Use of Marker Assisted Selection (MAS) in Crop Improvement

Tarkeshwar*, Ravi Prakash Chaudhary, Soni Singh, Govind Mishra and Shiva Nath

Dept. of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh (224 229), India

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Corresponding Author

Tarkeshwar
e-mail: tarkeshwar.barhaj2014@gmail.com

Abstract

Pyramiding multiple genes with potential characteristics into a single genotype through marker-assisted selection (MAS) can improve the efficiency of generating new crop varieties exhibiting disease resistance, as well as other desirable traits. Although markers can be used at any stage during a typical plant breeding programme, MAS is a great advantage in early generations because plants with undesirable gene combinations can be eliminated. Conventional breeding has got tremendous success towards feeding the world. But future demands, continuous development of new crop varieties to suitable to fight diverse problems in less time future. To address this problem MAS can be supplementary to conventional breeding programme.

Introduction

Markers are signpost used as reference to find out variations among the individuals. It can be morphological, biochemical or molecular/ DNA markers. Marker assisted selection (MAS) refers to the use of DNA makers that are tightly linked to DNA loci as a substitute for or to assist phenotypic screening. MAS is an indirect selection process where a trait of interest is selected 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.
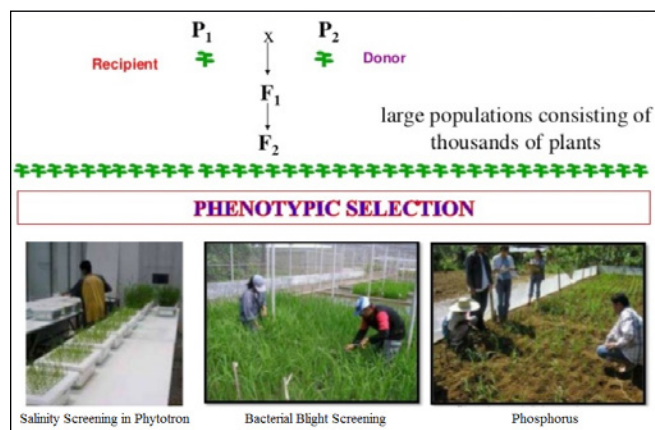

Figure 1: Conventional plant breeding

Potential Benefits from MAS

MAS is a simpler method compared to phenotype screening especially for traits with laborious screening. Here are the lists of some important advantages of MAS in crop improvement:

• It helps in more accurate and efficient selection of specific genotypes that may lead to accelerated variety development.

• It uses available resources more efficiently especially in the case of field trials.

• By the use of MAS selection can be done at seedling stage which is important for traits such as grain quality.

• Can select before transplanting in rice.

• It has increased reliability and no environmental effects.

• It can discriminate between homozygotes and heterozygotes and select single plants.
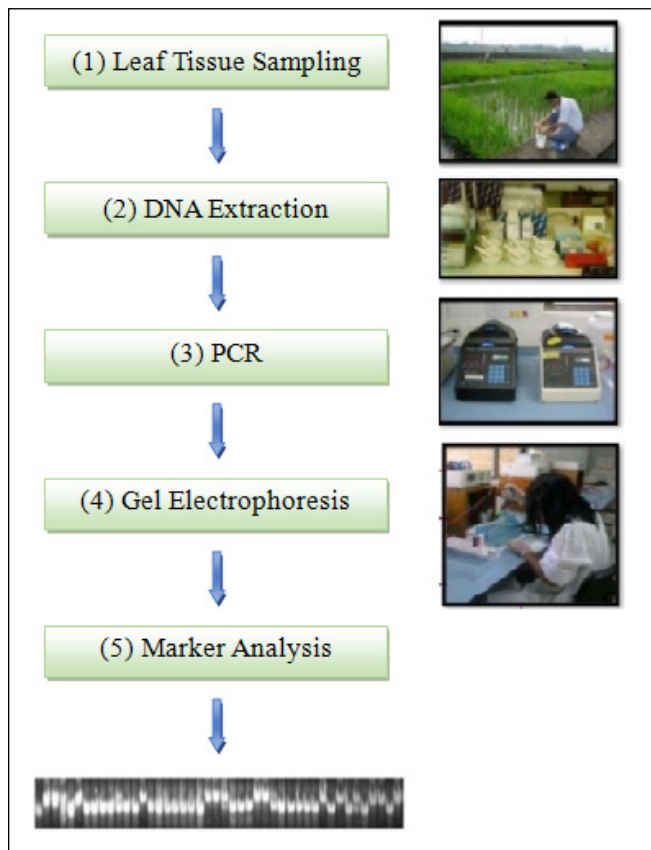
• May save time and resources.

