat mutant resources and for crop improvement. Over 400 services to national and international scientists have been provided to enhance their mutation induction efficiency. Ms Guo was also involved in establishing the TILLING platform in wheat which has been used to discover novel mutant alleles relevant to wheat quality and disease related traits.

Among these, novel mutant alleles of the gene TaAGP.L-B1 resulted in the decrease of grain starch content (Frontiers in Plant Science 2017, 8:1404). Novel mutant alleles of the gene TaSSIVb-D resulted in the reduction of starch granule number per chloroplast (BMC Genomics 2017, 18:358; Genes 2019, 10:307). Alleles of another two homoeologous genes have been discovered and pyramided to develop double and triple mutants of TaSSIVb, which enhanced the elucidation of gene interaction in hexaploid wheat (manuscript in preparation).

These favourable mutant alleles have been utilized in wheat improvement. Meanwhile, the TILLING approach has been transferred to over 150 researchers from other Member States through training courses hosted by the Wheat Mutation Breeding Team.

A wheat mutant library with broad spectrum has been developed by heavy ion beams irradiation as well as other mutagens. The resource contains more than 4000 stable mutant lines with various morphological mutations, e.g., plant architecture, leaf, spike, seed and root morphologies, stress resistance, processing quality, etc. This resource enhanced the genetic diversity of wheat germplasm. The mutants have been used to mine favourable alleles (BMC Genetics 2019, 20:102; PLoS ONE 2019, 14:e0211492), novel mutant genes (Journal of Integrative Agriculture 2020, 19:1721–1730) and to expound the characteristics of mutagens (Journal of Radiation Research 2020, 61 :44–57; Scientific Reports 2017, 7:2731). The seven new mutant wheat varieties that have been developed and officially released as a co-breeder have been cultivated on more than 5.54 million hectares in China. This benefits thousands of farmers with significant socio-economic impacts.



Tillering mutants in wheat.



Mutants with different spike characteristics in wheat.

INDIA

Ms Kavera Biradar

University of Agricultural Sciences



Ms Kavera Biradar has focused on mutation breeding in peanut resulting in the release of three new varieties. Mutation breeding involving two cultivars of peanut ('GPBD-4' and 'TPG-41') with the objective of genetic enhancement for oil quality through induced mutagenesis (200 and 300 Gy gamma rays) resulted in the release of two mutant varieties with improved fatty acid profile and higher yield ('G2-52' and 'Dh 245') for cultivation in the Karnataka State. The mutant 'GM 4-3-12' ('GPBD-4' derivative) was utilized in hybridization programme leading to the development of the variety, 'Dh 256', released for cultivation in the Peninsular Zone V of India. Ms Bi radar's research has led to the isolation of several desirable mutants using gamma ray (200 Gy). Transgressive mutants for 100 seed weight (107), oil content (30), protein content (92) and oil quality (138) were identified for further utilization in the breeding programme. She also succeeded in the molecular characterization of the *ahFAD2B* (oleoyl PC Desaturase) gene by cloning and sequencing. The variety 'G2-52' is a Spanish bunch variety that is the derivative of 'GPBD-4' (200 Gy) and was released for cultivation in the Northern Transitional Zone 8 of Karnataka for Kharif in 2013 [S.O. 2860 (E)].

It has high-yield-potential (3.8 t/ha) with moderate oil quality (55% oleic acid). The variety 'Dh 245' is a high-oleic (>70%) mutant that was identified from GPBD-4 (48-50% oleic acid) (300 Gy) and released as 'Dh 245' variety for the Northern Dry Zone 3 and Northern Transitional Zone 8 of Karnataka for Kharif in 2017 [S.O. 6318 (E)]. It is the first indigenous variety with higher oleate content and increased pod yield (2.8 t/ha). Oil with higher oleate fetch 2–3 times higher price due to improved nutritional profile (lowering blood cholesterol) and shelf life (10 times greater auto-oxidation stability).

The variety, 'Dh 256', is derived from the cross 'R-2001-2' × 'GM-4-3-12' (mutant). It has mid-season drought tolerance and higher yield (3.25 t/ha). The variety has been

released for cultivation in the All-India Peninsular Zone V for Kharif due to its wider adaptability and productivity.

The varieties 'G2-52', 'Dh 245' and 'Dh 256' are resistant to foliar diseases (late leaf spot and rust). The foliage remains green till harvest with higher haulm yield and quality fodder for animals fetching an additional income of Rupees (Rs) 1500 to 2500 per hectare. These varieties have acceptable pod and kernel features along with resistance to disease, which is lacking in the peanut germ plasm. In terms of socio-economic impact, the released varieties have an increase in pod yield by 17.70 to 35.00% with additional net returns of Rs 3100 to 10 200 per hectare over the traditional variety ('TMV 2') with additional economic gain of Rs 1500 to 2 500 per hectare from quality fodder. The variety 'G2 52' has covered an area of 54 000 hectares (2020–21) in three districts of Karnataka. The economic gain by growing 'G2 52' over 'TMV 2' will be to the extent of Rs 1.7 billion to the State. 'Dh 245' with its inherent trait for higher oleate may occupy greater area in the coming years as farmers can fetch 2–3 times higher price over other varieties for their quality produce as already witnessed in high oleate sunflower. 'Dh 256' is released at All India level and the area under this is also expected to increase since it is tolerant to mid-season drought stress. This is especially important as peanut is mainly a rainfed crop in India. In the state of Karnataka seven of thirty districts account for 70% of groundnut area. Greater adoption of the improved variety ('G2-52') from 56 to 81% has been seen in three districts. 'Dh 245' (218 hectares) and 'Dh 256' (1050 hectares) are slowly expanding in area.

The variety, 'G2 52', has replaced the widely cultivated variety 'TMV2' in Karnataka (56–81%). Varietal expansion has been taken up through on farm testing, front line demonstrations and trainings. Availability of quality seeds is accomplished through the Seed Hub of University with farmer participatory approach.



'G2-52': Spanish bunch peanut variety resistant to foliar diseases developed through induced mutagenesis.

