

Marker Assisted Selection

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Introduction

The association of simply inherited genetic marker with a quantitative trait in plants was first reported by Saxon in 1923. He observed segregation of seed size associated with segregation for a seed coat color marker in common bean [*Phaseolus vulgaris*]. In 1935, Rasmusson demonstrated linkage of flowering time [a quantitative trait] in peas with a simply inherited gene for flower color. A trait of interest is chosen based on a marker (morphological, biochemical, or DNA/RNA variation) linked to a trait of interest (e.g., productivity, disease resistance, abiotic stress tolerance, and quality), rather than on the trait itself, in an indirect selection process known as marker assisted selection, or marker aided selection (MAS). This method has been thoroughly studied and suggested for the breeding of plants and animals.

For instance, rather than focusing on the degree of disease resistance, MAS is used to select individuals who have disease resistance by identifying a marker allele that is associated with disease resistance. It is assumed that the marker's high frequency of association with the gene or quantitative trait locus (QTL) of interest results from genetic linkage, which is the close chromosomal proximity between the marker locus and the locus that determines disease resistance. When selecting for qualities that are expensive or difficult to quantify, have little heredity, or manifest late in development, MAS might be helpful. The specimens are inspected at specific stages of the breeding process to make sure they exhibit the desired characteristic. Identifying individual genes or QTLs (Quantitative Trait Loci) that significantly affect specific traits through their linkage to molecular markers can greatly improve the efficiency of incorporating desired traits into elite germplasm.

Classification of molecular markers DNA or molecular markers are classified in different groups on the basis of:

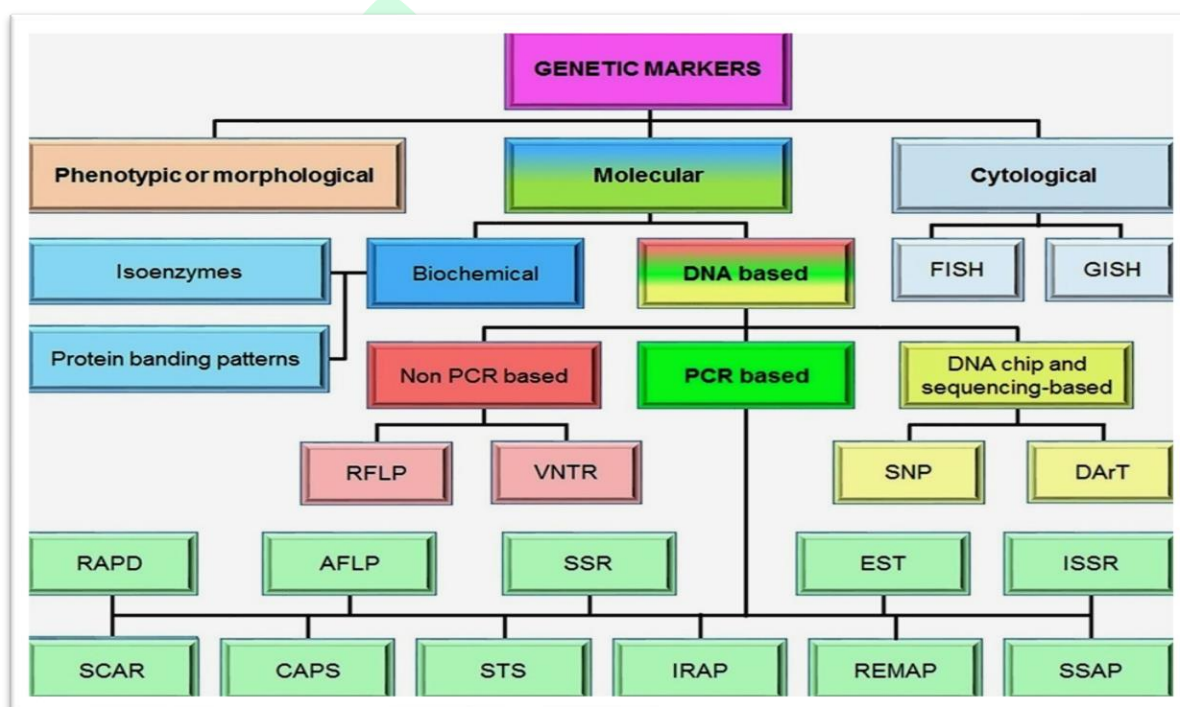
1. Nature of gene action (dominant or co-dominant markers)
2. Detection methods of molecular markers (PCR based molecular markers or hybrid based molecular markers)

3. Transmission mode of molecular markers (maternal organelle inheritance, paternal organelle inheritance, maternal nuclear inheritance, or biparental nuclear inheritance).

