AgroSynapsis

WORKSHOP

How to set up a Marker-Assisted Selection Pipeline

Information Package

www.agrosynapsis.com

TARGET AUDIENCE

- Plant breeders
- Plant PreBreeders and Molecular Geneticists
- MSc/PhD students in genetics or breeding
- Researchers involved in plant breeding projects
- Technical staff in seed companies or gene banks

DURATION

- 5 hours including Q&A, divided in two days
- Format: live webinar
- Maximum number of participants: 15

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 (60)

- 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-Assosiation Mapping
- Validate Trait Markers
- Demonstrate a real QTL case study: from discovery through validation to deployment in a breeding program

Interactive Activity and QA : Hands-on analysis of a ready-to-use dataset using QTL IciMapping **(60 minutes)**

DAY-2

How to use markers traits for selection (60 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 in groups: Hands-on use of AI tools (e.g. ChatGPT) to identify stable and major QTLs from published datasets, and to design a theoretical molecular breeding pipeline for their validation and deploymen**t (60 minutes)**

The Logistics of implementing a Marker-Assisted Selection Pipeline (35 minutes)

- Options of DNA extraction and Genoyping platforms
- Databases for data storing and management of routinary MAS tasks
- Demostration of SNP visualization and filtering with FlapJack software.
- Create a core set of SNPs for your crop and its use in downstream applications

Q&A + Wrap-Up

- 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