JAPAN

Ms Tomoko Abe

RIKEN Nishina Center for Accelerator-Based Science



Ms Tomoko Abe has developed a unique technology to induce mutations using energetic heavy ions at the RI Beam Factory (RIBF). This development was achieved through an efficient synergic link between agricultural science and accelerator physics. At relatively low doses, ion beams induce mutations at a high rate without severely inhibiting growth. The irradiation treatment can be given to various plant materials and quick irradiations lasting between seconds and a few minutes are enough to induce mutation. Heavy ions can produce dense and localized ionization reactions in matter along the ion track with their high linear energy transfer (LET). Ms Abe has concluded that the localized and dense ionization can cause double-strand DNA breaks, which are not easily repaired, resulting in higher mutation rates compared to single-strand breaks with X and gamma rays. She investigated the effect of LET on mutation induction using the model plant *Arabidopsis thaliana*. The most effective LET for mutation induction and lethality was 30 keV/ μm and 290 keV/ μm , respectively. This highly mutation efficient LET for seeds was designated as LETmax. Subsequently, Ms Abe has reported detailed analyses on the molecular nature of DNA alterations induced by heavy-ion irradiation with LET max using morphological mutants. The majority of mutations were small deletions ranging from several to several tens of base pairs which were sufficient to disrupt a single gene.

On the other hand, irradiation with 290 keV/ μm ions showed a different mutation spectrum from that at LETmax. The proportion of small deletions was low, while that of large deletions and rearrangements was high. She proposed a tailor-made mutagenesis. When a user wishes to obtain mutants with null mutations at a high efficiency, irradiation with C-ions should be selected. Among the C-ion irradiation levels, LETmax is effective for breeding because of its very high mutation frequency. The most common mutations are small deletions, suitable for disrupting a single gene. If a user requires mutations with large deletions or chromosomal rearrangements, Ar-ion

irradiation is suitable. It is a promising new mutagen suitable for functional analyses of tandem duplicated genes. Heavy ions with higher LETs, such as Ar and Fe, are more effective for the mutation breeding of microbes.

Ms Abe has collaborated with flower companies and public agricultural experimental stations since 1996 on the potential of practical breeding using heavy ion beams. Three new varieties were generated by irradiated samples in 1998, including verbena 'Temari Coral Pink' which became the first plant registered under the Seed and Seedling Law resulting from ion beam irradiation. She formed an Ion Beam Breeding Consortium for RIBF users in 1999. The consortium, which started with 24 users, now has 180 domestic and 20 overseas users. For example, all the agricultural experimental stations in each prefecture are users, except for two prefectures. There are four accelerator facilities in Japan that use breeding. The Ion Beam Breeding Society was organized in 2004. Mutation breeding by ion-beam irradiation was previously performed mainly for flowers and ornamental plants. Recently, beneficial variants have been developed for various crop species. Over 70 new varieties of plants and microbes have been created by ion-beam irradiation in Japan. The ion beam is thus a highly efficient tool for improving crops through mutation breeding.



Mutant rice under field evaluation during flowering.



Mutant rice under field evaluation during grain filling.

KENYA

Ms Miriam Kinyua

University of Eldoret



Ms Miriam Kinyua has applied mutation breeding techniques and efficiency enhancing technologies since 1995 and has made important achievements in the field. She has released the mutant bread wheat varieties, 'Eldo Mavuno' and 'Eldo Baraka'. 'Eldo Mavuno' is the most preferred variety in Kenya today based on seed enquiries from farmers. 'Eldo Mavuno' resulted from gamma irradiation of the parental variety 'Njoro BW II', and it was released in 2014. The mutant variety shows resistance to the stem rust disease and has a yield of 6–7 t/ha. The mutant variety 'Eldo Baraka' was also released in 2014, from irradiation of the parent, 'Kwale'. It also shows resistance to stem rust and has a yield of 5 t/ha.

Ms Kinyua has supervised more than five MSc and two PhD students where the thesis work focused on the application of mutation techniques to crop improvement. This has led to the selection of three mutant cassava and four mutant potato lines which are presently in their second (and last) season of national performance trials for release to farmers. Seed multiplication is ongoing with farmers. The research of the students also resulted in theses and journal papers that advance the application of mutation techniques to crop improvement.

Ms Kinyua also has been lecturing in the MSc course ABT 841 on mutation breeding for over 10 years and guiding students to apply these techniques at their duty stations. The curriculum for this course was developed within her project with the IAEA.

She has been a consultant to many African countries for mutation breeding projects for more than 10 years and has advised them on research in crop improvement through mutation breeding and biotechnology techniques. Due to her expertise in mutation breeding and efficiency-enhancing techniques, she was involved in writing a paper for nuclear application in agriculture for the African Commission on Nuclear Energy (AFCON) in 2020 and gave an invited presentation at WIN-A (Women in Nuclear in Africa) conference in 2020.



Field evaluation of wheat mutants.



Demonstration of mutation breeding to national trainees.

REPUBLIC OF KOREA

Ms Min Jeong Hong

Korea Atomic Energy Research Institute



Ms Min Jeong Hong is a researcher focused on breeding and basic research in *Triticeae*. She joined the Korea Atomic Energy Research Institute (KAERI) first as a post-doctoral researcher in 2013 and continues as a Senior Researcher since 2016. Her research in mutation breeding has centred on wheat, barley, oat, grasses and *Brachypodium*. She also works on marker development for increased precision and acceleration of breeding. Ms Hong has developed important genetic resources using mutation induction. She continues to analyse mutation mechanisms using genomics and molecular biology techniques. She employs an automatic high-throughput phenotyping platform for the analysis of plant phenotypes and is also involved in the development of new breeding techniques with biotechnology.

Ms Hong has registered one wheat variety, 'Trans', in 2013, and has also applied for registration of two new varieties. These include one soybean variety, 'Cheongmiwon', applied for registration in 2018, and one Lagerstroemia variety, 'Rosy Lovely', applied for registration in 2020. Her work also led to the development of genetic resources in major crops, namely, around 1200 coloured wheat mutant lines, 300 common wheat mutant lines, 250 oat mutant lines and 200 barley mutant lines.

