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MARKER ASSISTED SELECTION: ONE STEP TOWARDS FOOD SECURITY

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Introduction

Conventional plant breeding is primarily based on phenotypic selection of superior individuals among segregating progenies resulting from hybridization. Although significant studies have been made in crop improvement through phenotypic selections for agronomically important traits, considerable difficulties are often encountered during this process, primarily due to genotype-environment interactions. The markers have been used over the years for the classification of plants. Markers are any trait of an organism that can be identified with confidence and relative ease, and can be followed in a mapping population. In other words, they can be defined as heritable entities associated with the economically important trait under the control of polygenes (Beckman and Soller, 1986).

'Marker-assisted selection' (also called 'marker-assisted breeding' or 'marker-aided selection') may greatly increase the efficiency and effectiveness in plant breeding compared to conventional breeding methods. There are two types of markers: morphological markers and non-morphological markers (molecular markers). Morphological markers are those genetic markers whose inheritance can be followed with the naked eye.eg. plant height, colour of flowers, fruits and seeds, etc. Strauss *et al.* (1992) divided the molecular markers into two classes, biochemical molecular markers (eg. Isozymes) and genetic molecular markers (eg. RFLP, RAPD,etc). Genetic molecular markers are specific fragments of DNA that can be identified within the whole genome. They are found at specific locations of the genome. They are used to 'flag' the position of a particular gene or the inheritance of a particular characteristic. In a genetic cross, the characteristics of interest will usually stay linked with the molecular markers. Thus, individuals can be selected in which the molecular marker is present, since the marker indicates the presence of the desired characteristic. DNA based markers are used in cultivar identification, germplasm management, characterization of genetic diversity, population structure of wild relatives, phylogenetic analysis and marker assisted selection.

A. Morphological markers

Morphological markers are those traits that are scored visually or these are those genetic markers whose inheritance can be followed with the naked eye. The traits included in this group are plant height, disease response, photoperiod, sensitivity, shape or color of flowers, fruits or seeds etc. Although they are generally scored quickly, simply and without

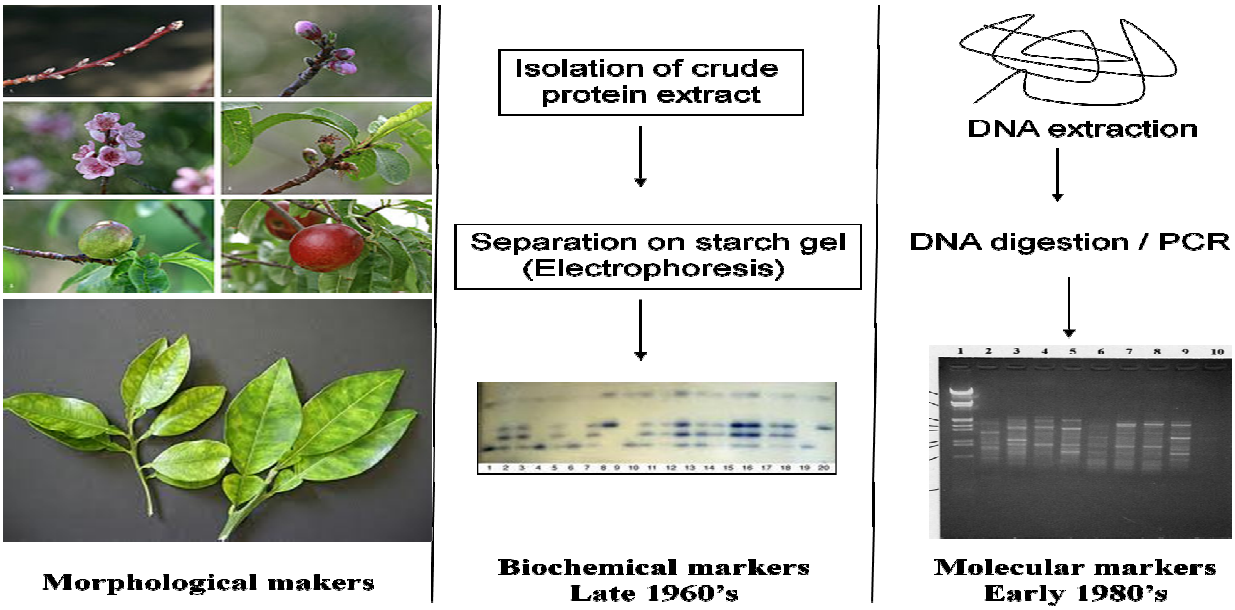
laboratory equipments, such markers are not put under too much use because of the following reasons: genotypes can be ascertained generally at whole plant or plant organ level and frequently the mature plant is used. Such markers frequently cause major alterations in the phenotype which is undesirable in breeding programs. Dominant, recessive interactions frequently prevent distinguishing all genotypes associated with morphological traits. Morphological markers masks the effect of linked minor gene, making it nearly impossible to identify desirable linkages for selection and are limited in number, influenced by environment and also specific stage of the analysis.

