

# Marker Assisted Selection: A Potential Tool in Crop Improvement

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MAS is most widely used to select desirable lines based on genotype rather than phenotype and is an indirect form of selection. Marker assisted selection (MAS) is linked to genes that control the trait of interest and is based on the identification and use of markers. Breeders used molecular markers aided selection methods to increase the precision of selection in breeding efficiency. Marker assisted selection (MAS) offers an efficient opportunity for combining single gene traits. Variety developed by MAS are not considered genetically modified organisms (GMOs) and are easily accepted by local and international market thus allowing for time and cost saving.

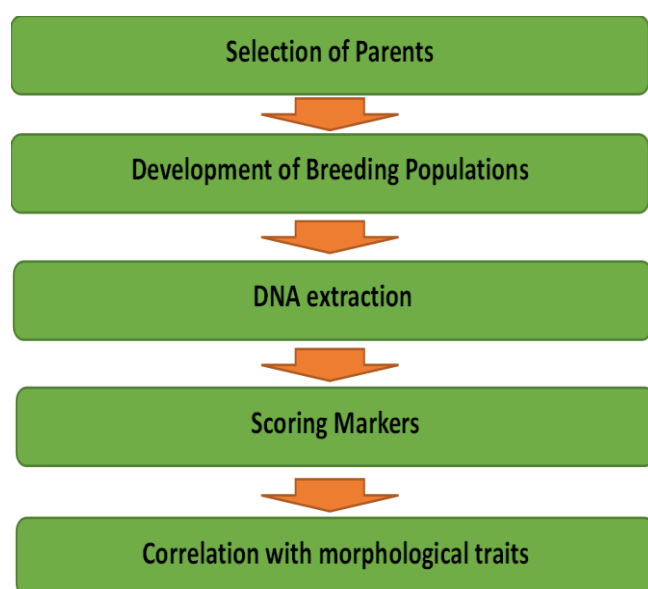
## Prerequisites for an efficient marker-assisted breeding program

- **High throughput DNA extraction:** An efficient DNA extraction system is needed for rapid selection of desired traits.
- **Genetic markers:** For a better marker assisted selection suitable markers are required. DNA markers are predominant types of genetic markers that are most commonly used in MAS programs however other markers (biochemical, morphological) can also be used. Some commonly used DNA markers are RFLP, SSR, RAPD, AFLP, SCAR, and SNP.
- **Genetic maps:** Linkage maps help identify marker-traits and choose markers for MAS.
- **Association between molecular markers and traits of interest:** For breeding program most crucial ingredient is knowledge of markers that are closely associated with traits.
- **Data management system:** An efficient system is required for labelling, storing, retrieving, and analysing large sets of data and producing reports useful to the breeder.

## Steps for Marker Assisted Selection

Various steps involved in Marker Assisted Selection (Figure 1) are:

- **Selection of Parents:** Selection of suitable parents for MAS should be done through germplasm screening and selection of homozygous (self-pollinated) or inbred (cross-pollinated) parents.
- **Development of Breeding Populations:** In this step the selected parents are crossed to obtain the F<sub>1</sub> population and detection of the marker alleles so as to remove false hybrids. Planting of segregating F<sub>2</sub> population along with screening of individuals and harvesting the ones with desired marker alleles. If F<sub>2</sub> population is homozygous then F<sub>3</sub> population can be used for screening of markers.
- **DNA extraction:** This involves DNA isolation from breeding population. For DNA isolation there is no need to wait for flowering or seed development stage as DNA isolation can be done through seedlings as well. The DNA is isolated with already available standard procedures. The isolated DNA is then digested and fragmented via restriction enzymes and then subjected to agarose gel electrophoresis.
- **Scoring Markers:** The marker polymorphism between the parents and their involvement in the recombinants in F<sub>2</sub> population is observed by using DNA probes. These DNA probes are labelled and helps in finding out the fragments having similarity. DNA probe hybridizes only with those fragments being complementary in nature.
- **Correlation with morphological traits:** Molecular markers are correlated with morphological and if the correlation is established then Marker assisted selection can be used effectively for genetic improvement of desired traits.