Ms Hong's research also led to the filing of a patent in 2021, specifically on the induction of amount of total fatty acids by FBA 1. Ms Hong has published about 48 original research papers in national and international journals including 21 papers on mutation breeding and 23 papers on basic research about crop breeding. She has given over 70 presentations at international seminars on plant breeding and has been the recipient of awards from the Korean Breeding Society Conference in the years 2017 and 2018, and the Genomic Publication Award in 2019. Ms Hong's most recent research involved the investigation of the effects of acute and chronic gamma irradiation on the cell biology and physiology of rice plants, and the dosage effect of gamma rays at different growth stages of *Arabidopsis thaliana* determined by high-throughput phenotyping.

Ms Hong participated in the regional project of the IAEA, RAS5070, during which she trained in Thailand in 2017. She also participated in the regional IAEA project RAS5077 where the national research emphasis was on the development of elite germ plasm and mutation detection technique in wheat and oat.



Recording observations on mutant wheat lines in the field.

MAURITIUS

Ms Saraye Banumaty

Food and Agricultural Research and Extension Institute



Ms Saraye Banumaty works as Senior Research Scientist at the Food and Agricultural Research and Extension Institute (FAREI) of Mauritius undertaking research on tomato. Tomato, an important cash crop cultivated locally, is highly vulnerable to heat stress. In the quest to find better performing tomato varieties tolerant to heat stress which will contribute to food security and adapt to climate change locally, Ms Saraye initiated a mutation breeding project, funded by the IAEA, on tomato in 2007.

Ms Saraye built up her knowledge and experience in the field of mutation breeding, the use of molecular markers for screening and detection of mutants and data analysis by following several training courses and fellowships. Ms Saraye contributed to the establishment of a fully equipped molecular laboratory at FAREI. She participated in the development and validation of low-cost methods for DNA extraction and quantification which is used for the training of fellows from Member States at the Plant Breeding and Genetics Laboratory (PBGL) of IAEA. Ms Saraye has shown how the low-cost Tilling/Scotilling method on agarose gel could be used successfully for the detection of polymorphisms as compared to LI-COR. This method is very useful especially for countries where LI-COR apparatus is not available due to high investment cost. Screening for heat stress in field is not always practical as temperature, humidity, wind, and sunlight cannot be controlled. A rapid, relatively cheap, and reliable pre-field screening methodology is required to screen large populations. Ms Saraye has developed a protocol for pre-screening of mutant tomato lines for heat stress at seedling stage in a growth chamber under controlled conditions.

This methodology is very useful for small countries like Mauritius where land is limited for screening large populations in the field and investment on sophisticated and costly greenhouses is not always possible.

Ms Saraye was successful in selecting three promising mutant lines, of which two have shown tolerance to heat stress. This was the first time that mutation breeding was used effectively and the first case ever of a successful mutation breeding programme in Mauritius. The three mutant lines were officially released under the names 'Summer King', 'Summer Star' and 'Rising Star' in September 2019. During the launching of the varieties, Ms Saraye presented the desirable characteristics of the mutants and gave seed sample to growers. She emphasized that seed production of these mutants by growers will reduce their cost of inputs.

To ensure seed availability to growers, she initiated a seed multiplication programme at FAREI and provided seed samples to the Seed Multiplication Department of the Ministry of Agro Industry and Food Security. She has arranged for the mutants to be officially registered in the Mutant Variety Database (MVD) of the IAEA. In addition, she requested the support of the processing unit of FAREI to assess the processing potential of these three mutant tomato lines. They were processed into different products such as Ketchup, puree, juice, nectar, jams and sundried.

The additional advantage of these three tomato mutants is that they are rich in lycopene, have uniform intense red colour and require no additive during processing. Thus, the production of tomato using these mutant lines can be a source of raw materials for entrepreneurs who are willing to engage in tomato processing at small scale. Ms Saraye has published several scientific papers, participated in international symposiums, and has also contributed to two articles published on the website of the IAEA.



Evaluation of mutant tomato lines.



Demonstration of mutant tomato at harvest.

NAMIBIA

Ms Lydia Ndinelao Horn

University of Namibia, Multidisciplinary Research Centre



Ms Lydia Ndinelao Horn was the first Namibian woman to lead the project on Plant Induced Mutation Breeding for Crop Improvement to Enhance Productivity in Namibia. Her role started in 2007 when she was appointed as a National Project Counterpart for the Technical Cooperation Project between the Namibian Government under the Ministry of Agriculture and Land Reform and the Joint FAO/IAEA Centre. In 2009, she was awarded a fellowship by the IAEA at the Joint FAO/IAEA Plant Breeding and Genetics Laboratory in Seibersdorf, Austria where she spent six months under intensive training, learning techniques in plant breeding using nuclear technology and biotechnology. She returned to Namibia the same year and used irradiated seed of various important crops of Namibia (*Pennisetum glaucum*, *Sorghum bicolor*, *Vigna unguiculata* and *Vigna subterranea*) to launch a national project on Induced Mutation Breeding. Ms Horn obtained a PhD degree in Plant Breeding from the University of KwaZulu-Natal, South Africa, under the sponsorship of the IAEA, making her the first female and Namibian to obtain this qualification. Her research on crop improvement using induced mutation breeding techniques led to the development of Namibia's first ever mutant germplasms of cowpea, pearl millet and sorghum.

She is the author of various articles on Induced Mutation Breeding in Namibia (especially in cowpea) which are well-documented in international Journals across the globe and can be accessible online. She has also written procedures on how to release varieties. Together with her technical team while at the ministry, various events (farmers' field and information days, regional training courses and participatory variety appraisal) were organized to bring together groups of farmers from different regions and from abroad.

Success stories about Namibia's project in mutation breeding has been documented by the Joint FAO/IAEA

Centre and has attracted much attention in the region. Under her leadership, she made sure her technical support staff got training and exposure through the IAEA-supported training and fellowships outside and within the country. She has been appointed to the high-level Steering Committee for Human Resource Development and Nuclear Resource Management (HLSC) of the African Regional Cooperative Agreement for Research, Development and Training to Nuclear Science and Technology (AFRA) 2018–2021. Ms Horn is continuing with her research on crop improvement at the University of Namibia where she also continues to influence young scientists and researchers to take up the field of induced mutation breeding techniques for crop improvement as a field of study.