Figure 2: An overview of marker genotyping platform

MAS Breeding Schemes

Four main breeding schemes are being used for marker assisted selection in plants *viz.,* marker assisted backcrossing, marker assisted pyramiding, early generation selection and combined approaches of above schemes.

1. Marker Assisted Backcrossing (MABC)

MABC has several advantages over conventional backcrossing *i.e.,* effective selection of target loci, minimizes linkage drag, accelerated recovery of recurrent parent *etc*. One of the most promising approaches of the MABC is the use of molecular markers to identify and select genes controlling resistance to those factors.

Selection of target gene or allele in MABC is of two types *i.e.,* foreground selection and background selection.

In order to select target gene or allele using markers that are tightly linked to the gene of interest is referred to as foreground selection, while background selection is the selection using markers that are not tightly linked to the gene of interest in order to select against other DNA from the donor parent.

2. Marker Assisted Pyramiding

Process of combining several genes, usually from two different parents, together into a single genotype. It is widely sued for combining multiple disease resistance genes for specific races or a pathogen. Pyramiding is extremely difficult to achieve using conventional methods *i.e.,* phenotyping a single plant for multiple form of seedling resistance almost impossible. It is very important method to develop durable disease resistance against different races.

3. Early Generation Selection

In this approach MAS is conducted at F_2 or F_3 stage. Plants with desirable genes or QTLs are selected and alleles can be fixed in the homozygous state *i.e.,* plants with undesirable gene combinations can be discarded.

Early generation selection gives advantage for later stages of breeding program because resources can be used to focus on fewer lines.

4. Combined Approaches

In some cases, a combination of phenotypic screening and MAS approach may be useful to following.

• To maximize genetic gain when QTLs have been identified from QTL mapping.

• Level of recombination between marker and QTL.

• To reduce population sizes for traits where marker genotyping is cheaper or easier than phenotypic screening.

Case Studies

• Pratap *et al.* (2017) introgressed Foc 2 gene in Pusa 256, an elite cultivar of *desi* chickpea and developed 5 highly wilt resistant lines.

• Hsu *et al.* (2020) derived five bacterial blight resistance genes (Xa4, Xa5, Xa7, Xa13 and Xa21) from a donor parent, IRBB66 and transferred into TNG82 via marker-assisted backcrossing breeding in order to improve TNG82's (Taiwanese *japonica* rice cultivar) resistance to bacterial blight.

• Tao *et al.* (2016) obtained ten BC3F5 lines by continuous backcrossing and selfing of Kanto 194 with Wuyujing 3, in conjunction with molecular marker-assisted selection (MAS) in order to improve resistance and quality of Wuyujing 3. The selected lines had homozygous Stv-biStv-biWx-mqWx-mq genotype and obtained agronomic traits similar to Wuyujing 3.

Conclusion

The fundamental basis of plant breeding is the selection of specific plants with desirable traits. Selection typically involves evaluating a breeding population for one or more traits. It may be simpler than phenotypic screening, which can save time, resources and effort. Selection can be carried out at seedling stage as well as single plants can be selected. These advantages can be exploited by breeders to accelerate the breeding process. Taget genotypes can be more effectively selected which may enable certain traits to be 'fast-tracked' resulting in quicker line development and variety release.

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