B. Non-morphological markers or molecular markers

Molecular markers are any kind of molecule indicating the existence of a chemical or a physical process. Strauss *et al.* (1992) distinguished the molecular markers into two classes: Biochemical molecular markers derived from the chemical products of gene expression i.e. protein based markers and molecular genetic markers derived from direct analysis of polymorphism in DNA sequences i.e. DNA based markers.

(i) Biochemical molecular markers

The first biochemical molecular markers used were the protein based markers. Proteins are attractive for direct genetic study because they are the primary products of structural genes. Changes in coding base sequence under many circumstances result in corresponding changes in the primary structure of proteins. One of the earliest protein based markers to be used was Isozyme. Market and Moller (1959) coined the term to describe the multiple molecular forms of the same enzyme with the same substrate specificity. In Isozyme analysis, crude plant extracts are subjected to electrophoresis using starch or polyacrylamide gels. Following electrophoresis, the enzymes of interest are detected by treating the gels with specific activity stains. Variation in bending patterns obtained between individual samples can be used to sort out genetically the varieties tested.



(ii) DNA based markers

DNA contains individual genetic blue print. The sequence of nucleotides in DNA of an individual is unique and thus determines its identity. The ultimate difference between

individuals lies in the nucleotide sequence of their DNA. The detection of such differences employing different molecular biological techniques led to the development of DNA markers. On plants DNA markers were first developed in 1985-86 by two groups of researchers working independently at native plants incorporated, USA and Cornell University Ithaca USA. DNA markers should not be considered as normal genes, as they usually do not have any biological effect and instead can be thought of as constant landmark in the genome. DNA markers are the identifiable DNA sequences found at specific locations on the chromosomes and transmitted by the standard laws of inheritance from one generation to the next one. They rely on DNA assay in contrast to morphological markers based on visible traits and biochemical molecular markers based on protein products by gene. So DNA is an ideal molecule for studying polymorphism.

Properties desirable for ideal DNA Markers

- Highly polymorphic nature: It must be polymorphic as it is polymorphism that is measured for genetic diversity studies
- Codominant inheritance: determination of homozygous and heterozygous states of diploid organisms
- Frequent occurrence in genome
- Selective neutral behaviours
- Easy access (availability): It should be easy, fast and cheap to detect
- Easy and fast assay
- High reproducibility
- Easy exchange of data between laboratories.

Marker Assisted Selection (MAS)

This is one of the important applications of molecular markers. MAS permit the breeder to make earlier decisions about the further selections while examining fewer plants. An added advantage in breeding for disease resistance behaviour is that this could be done in the absence of pathogen once marker information is available. Earlier markers were being developed for monogenic traits but present markers are developed for traits governed by multigenes or polygenes. Generally, the steps required for the development of markers for use in MAS includes: high resolution mapping, validation of markers and possibly marker conversion. Selecting plants in a segregating progeny that contain appropriate combinations of genes is a critical component of plant breeding. Moreover, plant breeders typically work with hundreds or even thousands of populations, which often contain large numbers (Witcombe and Virk, 2001). 'Marker-assisted selection' may greatly increase the efficiency and effectiveness in plant breeding compared to conventional breeding methods.