After nine years of research and field experiments, five mutant cowpea varieties were recommended for national release, making it the first Namibian bred varieties to be officially released in the country. The released cowpea varieties are 'ShR3P4', 'BrR4P11', 'NkR1P3', 'ShR4P1', 'BrR11P2' and 'ShR10P10'. These were selected for earliness, high yield, long pod size, big grain and/or high biomass yield. Parents were either Shindimba, Bira or Nakare. To meet the requirements of the Southern African Development Community (SADC), the national released varieties had to be tested in another country. The cowpea varieties were found to conform to the Distinct Uniform and Stable (DUS) by the Zimbabwean Ministry of Land, Agriculture, Water, Climate and Rural Settlement, under the Department of Research and Specialist Services (DR&SS) during 2020. Multiplication of the seed of released varieties started thereafter and it is reported that 2000 kg of improved seed has been multiplied for distribution to local farmers during 2021 cropping season under the supervision of the Ministry of Agriculture, Water and Land Reform in Namibia. According to the information obtained from the Senior Researcher responsible for seed at the Ministry of Agriculture, Water and Land Reform, so far 25 farmers received the seed for production.



Assessment of sorghum mutant lines in the field together with IAEA Technical Officer.

PERU

Ms Luz Rayda Gomez-Pando

Universidad Nacional Agraria La Molina



Ms Luz Rayda Gomez-Pando, Doctor of Agricultural Sciences, MSc and Agronomist Engineer, Principal Professor in Crop Science Department, Head (1998–2018), and Senior Researcher of Cereals and Native Grains Research Program of the Faculty of Agronomy at La Molina National Agrarian University in Lima, Peru.

Ms Gomez-Pando has a long history of research and achievements in plant mutation breeding. She started to work on improving barley, wheat and native grains in Peru using mutation breeding methodology since 1972. The main objective of her research work was and is to develop new and improved cultivars able to grow in adverse environmental conditions with suboptimal farming technology, but with better yield and quality for the small farmers in the Peruvian highlands. Since 1972 she has contributed to the development of two commercial cultivars in barley (*Hordeum vulgare*), ‘La Molina 95’ and ‘Centenario’, and one commercial cultivar of amaranthus (*Amaranthus caudatus*), ‘Centenario’.

In the Peruvian highlands between 3800–4000 m few crops can grow and produce. Barley contributes to 20% of the caloric intake and is the second source after potatoes that contributes with 21%. The released cultivars using induced mutations were improved for four characters: better yield, earlier maturity, better protein content and better test weight.

The combination of these characters with a good plant biomass and resistance to yellow rust made the barley cultivars very valuable for the highland farmers until today. The amaranthus cultivar ‘Centenario’ was improved in yield, storability, and plant colour. The three released mutant cultivars are still growing in the Peruvian highland, contributing significantly to improve food quality and the farmers' economy.

Her genetic improvement programme has developed advanced mutant lines of quinoa (*Chenopodium quinoa*) and new mutant lines of barley and amaranthus. These have greater tolerance to adverse weather environmental conditions (heat, drought, salinity) and have greater efficiency in the use of water and nutrients to withstand the adverse climate events occurring intensely and unpredictably in the marginal areas where these species are grown.

Ms Gomez-Pando's research works on mutation breeding have been published in scientific journals and in book chapters at the national and international levels and presented at national and international conferences. She teaches the subject of crop improvement at the undergraduate and postgraduate levels at La Molina National Agrarian University.

She has been teaching a chapter on the use of mutation induction annually to about 70 students for the last 40 years. She has advised numerous theses involving the use of induced mutations for crop improvement.

She has also contributed to the training of other researchers in Peru and other Latin American countries in the improvement of crops through plant mutation breeding.



Recording observations on mutant *Amaranthus* lines.



Field evaluation of quinoa mutant lines.

VIET NAM

Ms Vo Thi Minh Tuyen

Agricultural Genetics Institute



Mutagenesis is one of the experimental methods widely applied for crop improvement in the world and mutation breeding has significantly contributed to Viet Nam's food production. In Viet Nam, there are around ten organizations, institutions and universities that succeeded in the application of gamma irradiation for improving crop varieties. By the end of 2019, in Viet Nam, 80 mutant varieties have been developed and commercialized, which include 54 varieties of rice, 16 of soybean, and 10 others. The Agricultural Genetics Institute (AGI), where Ms Vo Thi Minh Tuyen is working, is a leading organization in the field of mutation breeding which has developed and commercialized 37 mutant varieties, which account for 46% of the total number of mutant varieties in Viet Nam. Among them there are 19 varieties of rice, that account for 35.2% of the total rice mutant varieties released in the country. Ms Vo Thi Minh Tuyen was very fortunate to start her career in the AGI where she has had the chance to learn the methods of mutagenesis in rice breeding from leading scientists since 1995.

From 2010 to present, Ms Vo Thi Minh Tuyen and her colleagues have participated in the development and commercialization of three mutant rice varieties: 'DT80' (carried saltol gene), 'CNC11', 'VDT99'. The 'DT80' mutant rice variety was released in 2019. It has an average yield of 6–7 t/ha, leading to increased earnings of US \$330 per hectare compared to the widely grown rice variety, 'TL6.3', which was used as the parent. This results from its increased yield of 15% and better tolerance to salinity. The cumulative area of this mutant since its release in 2019 is 15 000 hectares.

The CNC11 mutant rice variety was also released in 2019. Its average yield is 6–6.5 t/ha and it provides an increased income of US \$315 per hectare compared to its parent variety, 'BT7'. This results from the increased yield of 10% and good agronomic performance of 'CNC11'. The

estimated cumulative area under its cultivation since release in 2019 is 10 000 hectares.

The promising mutant 'VDT99' was sent to the National Testing Center for Crops to test for Value of Cultivation and Use of Crop in 2020. Its average yield is 6.5–7.5 t/ha. 'VDT99' provides an additional value of US \$350 per hectare compared to the 'KD 18' rice variety, which is the parent, and a popular rice variety in production. This results from the increased yield of 17% and good agronomic performance of 'VDT99'.

