# MARKER ASSISTED BREEDING TECHNIQUES

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Marker assisted selection or marker aided selection (MAS) is an indirect selection process where a trait of interest is selected based on a marker linked to a trait of interest (e.g. productivity, disease resistance, abiotic stress tolerance, and quality), rather than on the trait itself. This process has been extensively researched and proposed for plant and animal breeding.

1. Marker Assisted selection
2. Marker-Assisted Backcrossing
3. Marker-Assisted Gene Pyramiding
4. Marker-Assisted Recurrent Selection
5. Genomic Selection

## ❖ MARKER ASSISTED SELECTION

- Marker Assisted Selection (MAS): Indirect selection for a desired plant phenotype based on the banding pattern of linked molecular (DNA) markers.
- MAS is based on the concept that it is possible to infer the presence of a gene from the presence of a marker which is tightly linked to the gene of interest.

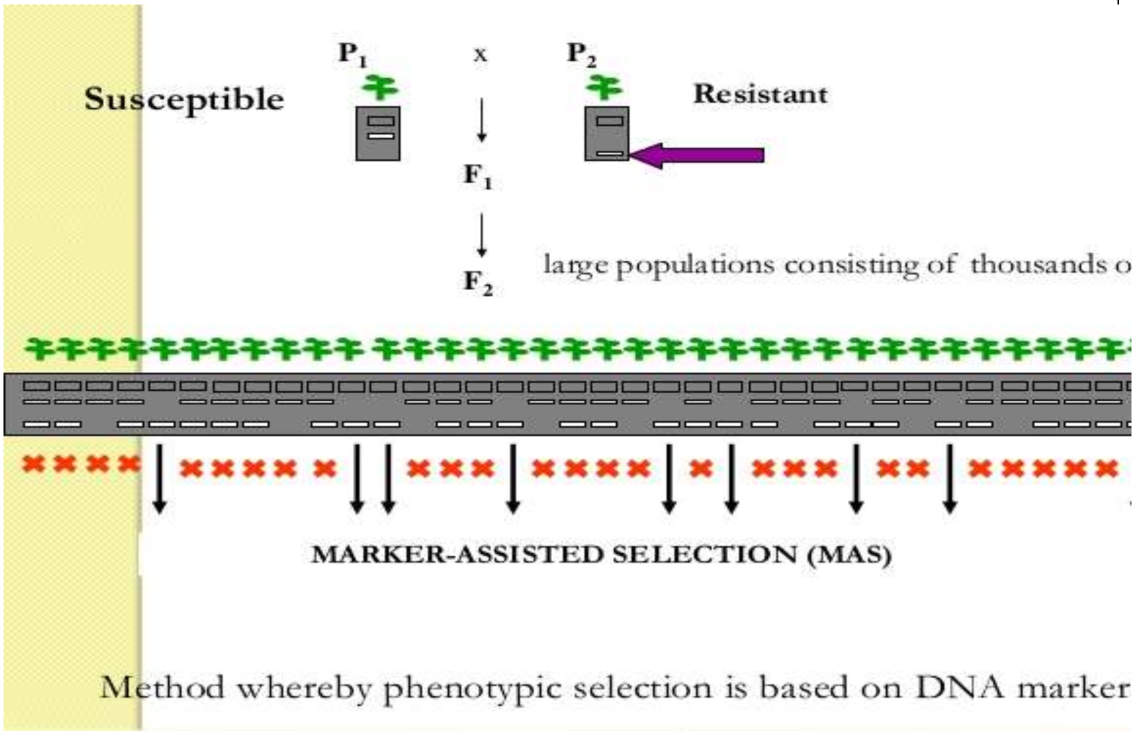
### ❑ Features of Marker Assisted Selection (MAS):