Types of Markers

Mainly it is of three types

1. Molecular markers
2. Cytological
3. Morphological/phenotypic



Important Features of Different Types of Markers

Feature	RELP	RAPD	RFLP
PCR based	No	Yes	Yes
DNA quality	High	High	Moderate
Dominance	Codominant	Dominant	Codominant
Reproducibility	High	Unreliable	High
automation	Low	Moderate	Moderate
Cost per analysis	High	Low	Moderate
Need for sequence data	Yes	No	No
Accuracy	Very high	Very low	Medium

Level of polymorphisam	Low	Low to moderate	Low to moderate
Detecion of alles	Yes	No	No
Genome abundance	High	Very high	Very high
Radioactive detection	Usually yes	No	No

Advantages of marker assisted selection

1. It has many advantages as mentioned below
2. High speed
3. Detection of recessive alles
4. Consistency of results
5. Biosafety
6. High efficiency
7. Useful for mapping of Complex traits such as QTL mapping

Disadvantages of MAS

1. High initial cost
2. Require specialized skills and knowledge
3. Limited marker availability for some crop traits
4. Laborious process detection of various DNA marker
5. Genetic Background Effects
6. Ethical and Regulatory Issues: The use of genetic markers and biotechnology in breeding can raise ethical and regulatory concerns, particularly in regions with strict regulations on genetically modified organisms (GMOs).
7. Integration with Traditional Breeding: Integrating MAS with traditional breeding methods can be challenging, requiring careful planning and coordination

The success of a marker-based breeding system generally relies on three main factors:

- A genetic map with a sufficient number of evenly spaced polymorphic markers to accurately locate desired QTLs or major genes.
- Close linkage between the QTL or major gene of interest and nearby markers.
- Adequate recombination between the markers and the rest of the genome.
- The ability to analyze many plants in a time- and cost-effective manner

Mas Contribution to Crop Improvement

The intention of biotechnology in conjunction with traditional breeding is growing as a result of the genetic mapping of key genes and quantitative trait loci (QTLs) for numerous significant agricultural features. Through marker-assisted selection (MAS) of the traits throughout the breeding process, it is possible to take advantage of the information obtained from the map position of traits with agronomical relevance and of the associated molecular markers. The success of MAS, however, is dependent on a number of variables, such as the genetic basis of the traits, the number of individuals that can be analyzed, and the genetic background in which the target gene needs to be transferred, as demonstrated by empirical implementations of this process. In breeding programs, MAS for merely inherited traits is becoming more and more significant, enabling acceleration in plant breeding. Some significant examples of a potential routine use of MAS are traits linked to disease resistance to pathogens and to the quality of certain crop products. Even though there are a few successful applications in enhancing quantitative traits, a number of constraints have set serious limitations on the efficient exploitation of MAS in plant breeding for more complicated traits, such as yield and abiotic stress tolerance. A helpful tool for choosing genotypes with better agronomical performances is being made available by recent developments in genotyping technologies combined with comparative and functional genomics techniques.

Recent advances in Marker-Assisted Selection (MAS) have significantly enhanced plant breeding programs.

- **Improved DNA Markers:** The use of advanced DNA markers, such as Single Nucleotide Polymorphisms (SNPs) and Simple Sequence Repeats (SSRs), has increased the accuracy and efficiency of identifying desirable traits.
- **Genomic Selection (GS):** This approach uses genome-wide information to predict the breeding value of plants, allowing for more precise selection of traits. It has been particularly useful for complex traits influenced by multiple genes³.
- **Genome Editing:** Techniques like CRISPR/Cas9 enable precise modifications to plant genomes, accelerating the development of new varieties with improved traits.
- **High-Throughput Genotyping:** Advances in genotyping technologies have made it possible to analyse large numbers of samples quickly and cost-effectively, speeding up the breeding process.

- **Integration with Other Technologies:** Combining MAS with other genomic tools, such as Genome-Wide Association Studies (GWAS), has improved the understanding of genetic diversity and trait heritability