Apart from these new rice mutant varieties released, 198 promising mutant rice lines have been developed. Among them, 45 mutant lines are resistant to bacterial leaf blight, 27 mutant lines are resistant to blast, 43 mutant lines are salt-tolerant, 36 mutant lines are drought-tolerant, 47 mutant lines have shorter growth duration (85–90 days in summer season) and high-temperature tolerance.

These are the sources of precious genetic material for the selection and development of new rice varieties adapted to climate change. Besides this, Ms Vo Thi Minh Tuyen and team have published 10 papers on rice mutation breeding in specialized agricultural journals. These achievements were used as the basis for the institute to appoint Ms Vo Thi Minh Tuyen as the Head of Mutation and Heterosis Breeding Department within the AGI since 2020.

In this new position, she will continue her research on rice mutation breeding, educate students and young scientists in mutation breeding for the development of new rice varieties, as well as new varieties of other crops.



Recording observations on mutant rice lines in the greenhouse.



Field evaluation of mutant rice variety.



Joint FAO/IAEA Centre
Nuclear Techniques in Food and Agriculture

Young Scientist Award

AWARDS 2021
PLANT MUTATION BREEDING

CHINA

Mr Zhen Yang

Institute of Nuclear Agriculture Sciences and Space
Mutagenesis Breeding

Hunan Academy of Agricultural Sciences



Mr Zhen Yang focuses on plant mutation breeding research and associated biotechnologies at the Institute of Nuclear Agriculture Sciences and Space Mutagenesis Breeding of the Hunan Academy of Agricultural Sciences. From 2008 to now, Mr Yang has been working on rice mutation breeding and molecular biotechnology. His achievements are in the areas of technology development, pioneering a research platform and the development and release of improved rice varieties.

Mr Yang's research has succeeded in the development of a method of directional selection of mutants of target traits (controlled by major genes) from irradiated rice mutation population using molecular biology technology at the seedling stage. He has recently established a platform for the use of high-energy electron accelerator, heavy ion beams and ^{60}Co - γ for mutagenesis and radiation-induced mutation breeding in rice.

More than 20 new and improved rice mutant lines with early heading, good salt-tolerance, low cadmium absorption, nitrogen use efficiency and different amylose content have been developed and introduced to cultivation in the past few years.

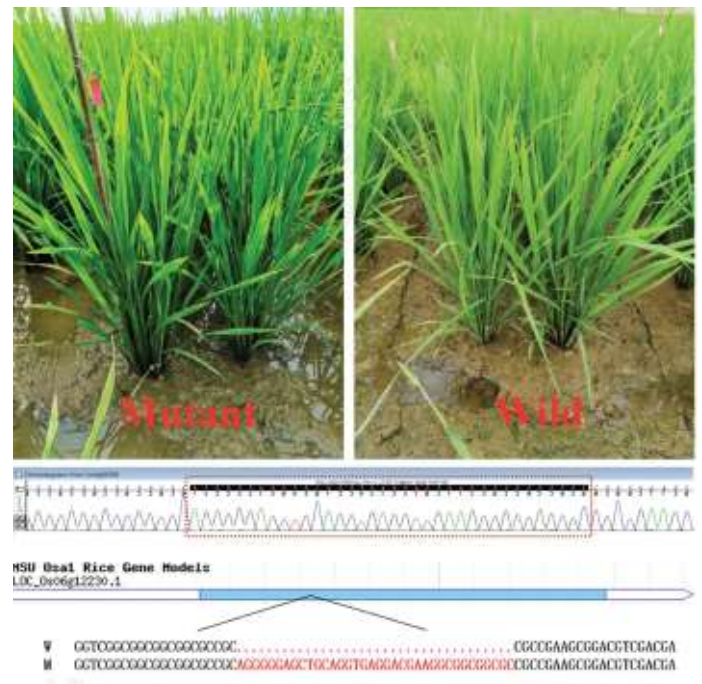
Mr Yang combines mutation induction with hybridization for the development of new and improved rice varieties. His research efforts led to the development of a new two-line hybrid rice variety C 'Liangyou 266' from the parents

'C58S/R266' in 2013. The variety has low cadmium accumulation, an average yield of 8.1 t/ha, good grain quality and has been in cultivation since 2014. Since its release for cultivation, the variety has been planted on more than 0.31 million hectares. The peak area covered by the variety to date was 0.12 million hectares in the year 2017. It was awarded the Second Award of Hunan Science and Technology Progress in 2019.

Mr Yang has also been involved in the IAEA activities in workshops and training courses in recent years. He has been carrying out the science popularization work of rice mutation breeding in the Hunan Province of China.



'Yliangyou 1166', released as a national variety in 2021 from gamma ray mutagenesis (300 Gy).



'OsTCP19' gene mutation related to nitrogen use efficiency, resulting from heavy ion beam treatment (125Gy).

INDIA

Mr Dhanasekar Punniyamoorthy
Bhabha Atomic Research Centre



Mr P. Dhanasekar has been nominated for his outstanding and meritorious achievement of developing and deploying four pulse varieties through mutation breeding.

India is the largest global producer, consumer, and importer of pulses in the world. The drastic reduction in annual import of pulses, from five million tons (2013) to 1.5 million tons (2020) has curtailed the foreign exchange losses correspondingly from US \$3 billion to about US \$1 billion. Mutation breeding and release of superior varieties has contributed to the recent uptrend in pulses productivity (661 kg/ha to 967 kg/ha) towards self-sufficiency. Mr P. Dhanasekar is actively involved in the genetic improvement of two pulse crops: pigeonpea and cowpea, through mutation and recombination breeding approaches. His strenuous and dedicated research efforts have culminated in the release and notification of four high yielding mutant varieties by the Indian government for commercial cultivation: three in pigeonpea and one in cowpea. In the Central Zone of India, the dearth of suitable early maturing pigeonpea varieties for almost 15 years ended with his two mutant varieties 'TT-401' in 2007 and 'TJT-501' (in collaboration with JNKVV, Jabalpur) in 2009. For this Indian Council of Agricultural Research conferred the Institute with a certificate of honour. These mutant derivatives are endowed with resistance to fusarium wilt and sterility mosaic diseases along with earliness, semi-spreading growth habit, and increased harvest-index. In 2013, another mutant variety of his, 'PKVTARA' (in collaboration with Dr P.D.K.V. Akola), with tolerance to the pod borer complex was released for the Maharashtra State.