- **Pre-Requisites:**
  - ✓ A tight linkage between molecular marker and gene of interest, and
  - ✓ High heritability of the gene of interest.
- **Application:**
  - ✓ MAS is applicable for genetic improvement of plants as well as animals. In plants, it is equally applicable in both self-pollinated and cross pollinated species.
- **Efficiency:**
  - ✓ MAS is more efficient than purely phenotypic selection in quite large populations.
- **Accuracy:**
  - ✓ Molecular markers have very high accuracy. They are not affected by environmental conditions.
- **Speed of Progress:**
  - ✓ MAS is a rapid method of crop improvement. MAS permits identification of recessive alleles even in heterozygous condition and thus speeds up the progress of crop improvement work.
- **Traits Improved:**
  - ✓ MAS can be used for improvement of both oligogenic and polygenic traits.
- **Material Developed:**
  - ✓ MAS leads to development of non-transgenic genotypes or cultivars.

- **Cost:**
  - ✓ MAS is very costly as compared to phenotypic selection. MAS requires sophisticated and well equipped laboratory.

## APPLICATIONS OF MAS IN PLANT BREEDING

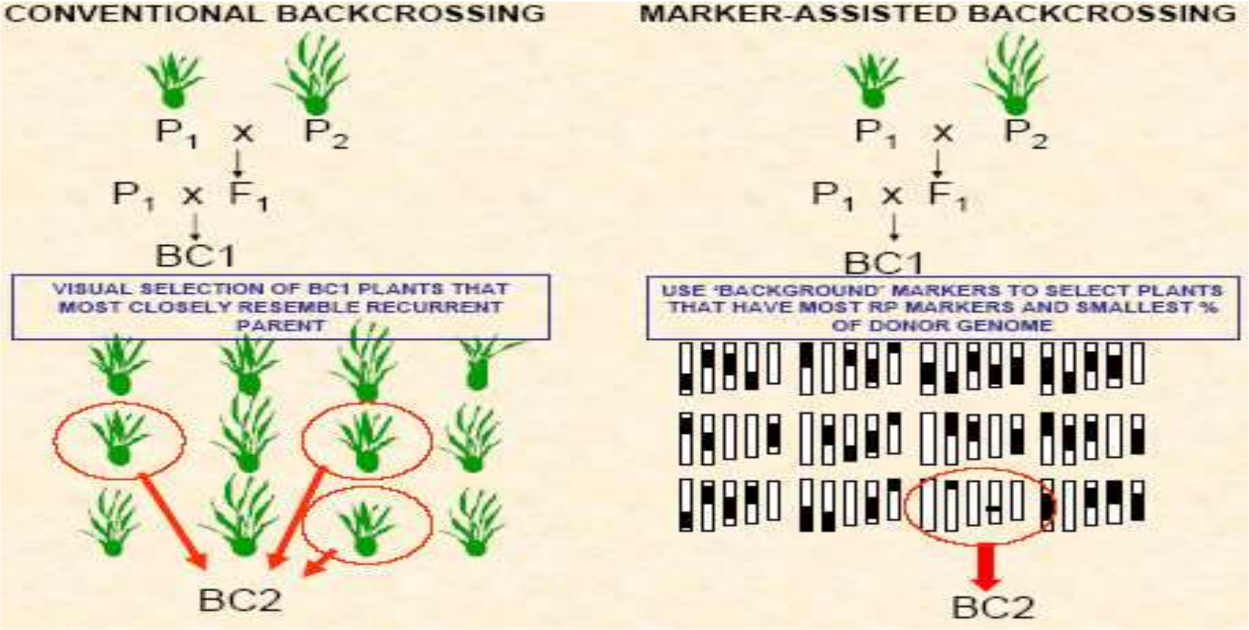
- ✓ MAS is very effective, efficient and rapid method of transferring resistance to biotic and abiotic stresses in crop plants.
- ✓ It is useful in gene pyramiding for disease and insect resistance**.**
- ✓ It is being used for transfer of male sterility and photo period insensitivity into cultivated genotypes from different sources.
- ✓ MAS is being used for improvement of quality characters in different crops.
- ✓ MAS can be successfully used for transferring desirable transgene from one cultivar to another.
- ✓ MAS is very effective in introgression of desirable genes from wild into cultivated genotypes.
- ✓ MAS is equally effective in genetic improvement of plants and animals.
- ✓ MAS is useful in genetic improvement of tree species where fruiting takes very long time (say 20 years) because for application of phenotypic selection we have to wait for such a long time.
- ✓ MAS has wide application for genetic improvement of oligogenic traits as compared to polygenic traits.