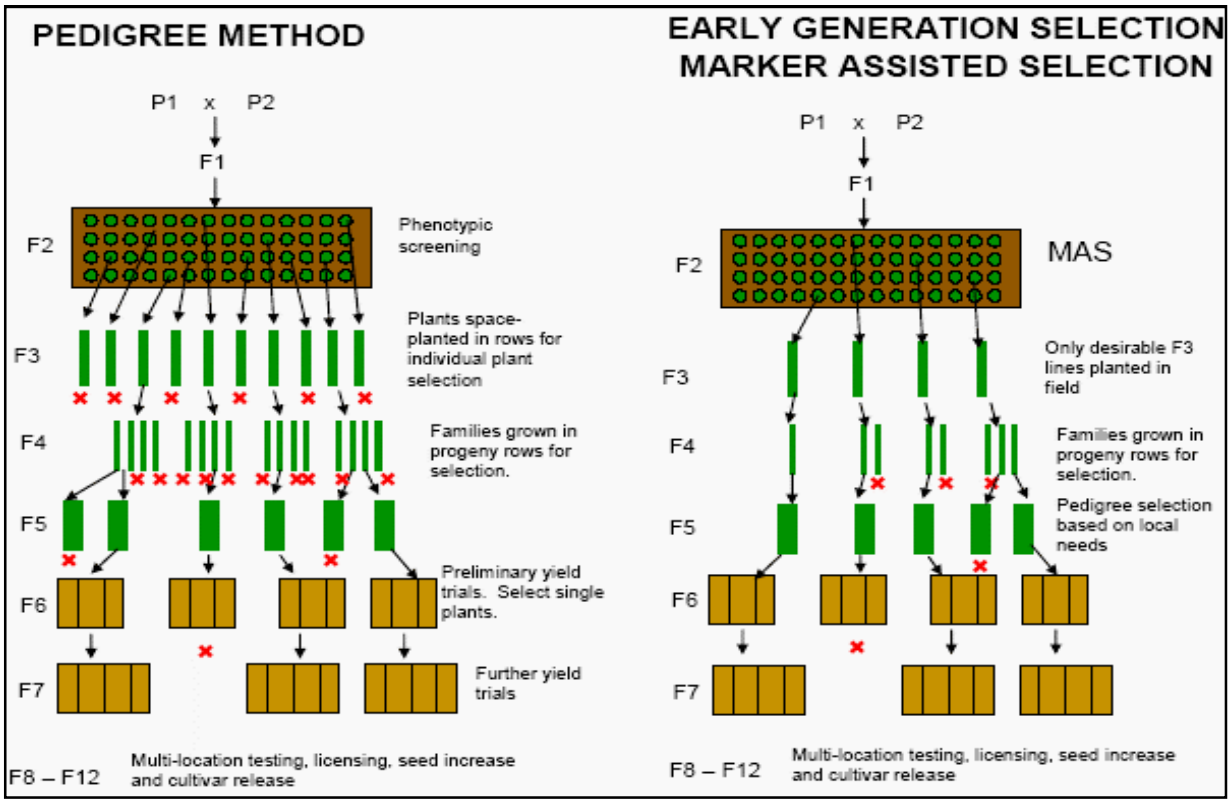
The advantages of MAS include

- Time saving from the substitution of complex field trials (that need to be conducted at particular times of year or at specific locations, or are technically complicated) with molecular tests.
- Elimination of unreliable phenotypic evaluation associated with field trials due to environmental effects.
- Selection of genotypes at seedling stage.
- Gene pyramiding or combining multiple genes simultaneously.

- Avoid the transfer of undesirable or deleterious genes ('linkage drag'; this is of particular relevance when the introgression of genes from wild species is involved).
- Selecting for traits with low heritability.