Mr Dhanasekar's gamma rays induced direct mutant cowpea variety 'TC-901' released recently in 2018 and has the distinction of being the nation's first summer suitable cowpea variety. It is bestowed with early and synchronous maturity, resistance to diseases, high protein (27%), fodder and seed yield (1000–1200 kg/ha). 'TC-901' has been

included as a national check in the coordinated summer varietal trials.

His breeding pursuit in the hitherto difficult domain of restructuring pigeonpea resulted in compact plant-type 'IDT2004-1' carrying a novel GA_3 -insensitive D_0 -dwarf mutation. Molecular markers (OPF04₇₀₀ and OPA0₁₃₇₅) tightly linked with the monogenic recessive compact-dwarf trait were established. Mr Dhanasekar has identified 63 valuable cowpea mutants and 13 of his exemplary high yielding mutant derivatives are under varietal evaluation trials. A novel SNP mutation in VuTFL1 gene has been deciphered by him as the cause for determinacy in a cowpea mutant.

He also has developed DNA fingerprinting of important cowpea mutants. The three pigeonpea varieties resulting from Mr Dhanasekar's research are in great demand and are widely cultivated by farmers in the Central Zone of India, the hub of pigeonpea cultivation. The varieties annually garner about 11 % of the national breeder seed indent (peaked 23% during 2017–2018). To meet the burgeoning demand of 'TJT-501' that occupies nearly 60% of pigeonpea area in Madhya Pradesh, 106.1 tons of breeder seeds were produced (2015–2018). As estimated, these varieties were cultivated by two million farmers in over 2.5 million hectares with cumulative production of 4.35 million tons (2013–2020). The farmers by adopting these varieties have earned additionally US \$600 per hectare. The recently released cowpea variety 'TC-901' yet to complete the breeder-foundation-certified seed cycle, is expected to immensely contribute to the National Food Security Mission by augmenting summer pulse production.



Cowpea mutant variety, 'TC-901'.



Pigeonpea variety, 'TJT-501'.

MADAGASCAR

Mr Harimialimalala Jhonny Rabefiraisana
Faculty of Sciences, University of Antananarivo



Mr Harimialimalala Jhonny Rabefiraisana of the University of Antananarivo is recognized for his mutation breeding work in the identification of rice and maize mutant lines with resistance to the parasitic weed, *Striga asiatica*.

Rice, followed by cassava and maize, are the main food crops in Madagascar, whose population is growing, resulting in a continuous increase in demand for rice and maize and pressure to increase production. However, upland rice and maize cultivation in the Middle-West of Madagascar are threatened by climatic and pedological unfavourable conditions, including weeds, pests, and parasites. Among these problems, the parasitic weed, *Striga asiatica*, appears to be one of the major issues causing significant production losses for upland rice and maize. In severe situations of *Striga* infestation, losses in rice and maize yield in the Middle-West of Madagascar may reach up to 90–100%. Employment of several management strategies, with quarantine imposed on contaminated regions, control of farm equipment movement between infected and uninfected regions, intensive herbicide application, and reduction of *Striga* seed through injection of ethylene gas, has caused success in the control of *S. asiatica*. However, these approaches are costly and are not generally accessible to the small farmer in the areas infested with *Striga*.

In these areas the *Striga* problem is, in general, linked with low economic resources, low soil fertility, marginal environments with continued cereal monoculture, and newly infested areas regrettably expanded due to several human and agricultural actions. The development of rice and maize lines with increased genetic resistance or tolerance to *S. asiatica* is a crucial way to meet the growing food demand. To deal with this problem of damage caused by *Striga*, the team contribution is based on creating new sources of resistance to *S. asiatica* induced by gamma-ray irradiation in upland rice and maize. The rice variety, 'B22', and the maize variety 'Irat-200' and 'PLATA',

which are highly appreciated by consumers and popularly planted by farmers in the middle west of Madagascar are identified as susceptible to *S. asiatica*. These were subjected to mutation induction to create new sources of resistance to *Striga asiatica*. The support from the Joint FAO/IAEA Centre with the MAG5025 project entitled 'Enhancing biocontrol of *Striga asiatica* (L.) Kuntze through the development of tolerant rice and maize lines and its links with microbiological and ecological functioning of soil', and the MAG5026 project entitled 'Enhancing rice and maize productivity through the use of improved lines and agricultural practices to ensure food Security and increase rural livelihoods' and the CRP D25005 entitled 'Mutation breeding for resistance to *Striga* parasitic weeds in cereals for food security" allowed the team to identify advanced mutant lines in both rice and maize with tolerance or resistance to the weed.

These include 13 rainfed mutant rice lines and 16 mutant maize lines that are resistant to *S. asiatica*, and another 24 mutant rice lines and 28 mutant maize lines that are tolerant to the witchweed. The official release process of the rice lines and maize lines resistant or tolerant to *S. asiatica* is in progress.



Greenhouse screening for resistance to *Striga*.



Early field assessment of *Striga* infestation in mutant maize fields.

PAKISTAN

Mr Muhammad Kashif Riaz Khan
Pakistan Atomic Energy Commission



Mr Muhammad Kashif Riaz Khan, Principal Scientist, Cotton Group at the Nuclear Institute for Agriculture and Biology (NIAB) has more than 20 years cogent R&D and teaching experience in the field of mutation breeding coupled with molecular genetics and genomics in cotton. This award recognizes contributions in the evolution of three famous cotton cultivars, ‘NIAB KIRAN’, ‘NIAB-112’ and ‘NIAB-878/B’ in Pakistan since 2010.

These varieties proved to be well-adapted under changing climatic scenario in Pakistan and help in uplifting the profitability of cotton growers in the country.