## MARKER ASSISTED BACKCROSSING

- MABC aims to transfer one or a few genes/QTLs of interest from one genetic source into a superior cultivar or elite breeding line to improve the targeted trait.

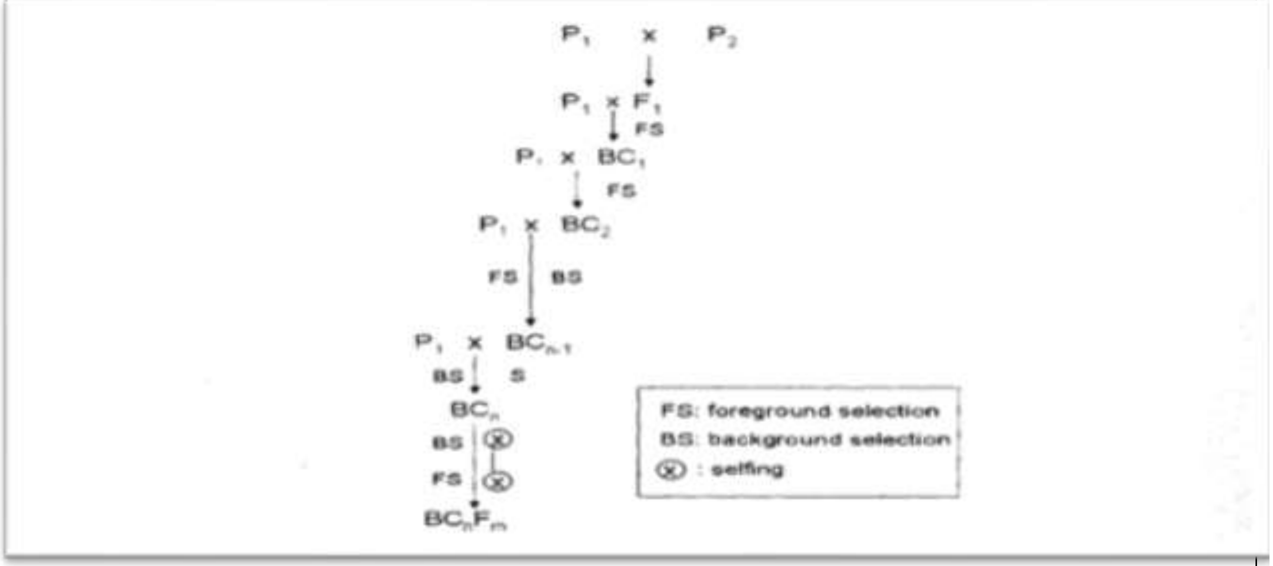
- Two levels of selection in which markers may be applied in backcross breeding.
- Select backcross progeny carrying the target gene which tightly linked to flanking markers (foreground selection)
- Select backcross progeny with background markers (background selection) to accelerate the recovery of the recurrent parent genome.