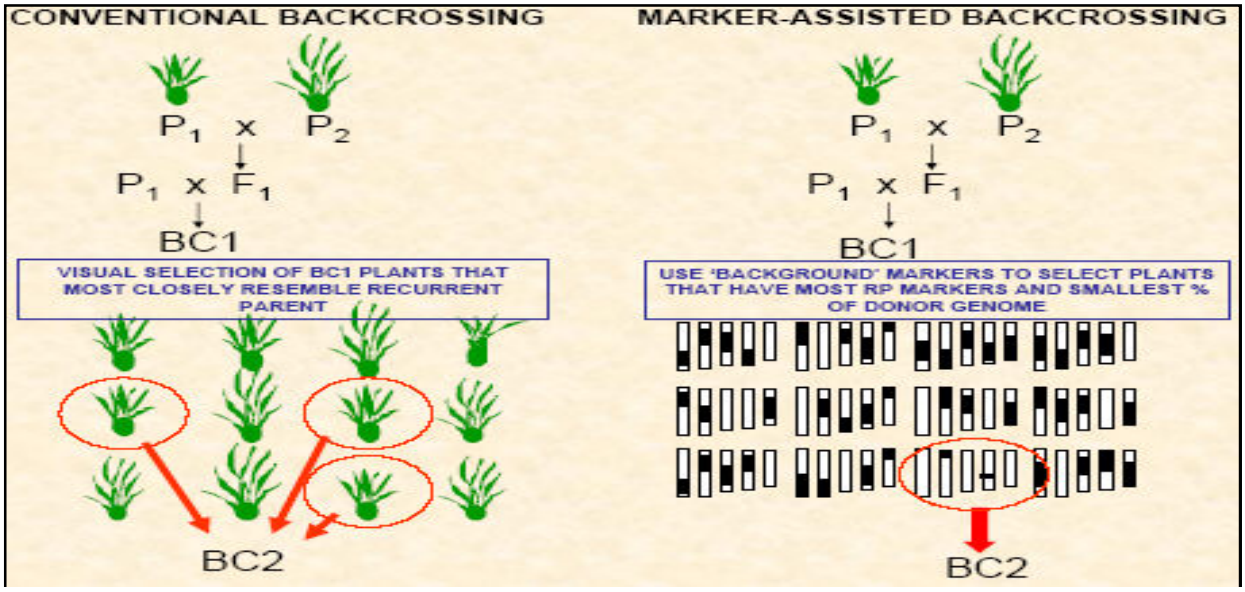
MAS requirements

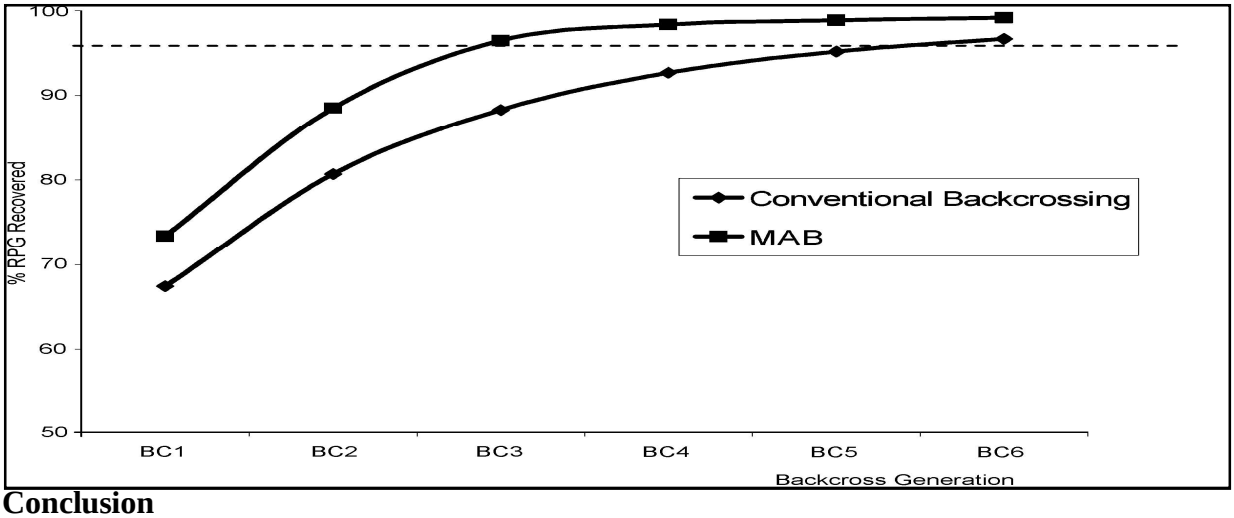
(i) A genetic map with an adequate number of uniformly-spaced polymorphic markers to accurately locate desired QTLs or major genes.
(ii) Close linkage between the QTL or a major gene of interest and adjacent markers.
(iii) Adequate recombination between the markers and rest of the genome.
(iv) An ability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



Marker assisted backcrossing

There are three levels of selection in which markers may be applied in backcross breeding. In the first level, markers may be used to screen for the target trait, which may be useful for traits that have laborious phenotypic screening procedures or recessive alleles. The second level of selection involves selecting backcross progeny with the target gene and tightly-linked flanking markers in order to minimize linkage drag. We refer to this as 'recombinant selection'. The third level of MAB involves selecting backcross progeny (that have already been selected for the target trait) with 'background' markers. With conventional backcrossing, it takes a minimum of five to six generations to recover the recurrent parent. Data from simulation studies suggests that at least two but possibly three or even four backcross generations can be saved by using markers.





Conclusion

Molecular markers have been widely applied to food and fiber crops. MAS can be effectively used in diverse and back cross breeding to produce new promising cultivars and to introduce desirable genes in existing well adapted cultivars. During the last few decades, the use of molecular markers, revealing polymorphism at the DNA level, has been playing an increasing part in genetics studies. Day by day development of new and specific types of markers makes their importance in understanding the genomic variability and the diversity between the same as well as different species of the plants.

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