Moreover, as team member of Cotton Group he was actively involved in the final evaluation of ‘NIAB-111’ which was the first virus-tolerant variety having fine fibre in 2004. It covered a significant area in the Punjab province since its release for cultivation up to 2014–2015 with an impact of billion rupees on the national economy. The recently evolved cotton varieties viz, ‘NIAB KIRAN’ (2013 in Punjab and 2016 in Sindh provinces), and ‘NIAB-878/B’ (2017) have the ability to withstand severe climatic conditions under prevailing climate change and have more

than 40% share in the seed production system, which is the candid proof of these varieties to cover the same proportionate area in Punjab (2018–2020) with billion rupees impact on national economy. ‘NIAB KIRAN’ covered about 67% area against NON-GMO varieties in Sindh during 2017–2018 and proved to be the best cotton variety in Baluchistan province (2019–2020) for organic cotton production. ‘NIAB-878/B’ proved as climate resilient with its ability to unlock its yield potential under the changing climatic scenario of the country with 30–40% loss recovery of yield against peak heat stress period (July–August). ‘NIAB-112’ has the ability to tolerate severe threat of CLCuD and common grower variety because of less input’s requirement. The impact of mutant background varieties of Pakistan can be envisaged from the IAEA success stories.



NIAB-112 field view.



Cotton mutants in the greenhouse.

UNITED REPUBLIC OF TANZANIA

Mr Salum Faki Hamad

Zanzibar Agricultural Research Institute



Mr Salum Faki Hamad of Zanzibar Agricultural Research Institute is recognized for his research in mutation breeding of rice and the release of the mutant rice variety, SUPA BC (TARI-RIC1) that has been in cultivation in Zanzibar since 2014 and currently occupies the majority of the area under rice.

The IAEA supported the rice improvement project in Zanzibar through training of Zanzibar Agricultural Research Institute (ZARI) staff and scientists on mutation breeding techniques and assisting the research institute with the radiation facilities to induce mutation to local and improved varieties, and the provision of laboratory and field equipment to ZARI. Through the Technical Cooperation Project (TCP) with the IAEA, ZARI has been conducting mutation breeding projects to improve rice production in Zanzibar. The first mutant variety named 'SUPA BC' was released for multilocation trial in 2011 and passed official release for farmer cultivation in Zanzibar in 2014. Since its release, the 'SUPA BC' variety has gained popularity and is widely accepted by farmers and rice consumers in Zanzibar. Based on baseline survey data conducted by the Extended Rice Research Project (ERPP) in the 2016/2017 season, more than 70.6% of the farmers cultivated the 'SUPA BC' rice variety.

An ERPP project conducted a participatory field trial to assess farmers' preference on varieties of rice. Sixty five percent of farmers chose 'SUPA BC'. When asked about the reason of choosing 'SUPA BC', farmers said that 'SUPA BC' has higher aroma, high yield, and better market price. The 'SUPA BC' variety was developed with technical support from the Joint FAO/IAEA Centre through the TCP, URT5020. The aim of the project was to enhance crop production through radiation techniques. The irradiation process was initiated in collaboration with rice scientists from the Sokoine University of Agriculture (SUA), mainly, Dr Ashura Luiz Kihupi. ZARI participated in the development of the variety in all stages of selection

and development from M_1 to M_4 until the selection of the final successful variety. Initially, ZARI received 24 mutant lines from SUA for evaluation and assessment of adaptability and suitability in Zanzibar.

During the selection process, the mutant 'SUPA BC 100' emerged as the better performing line. The 'SUPA BC 100' mutant was then backcrossed with its parent variety SUPA to restore some of the good traits of the parent and hence the name 'SUPA BC' (SUPA Back Cross). Currently, the team is intensively working on seed multiplication of 'SUPA BC' and the dissemination of quality seed to farmers. The team is producing pre-basic seed of 'SUPA BC' in contract with farmers who have been trained on the production of Quality Declared Seed (QDS). 'SUPA BC' is multiplied as QDS and disseminated to other farmers, thus increasing the area under SUPA BC cultivation. Currently, 'SUPA BC' covers 70% of the total area under rice cultivation in Zanzibar, which is about 810 hectares.

Mr Hamad and team expect to double the area of production of 'SUPA BC' in 2021 following government expansion of area of irrigation from 810 hectares to 2527 hectares in 2020 (CCM Manifest 2020–2025; CCM is a ruling part of Zanzibar and Tanzania). As there is no official seed certification agency yet in Zanzibar, the Quality Declared Seed System is used currently. The process of establishing seed certification is in the final stages in the country. 'SUPA BC' was registered in 2020 in mainland Tanzania by the Tanzania Agricultural Research Institute (TARI) and given registration name, 'TARI-RIC1'.



ZARI Laboratory Technician staffs preparing local rice seeds for sending to Vienna for irradiation.



Rice mutants (M_3) for phenotype screen for rice blast disease resistance at Kibonde Mzungu Irrigation scheme in Zanzibar.

VIET NAM

Mr Nguyen Van Manh

Agricultural Genetics Institute



Mr Nguyen Van Manh has been working at the Agricultural Genetics Institute (AGI) of Viet Nam since 2009 in plant mutation breeding using gamma irradiation (gamma cell) and chemical mutagenesis. AGI is the only institute in Viet Nam with the Department of Mutation and Heterosis, and Mr Manh has significantly benefited from the guidance of leading professors in the science. To date, AGI has developed 48 of the 71 mutant crop varieties in the country (accounting for 68%). This includes 33 rice varieties, 11 soybean varieties, two chrysanthemum varieties and two maize varieties. Recently, in collaboration with Japanese scientists, Mr Manh and team have started the application of ion beam for mutation induction. The target crops for Mr Manh's group are soybean and groundnut, which play important roles in providing nutrition for people, especially ethnic minority groups in remote mountain regions of the country. Further, in lowland areas soybean is one of the traditional food crops and plays an important role in crop rotation, as it is planted between two rice crop seasons. This helps soil improvement, providing food for humans and livestock, and additional income for farmer from a land unit. The yield has been below optimum for previously existing soybean varieties in the country. The main causes have been the limitations of existing soybean varieties in adaptation to local climate conditions, and the lack of resistance to pest and diseases.

Mr Manh's main achievement in soybean mutation breeding is the development of three national varieties ('DT2008', 'DT2010', 'DT215') and 120 promising lines (50 lines with high productivity (>3 t/ha); 15 lines resistant to rust; 20 lines resistant to powdery mildew; 20 lines with high-protein (>40%); and 15 lines with drought-tolerance).