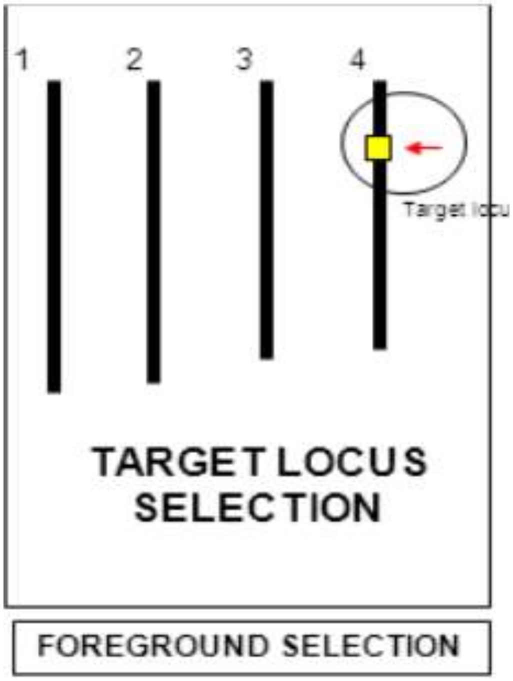
## Situations under which MABC is useful

(a) Phenotyping is difficult and/or expensive or impossible;
(b) Heritability of the target trait is low;
(c) The trait is expressed in late stages of plant development and growth, such as flowers, fruits, seeds;
(d) The traits are controlled by genes that require special conditions to express;
(e) The traits are controlled by recessive genes; and
(f) Gene pyramiding is needed for one or more traits.

## Procedure of MABC

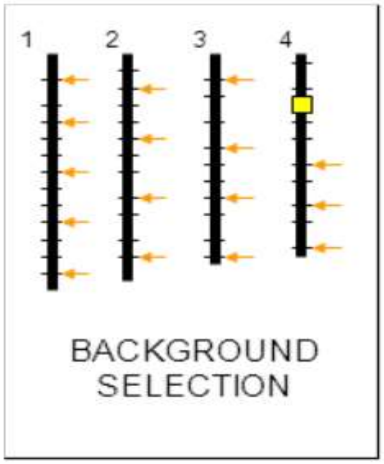


## Foreground selection



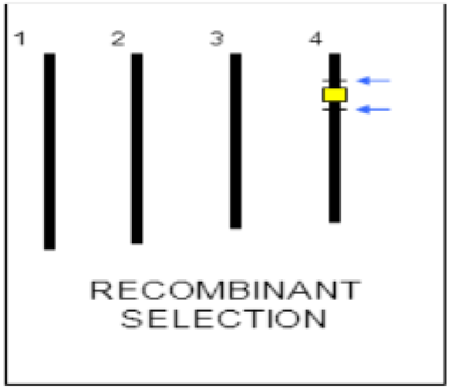
- Marker-assisted foreground selection was proposed by **Tanksley** (1983) and investigated in the context of introgression of resistance genes by Melchinger (1990).
- Foreground selection refers to **markers that are tightly linked to the gene of interest in order to select for the target allele or gene.**
- Markers that are flanking the target gene in the donor genotype are used for the selection of target gene.
- Useful for the traits that are difficult to evaluate
- Useful for recessive gene

## Background selection



- Marker-assisted background selection was proposed by **Young and Tanksley** (1989) to accelerate recovery of the recurrent parent genome (RPG).
- Background selection refers to markers that are not tightly linked to the gene of interest in order to select against other DNA from the donor parent Use unlinked markers to select against donor genome
- Accelerates the recovery of the recurrent parent genome
- Savings of 2, 3 or even 4 backcross generation may

