



Marker Assisted Selection in Crop Breeding

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Marker-assisted selection (MAS) is a powerful tool in crop breeding that enables plant breeders to select plants with desired traits more efficiently and accurately. It involves the use of molecular markers, such as DNA sequences or proteins, to identify and select plants with specific genes or traits of interest. This method has revolutionized crop breeding by accelerating the breeding process and increasing the precision of trait selection. Here's how marker-assisted selection works in crop breeding:

(a) **Trait Identification:** The first step in MAS is to identify the target trait or gene of interest.

(b) **Marker Development:** Once the target trait or gene is identified, molecular markers are developed that are closely linked to the trait.

(c) **Genotyping:** In the genotyping step, DNA samples from a population of plants are analyzed to determine the presence or absence of the marker sequences.

(d) **Data Analysis:** The genotyping data is then analyzed to determine which plants carry the desired trait or gene based on the presence or absence of the molecular markers.

(e) **Selection of Plants:** Using the marker information, breeders can select plants with the target trait or gene with high accuracy.

(f) **Crossover and Backcrossing:** Selected plants can be crossed with other plants to introduce additional genetic diversity. Backcrossing can be used to gradually introduce the trait into the background of elite or commercial varieties, which can make the new variety more acceptable to growers and consumers.

(g) **Field Testing:** The selected plants and their offspring are grown and evaluated in field trials to ensure that they perform well under real-world conditions.

(h) **Commercialization:** Once a new variety is deemed successful in field trials, it can be released for commercial production.

Advantages of Marker-Assisted Selection in Crop Breeding

(a) **Increased Precision:** MAS allows for the selection of plants with the target trait at a very early stage, increasing the precision of breeding efforts.

(b) **Faster Breeding:** It accelerates the breeding process by reducing the time required to develop new crop varieties.

(c) **Reduced Costs:** It can reduce the cost of field trials, as plants are pre-selected based on genetic markers before field testing.

(d) **Disease Resistance:** It is particularly valuable for identifying and incorporating disease-resistant genes into crop varieties.

(e) **Preservation of Desired Genetic Background:** MAS allows breeders to preserve the genetic background of elite varieties while introducing specific traits, which is critical for maintaining desirable agronomic characteristics. Marker-assisted selection has significantly

advanced the field of crop breeding, enabling the development of new varieties with improved traits and resistance to diseases and pests. It has the potential to contribute to global food security by increasing the efficiency and precision of crop improvement.

Salient requirements for MAS

In general, the success of a marker-based breeding system depends on these main factors:

- (i) A genetic map with an adequate number of uniformly-spaced polymorphic markers to accurately locate desired QTLs or major genes.
- (ii) Close linkage between the QTL or a major gene of interest and adjacent markers.
- (iii) Adequate recombination between the markers and rest of the genome.
- (iv) Ability to analyse a larger number of plants in a time and cost-effective manner.

Strategies for Marker-Assisted Selection

(1) The recent advances in genomics have paved the way for clear and reliable methods for MAS in plants: from QTL identification, NIL development and fine-mapping to transferring the QTL into popular varieties using a precise marker assisted backcrossing (MABC) strategy. MABC involves the manipulation of genomic regions involved in the expression of particular traits of interest through DNA markers, and combines the power of a conventional backcrossing program with the ability to differentiate parental chromosomal segments.

(2) **Foreground selection and background selection:** Molecular markers are now increasingly being employed to trace the presence of target genes (foreground selection) as well as for accelerating the recovery of the recurrent parent genome (background selection) in backcross programmes.

Marker assisted selection in crop breeding

Backcrossing has been a widely used technique in plant breeding for almost a century. Backcrossing is a plant breeding method most commonly used to incorporate one or a few genes into an adapted or elite variety. In most cases, the parent used for backcrossing has a large number of desirable attributes but is deficient in only a few characteristics. The method was first described in 1922 and was widely used between the 1930s and 1960s.

Traits improved by MAS

- (1) **Barley:** Barley Yellow Dwarf Virus Resistance, Yellow Mosaic Virus Resistance, Stripe Rust Resistance, and Leaf Rust Resistance, and Yield Improvement
- (2) **Maize:** Corn Borer Resistance, Earliness and Yield Improvement
- (3) **Rice:** Bacterial Leaf Blight Resistance, Blast Resistance, Submergence Tolerance, Brown Plant Hopper Resistance, Fertility Restoration, Waxiness, Root Traits and Aroma
- (4) **Wheat:** Powdery Mildew Resistance.

Constraints in MAS

- (a) Identification of a limited number of major (QTLs) controlling specific traits.
- (b) The notion that QTL identification is required whenever additional germplasm is used.
- (c) Inadequacies/ experimental deficiencies in QTL analysis leading to either overestimation or underestimation of the number and effects of QTLs.
- (d) Lack of universally valid QTL marker associations applicable over different sets of breeding materials.
- (e) Strong QTL – environment interaction.
- (f) Difficulty in precisely evaluating epistatic effects.

Recent Advances in MAS Strategies and Genotyping Techniques

- (a) Single large-scale MAS
- (b) Pedigree MAS
- (c) Breeding by Design

Current Status of Applications of MAS in Agriculture

Most of the traits of agronomic importance are complex and regulated by several genes. Unlike the case of simply inherited traits that are controlled by one or a few major genes, improvement of polygenic traits through MAS is a complex endeavour. The difficulty in manipulating quantitative traits is related to their genetic complexity, mainly the number of genes involved in their expression and interactions among genes (epistasis).

Applications of MAS in plant breeding

(a) Marker-assisted evaluation of breeding material Cultivar identity/assessment of 'purity'
(b) Assessment of genetic diversity and parental selection (c) Study of heterosis (d) Identification of genomic regions under selection (e) Marker-assisted gene pyramiding (f) Early generation marker-assisted selection (g) Combined marker-assisted selection.

Conclusion

MAS could greatly assist plant breeders in reaching this goal although, to date, the impact on variety development has been minimal. For the potential of MAS to be realized, it is imperative that there should be a greater integration with breeding programmes and those current barriers be well understood and appropriate solutions developed. The exploitation of the advantages of MAS relative to conventional breeding could have a great impact on crop improvement. The high cost of MAS will continue to be a major obstacle for its adoption for some crop species and plant breeding in developing countries in the near future. Specific MAS strategies may need to be tailored to specific crops, traits and available budgets.

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