He has published 14 research articles, together with his team, on breeding mutant soybean in Viet Nam.

Three national varieties ('DT2008', 'DT2010', 'DT215') have been released for large scale production. They are widely in cultivation now in all provinces of Viet Nam. Below are the main characteristics of the released national varieties: 'DT2008' was developed with ^{60}Co gamma irradiation at the dose of 180 Gy on dry seeds of the hybrid line '2001HC' ('DT2001' x 'HC100'). It has a high yield of 2.0–4.0 t/ha (23.1–45% higher than the common variety 'DT84'), good tolerance to drought, good resistance to the diseases of rust, downy mildew, and bacterial infections. During the period of 2010–2020, 'DT2008' was tested and introduced into production in many provinces in the whole country such as Ha Noi, Thai Nguyen, Tuyen Quang, Cao Bang, Phu Tho, Yen Bai, Ha Giang, Dak Lak and Dak Nong. The variety was cultivated by 1.5 million farmers over an area of 30 000 hectares.

'DT2010' is an indirect mutant developed by hybridization between the mutant varieties 'DT2008' and 'DT99'. It has a short growth duration of 80–88 days (equal to the common variety 'DT84') but higher yield of 2.2–2.5 t/ha (over 10% compared to the common variety 'DT84'), good resistance to rust and drought tolerance. Thanks to its short growth duration and high yield, it has the prospect of replacing 'DT84' in cultivation, especially in the cropping system in the Red River Delta in two-crop rice lands in winter. The variety was cultivated by 0.05 million farmers on an area of 1500 hectare and contributed to increasing the income of famers by about 20%. 'DT215' was developed by ^{60}Co gamma irradiation at the dose of 200 Gy on dry seeds of 'DT2008'. It has black seed coat. Compared to the parent 'DT2008', 'DT215' has the same good growth and development, mild infection of some diseases (rust, downy mildew) and high yield (2.46–3.18 t/ha) but higher nutrient contents (carotenoids, omega 3, omega 6 which are 59, 30 and 12% higher than the parent variety, respectively) and 5–8 days shorter growth duration (90–100 days). The variety has been cultivated on an area of 500 hectares and has contributed to increasing the income for famers by about 50%. Mr Manh is the Deputy Head of Department of Mutation and Heterosis and team leader of soybean research and breeding at AGI since 2020.



'DT2010' soybean variety in Vinh Phuc Province.

ZIMBABWE

Mr Prince M. Matova

Crop Breeding Institute, Department of Research and Specialist Services

Ministry of Agriculture



Mr Prince M Matova is recognized for his contributions to the development and release of the cowpea mutant variety, CBC5, the first mutant variety to be released in Zimbabwe. Collaborating with researchers in South Africa, Mr Matova conducted studies to evaluate the potential of using gamma mutation induction and chemical mutagenesis in improving cowpea and tepary bean respectively. The two crops are important to smallholder farmers in the semi-arid to arid areas of Sub-Saharan Africa because of their inherent drought tolerance and high nutrient density. Mr Matova also implemented for the first time, research to optimise maize mutation breeding with gamma irradiation on maize inbred lines and open-pollinated varieties (OPVs) and optimal irradiation doses were determined and recommended. The cowpea variety, 'CBC5', is drought tolerant, has grains that are 10% larger than those of its parent 'CBC1' and performs 20% better in terms of grain yield potential compared with most farmer-preferred varieties in Zimbabwe. The variety was released in 2017 and commercialised in 2018. It is adapted to all the agro-ecological zones of Zimbabwe and has a niche advantage in natural regions four and five which receive very little rainfall per annum and there is huge livestock rearing activities which can be partly sustained by the residues of the cowpea crop during the dry seasons. With the consent of the parent institute, the Crop Breeding Institute and the Department of Research and Specialist Services, 'CBC5' can now be commercialised in other countries. The variety was licensed to National Tested Seeds, a private seed company in Zimbabwe that is doing commercial seed production and marketing of the variety on behalf of the Crop Breeding Institute.

Parallel to that, the variety together with other experimental mutant varieties that are even more drought tolerant and endowed with farmer preferred traits such as

pods above canopy better resistance to insect pests and diseases, have been introduced into various farmer communities across Zimbabwe through on-farm testing and on-farm seed production trainings. The Crop Breeding Institute collaborated with an NGO called Practical Action under the Benefit-sharing Fund project funded by FAO from 2016 to 2018 and through the project, CBC5 and other advanced mutant varieties were disseminated to four districts of Matebeleland South province in Zimbabwe, which receives an average of <250 mm of rainfall per year. The variety is being used by communal farmers across the country, particularly women farmers. At present, the cowpea breeding programme has six advanced mutant lines that were screened for drought tolerance with the International Institute of Tropical Agriculture (IITA) in Nigeria in 2014–2015. Further testing and validation were done in Zimbabwe, and the same materials were also sent to Vienna for further tests at the Plant Breeding and Genetics Laboratory in Seibersdorf. The varieties have enhanced drought tolerance, large seed sizes, improved yield potential and an interesting characteristic of pods growing above the canopy. Mutation breeding in the maize programme started in 2016, and 31 populations were irradiated and screened for agronomic performance and FAW tolerance. At present the programme is screening and evaluating the agronomic performance of 863 mutant lines at M₄. These pose a huge potential source of inbred lines for further breeding and parent extraction for hybrid constitution. Zimbabwe runs 13 breeding programmes under the Ministry of Agriculture; crops include major staples and crops important to smallholder farmers such as maize and cowpea. Mutation breeding in Zimbabwe will continue with particular focus on maize and cowpea. The objectives will be: (1) To improve grain yield and quality traits, (2) Improvement of insect pest resistance, FAW tolerance for maize and aphid tolerance for cowpeas. Gamma mutation induction will be done on improved maize lines and donor lines and cowpea lines with native resistance to fall armyworm and aphids respectively.



Radiosensitivity test in maize.

Websites and Links

- Plant Breeding and Genetics Section:
<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>
<https://www.fao.org/agriculture/fao-iaea-nuclear-techniques/en/>
- 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 \(fao.org\)](#)

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