## Recombinant selection



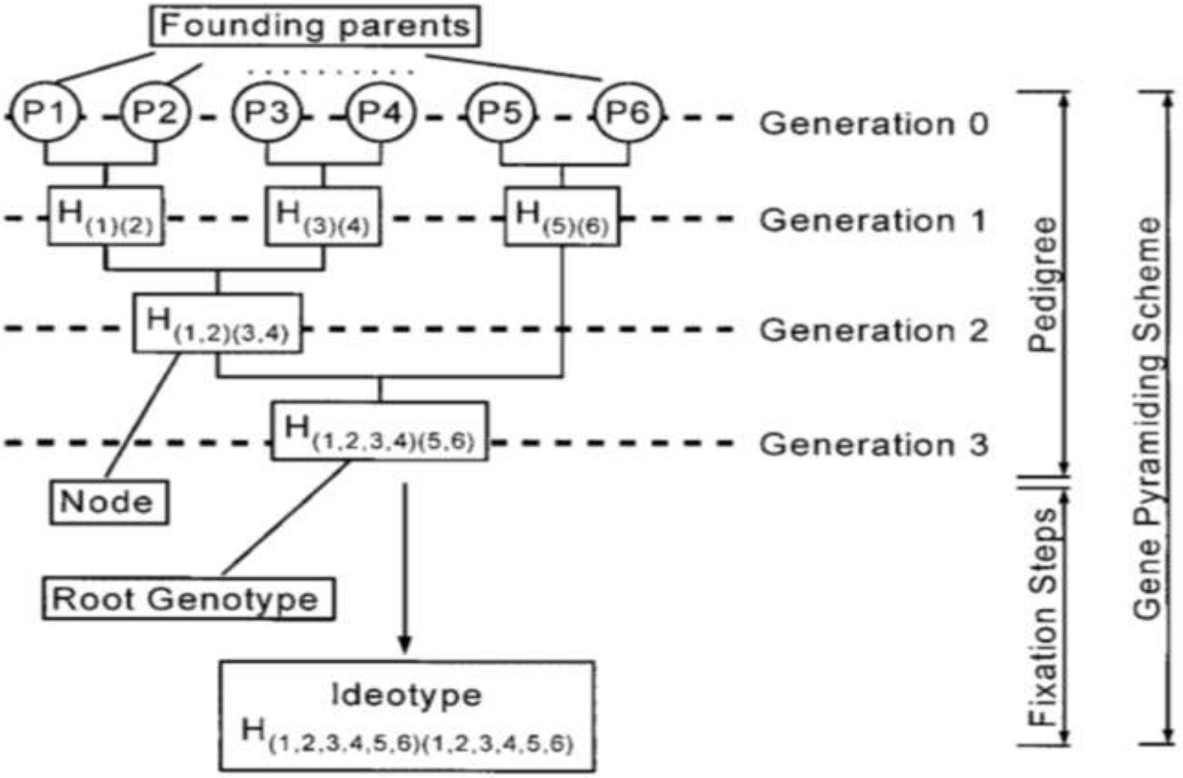
- ➢ Purpose: To reduce the size of the donor chromosome segment that is linked with the gene of interest.
- ➢ Linkage drag is minimized by using flanking markers (less than 5cM on either side) of target gene.
- ➢ Require large population sizes
- ➢ Depends on flanking markers from target

## ❑ Merits of MABC

(1) Efficient foreground selection for the target locus.
(2) Efficient background selection for recurrent parent genome.
(3) Minimization of linkage drag surrounding the locus being introgressed.
(4) Rapid breeding of new genotypes with favorable traits.

## ❖ Marker-Assisted Gene Pyramiding

- ➢ Pyramiding is the process of combining multiple gene/QTLs together into a single genotype. This is possible through conventional breeding but extremely difficult or impossible at early generations. DNA markers may facilitate because:
- ➢ DNA marker assays are non-destructive
- ➢ Markers for multiple specific genes/QTLs can be tested without phenotyping
- ➢ The most widespread application for pyramiding has been for combining multiple disease ressistance genes in order to develop durable disease ressistance.



A distinct gene pyramiding scheme cumulating six target genes.

## ❖ MARKER-ASSISTED RECURRENT SELECTION

- Marker-assisted recurrent selection (MARS) is a scheme which allows performing genotypic selection and intercrossing in the same crop season for one cycle of selection.
- Therefore, MARS could enhance the efficiency of recurrent selection and accelerate the progress of the procedure particularly helps in integrating multiple favorable genes/QTLs from different sources through recurrent selection based on a multiple-parental population.

