

WORKSHOP

How to set up a Marker-Assisted Selection Pipeline

Information Package

 TARGET AUDIENCE

- Plant breeders
- Decision makers who want to expand their knowledge
- MSc/PhD students in genetics or breeding
- Researchers involved in plant breeding projects
- Technical staff in seed companies or gene banks

 DURATION

- 4 hours including Q&A, divided in two days
- Format: live webinar
- Maximum number of participants: 12

 WEBINAR AGENDA**DAY-1****Welcome & Introduction (15 min)**

- Host and trainer introductions
- Overview of goals and schedule

How Marker -Assisted Selection benefits genetic gain (15 min)

- Basic Concepts of MAS
- Breeder's Equation
- How MAS unlocks Breeder's Equation
- Basic Structure of a MAS pipeline

How to Generate Markers Linked to Traits (45)

- How to look into published data for trait markers.
- The principles of Genetic Mapping
- Genetic Distance and Genetic Maps

- QTL mapping: types of mapping populations, phenotyping, software for analysis and interpretation of results.
- Demonstration of QTL analysis using QTL IciMapping software
- QTL mapping *versus* Genome-Association Mapping
- Demonstration how to navigate through a publication of QTL mapping
- Validate Trait Markers

Interactive Activity and QA : 45 minutes

DAY-2

How to use markers traits for selection (45 minutes)

- Criteria of choosing reliable markers for routine use in MAS
- Overview of Applications of MAS
- Strategy of QTL Deployment and Line Augmentation
- Foreground, background, and recombinant selection strategies (Backcross Strategy)
- A case study of Marker -Assisted Backcross program

Interactive Activity and QA (20 minutes)

The Logistics of implementing a Marker-Assisted Selection Pipeline (25 minutes)

- Options of DNA extraction and Genotyping platforms
- Databases for data storing and management of routinary MAS tasks

- Demonstration of SNP visualization and filtering with FlapJack software.
- Create a core set of SNPs for your crop and its use in downstream applications

Practical Considerations & Challenges (15 min)

- In house genotyping facilities *versus* outsourcing
- Collaboration between breeders, lab teams and geneticists
- Synergies between public and private sector
- When and how to integrate MAS into your program

Q&A + Wrap-Up (15 min)

- Participant questions and discussion
- Feedback form
- Resources shared: manuals, templates, reading materials

MATERIALS PROVIDED

- Slide handout (PDF)
- Certificate of participation
- Suggested reading and tools for further learning

BONUS / FOLLOW-UP OPPORTUNITIES

- Invitation to advanced MAS workshops
- Mailing list for follow-up resources and updates
- Optional personalized session for your own dataset (consulting offer)