



Virtual Training Workshop on Methods and Workflows for Establishing Genetic Associations Using Functional Genomic Tools for Mutation Breeding Applications

Seibersdorf, Austria

via Microsoft Teams

20 - 21 November 2025

Ref. No.: EVT2405245

Information Sheet

Introduction

Mutation breeding has emerged as a powerful tool for crop improvement, enabling the development of novel traits through induced genetic variation. With the advent of high-throughput sequencing and functional genomics technologies, researchers can now accelerate the identification of gene-trait associations and understand the molecular basis of induced mutations. The integration of mutation breeding with functional genomics has revolutionized the way we identify and characterize genes responsible for important agronomic traits. This master class introduces participants to cutting-edge mutation mapping approaches, including (i) QTL-seq (Quantitative Trait Locus sequencing) that combines bulked segregant analysis with whole-genome sequencing to rapidly identify genomic regions associated with quantitative traits, (ii) BSA-seq (Bulked Segregant Analysis sequencing) that involves mapping single-gene traits by sequencing pooled DNA from individuals with contrasting phenotypes, (iii) MutMap and MutMap+: Designed for mapping mutations in selfing populations using next-generation sequencing, and (iv) SHOREmap and NIKS: Tools for high-resolution mapping in forward genetic screens.

These approaches are complemented by functional genomics tools such as RNA-Seq, proteomics, and metabolomics, which provide insights into gene expression, protein function, and metabolic pathways. Together, they form a comprehensive workflow for establishing genetic associations and accelerating the development of improved crop varieties. This master class, organized by Murdoch University in collaboration Joint FAO/IAEA Plant Breeding and Genetics Laboratory, will provide a comprehensive overview of modern workflows that integrate mutation breeding with functional genomics tools. Participants will gain experience in applying genomics and bioinformatics to identify and validate candidate genes associated with desirable agronomic traits.

Objectives

1. Understand the principles of modern mutation breeding approaches for crop improvement.
2. Apply functional genomics tools (e.g., RNA-Seq, GBS, WGS) to analyze mutant populations.
3. Implement workflows for detecting genetic variants and linking them to phenotypic traits.
4. Validate gene-trait associations using molecular and computational approaches.

Target Audience

- Plant breeders and geneticists working in national/international agricultural research systems.
- Molecular biologists and biotechnologists involved in crop improvement.
- Bioinformaticians and data analysts supporting genomics research.
- Graduate students, postdoctoral researchers, and early-career scientists in plant sciences.
- Professionals from IAEA Member States engaged in mutation breeding and functional genomics.

Working Language

English

Participation and Registration

This training workshop will be open for remote access from 20 to 21 November 2025 using the virtual platform Microsoft Teams. All persons wishing to participate in the event have to be designated by an IAEA Member State or should be members of organizations that have been invited to attend.

Registration through the InTouch+ platform:

In order to be designated by an IAEA Member State or invited organization, participants are requested to submit their application via the InTouch+ platform (<https://intouchplus.iaea.org>) to the competent national authority (Ministry of Foreign Affairs, Permanent Mission to the IAEA or National Atomic Energy Authority) or organization for onward transmission to the IAEA by **30 September 2025**, following the registration procedure in InTouch+:

1. Access the InTouch+ platform (<https://intouchplus.iaea.org>):
 - Persons with an existing NUCLEUS account can sign in with their username and password;
 - Persons without an existing NUCLEUS account can register [here](#).
2. Once signed in, prospective participants can use the InTouch+ platform to:
 - Complete or update their personal details under 'Basic Profile' and upload the relevant supporting documents;
 - Search for the relevant event (EVT2405245) under the 'My Eligible Events' tab;
 - Select the Member State or invited organization they want to represent from the drop-down menu entitled 'Designating Authority' (if an invited organization is not listed, please contact InTouchPlus.Contact-Point@iaea.org);
 - Based on the data input, the InTouch+ platform will automatically generate Participation Form (Form A).
 - Submit their application.

Once submitted through the InTouch+ platform, the application, together with the auto-generated Form

A, will be transmitted automatically to the required authority for approval. If approved, the application, together with the Form A, will automatically be sent to the IAEA through the online platform.

For additional information on how to apply for an event, please refer to the [InTouch+ Help](#) page. Any other issues or queries related to InTouch+ can be sent to InTouchPlus.Contact-Point@iaea.org.

Selected participants will be informed in due course on the procedures to be followed with regard to administrative and technical matters. Candidates who successfully complete the virtual training course will receive a certificate.

No registration fee is charged to participants.

Participants are hereby informed that the personal data they submit will be processed in line with the [Agency's Personal Data and Privacy Policy](#) and is collected solely for the purpose(s) of reviewing and assessing the application and to complete logistical arrangements where required. Further information can be found in the [Data Processing Notice](#) concerning IAEA InTouch+ platform.

Organization

Scientific Secretary

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Subsequent correspondence on scientific matters should be sent to the Scientific Secretary and correspondence on other matters related to the event to the Administrative Secretary.