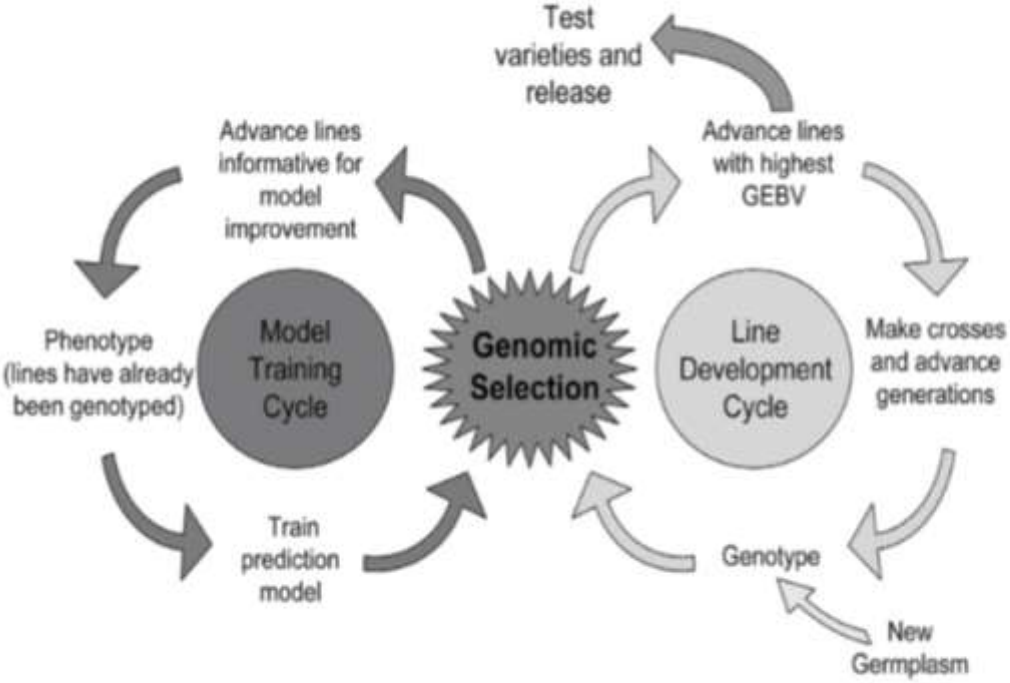
### ❑ Advantages of MARS over MABC

- ➢ When much of the variation is controlled by many minor QTLs (20-30 QTLs), MABC has limited applicability because estimates of QTL.
- ➢ Effects are inconsistent and gene pyramiding becomes increasingly difficult as the number of QTLs increases.
- ➢ A more effective strategy is to deploy MARS to increase the frequency of favourable marker alleles in the population.
- ➢ MARS breeding scheme give higher genetic gain as compared to MABC.

### ❑ Steps of MARS :

1) Defining a selection index for F2 or F2-derived progenies, use index to weight significant marker for target QTLs (20-30 QTLs).
2) Recombining selfed progenies of the selected individuals.
3) Repeat the procedure for a number of cycles.

## ❖ GENOMIC SELECTION



- Genomic selection (GS) is a new approach for improving quantitative traits in large plant breeding populations that uses whole genome molecular markers and combines marker data with phenotypic data in an attempt to increase the accuracy of the prediction of breeding and genotypic values.
- Breeding values are derived from Best Linear Unbiased Predictors (BLUPs) as the sum of BLUPs for all markers.
- Objectives of GS is to predict the breeding value of each individual instead of identifying QTL for use in traditional marker assisted selection (MAS) program.
- Require high-density molecular markers
- GS considers the effect of all markers together and captures most of the additive variation
- Marker effects are first estimated based on a so-called “training population” that needs to be sufficiently large (>300).
- Breeding value is then predicted for each genotype in the “testing population” using the estimated marker effects.

**References (if any)**

1. Advances in Plant Breeding Strategies: Breeding, Biotechnology and Molecular Tools, J. M. Khayri, S. M. Jain and D.V. Johnson, 1:431-472.
2. Molecular Plant Breeding, Yunbi Xu,286-327.

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