**Figure 1: Steps involved in Marker Assisted Selection**

## Applications of MAS

- ❖ Gene transfer of desirable trait from one species to other
- ❖ Improves the quality characteristics of cultivars of different crops
- ❖ Introgression of genes with desired traits from wild to cultivating variety
- ❖ Transfers resistance to biotic and abiotic stress in various crops
- ❖ Genetic improvement of tree species having late fruiting (around 20 years, which took long time for their phenotypic selection)
- ❖ Widely applicable for oligogenic traits than polygenic traits

## Recent Advances/ achievements /examples

Molecular marker technologies and the development of new plant varieties are the major areas for molecular breeding strategies. Introducing new varieties obtained via MAS is not subjected to restrictions as that of GM crop faces. Some examples of newly developed varieties using MAS are:

### Rice

The majority of people on earth eat rice as their main dietary source. Using markers in conjunction with selection has grown to be a common strategy for creating improved genotypes in rice. Through marker-assisted selection, it is possible to combine the desired traits from multiple genes into a single genotype. It is

typically employed for indirect selection of an important feature, such as disease resistance, productivity, or quality. Other traits of importance include biotic or abiotic stress tolerance. Microsatellites are the best molecular markers for plant breeding because they are widespread, have high rates of polymorphism, and are widely distributed throughout the genome. A variety of molecular markers have been utilised for marker-assisted breeding. The applicability of gene identification and pyramiding valuable genes has been substantially expanded by these molecular approaches. It is necessary to have thorough understanding of the genetic regulation of physiological qualities, the relationship between these physiological traits and molecular markers on chromosomes, and ultimately the genes underlying the traits. Researchers from all across the world have quickly embraced molecular markers as a useful and relevant tool for first studies addressing physiological features. Genetic linkage maps are a crucial tool for connecting marker loci to a particular plant trait.

Some examples with the gene or QTLs being introgressed or used for certain tolerance or resistance in plants are:

TRAIT	GENE/QTL	Reference
Submergence tolerance	<i>Sub1</i>	Rehman <i>et al.</i> , 2018
Drought tolerance	QTL	Jalil <i>et al.</i> , 2018
	<i>qDTY1.1, qDTY2.1, qDTY3.1</i> (QTLs) and <i>Sub1</i>	Sandhu <i>et al.</i> , 2019
Bacterial blight resistance	<i>xa13</i> and <i>xa21</i>	Balachiranjeevi <i>et al.</i> , 2018
	<i>xa21, xa3</i> and <i>xa5</i> ( <i>Samba mahsuri</i> )	Swamy <i>et al.</i> , 2020
Blast resistance	QTLs (On chromosome 1, 2, 11 and 12)	Srichant <i>et al.</i> , 2019
Salinity stress tolerance	<i>Saltol</i>	Yadav <i>et al.</i> , 2020
Pest resistance	<i>Bph3</i>	Qing <i>et al.</i> , 2019

Although susceptibility of rice to salt stress varies over the course of its life cycle. The effects are

most obvious during the seedling and reproductive stages. Therefore, use of MAS has proven to be the most effective method for creating improved salt-tolerant varieties. The bacterial blight disease *Xanthomonas oryzae* pv primarily affects rice. Pyramiding several resistance genes using MAS proved to be quite effective for *Oryzae*. A single rice variety with high yield, abiotic stress tolerance and biotic stress resistance as well as improved nutritional quality might be created using molecular markers with MAS in gene pyramiding.

### Wheat

Wheat is the oldest cereal crop and Marker assisted selection provides an opportunity for selecting desirable lines based on gene type rather than phenotype. Selection for a resistance gene can be carried out without exposing the plant to the pest, pathogen or environmental stress. Resistance in wheat against various diseases like leaf rust, stripe rust, stem rust etc is generally governed by few genes and can be tagged with any PCR based DNA marker. Developing resistant varieties for single disease would not be sufficient for saving plant product and to feed growing population of developing countries. So many diseases and environmentally reduced character together cause heavy yield loss therefore urges the need to redesign the experiments to develop multiple biotic and abiotic resistant varieties in wheat.

TRAIT	GENE/QTL	Reference
Powdery mildew resistance	<i>PmJM23</i>	Jia <i>et al.</i> 2020
Rust resistance	<i>Lr19, Lr24, LrTrK, S r26, Yr5, Yr10 and Yr15</i>	Mallick <i>et al.</i> 2021
	<i>Sr22, Sr26, and Sr50</i>	Randhawa <i>et al.</i> 2019
Moisture deficit stress tolerance	QTL	Puttamadanayaka <i>et al.</i> 2020
Soil-borne wheat mosaic virus	<i>Sbwm1</i>	Liu <i>et al.</i> 2020

### Conclusion

Plant breeding has made remarkable strides in crop improvement however the impact on variety development has been relatively small up to this point.

To utilize MAS to its full potential, greater breeding programme integration, a clear understanding of the current obstacles and the appropriate solutions are necessary. The use of various applications of MAS can have a great impression in crop improvement as opposed to traditional breeding. It is necessary to customise specific MAS tactics, such as how to use new marker technology to drastically cut the cost of MAS for certain crops, traits, and financial constraints, making MAS more generally usable for agricultural breeding operations.

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