



Molecular Breeding for Sustainable Crop Improvement

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Abstract

DNA markers have enormous potential to improve the efficiency and precision of conventional plant breeding via marker-assisted selection (MAS). The large number of quantitative trait loci (QTLs) mapping studies for diverse crops species have provided an abundance of DNA marker-trait associations. The advantages of MAS and its most widely used applications in plant breeding, providing examples from cereal crops. Crop improvement is dependent on identifying desirable genes and superior genotypes with such genes in a breeding population. Marker-assisted selection aids in the selection of such genes and genotypes (MAS). This article describes traits for which MAS is used in various crops, as well as MAS products developed in India.

Keywords: Germplasm, Genetic resources, introgression

Introduction

Crop improvement depends on finding the best genotypes in a breeding population that carry the desired genes. Marker-assisted selection makes it easier to choose these genes and genotypes (MAS). MAS is the technique of selecting genes or traits indirectly using morphological, biochemical, or DNA-based/molecular indicators that are connected. Breeders genotype the population in order to indirectly choose desired genes or associated phenotypes and directly select for the presence of the markers. By doing this, MAS negates the need for phenotypic selection, which can be challenging, expensive, time-consuming, and dependent on the environment.

Molecular markers and MAS in plant breeding

Markers have been used for improved access and utilization of germplasm resources, gene/QTL mapping and tagging, backcross breeding, pyramiding and stacking. It has been reported that MAS can reduce the breeding cycle by about 4 years which would amount to saving \$200 million in 25 years.

- **Construction of genetic linkage map:** Molecular markers could be used to construct a highly saturated genetic linkage map for fine mapping or tagging of desirable traits in the plants.
- **Mapping and tagging of genes:** A large number of monogenic and polygenic genomic loci for various traits have been identified in many plants and are currently being exploited by breeders. Tagging of useful genes responsible for conferring resistance to plant pathogens and tolerance to abiotic stresses is a major target. Molecular markers have facilitated the construction of physical and genetic maps of genes/QTL in the genome. Table 1 gives a summary of the traits for which MAS is being applied in different crops.

Table :1 Traits for which MAS is being applied in different crops

S. No.	Crop	Trait
1.	Cotton	Fiber strength
2.	Broccoli	Resistance to diamondback moth
3.	Dry bean	<i>Sclerotinia</i> white mold resistance
4.	Chickpea	drought tolerance, <i>Fusarium</i> wilt disease
5.	White bean	Bean golden yellow mosaic virus (BGYMV), common bacterial blight resistance.
6.	Tomato	Black mold resistance, acyl sugar mediated pest resistance, bacterial spot and speck resistance, fruit quality
7.	Pepper	Tobamo virus resistance, tomato spotted wilt virus resistance, root-knot nematode resistance, potyvirus resistance
8.	Cucumber	Yield contributing traits, multiple lateral branching
9.	Maize	Corn borer resistance, seedling emergence, quality protein maize (QPM), earliness and grain yield.
10.	Pearlmillet	Disease resistance and grain yield
11.	Potato	Root-knot nematode resistance, potato virus X and Y resistance, root cyst nematode, wart resistance.
12.	Groundnut	Rust and late leaf spot disease, high oleic acid content
13.	Rice	Blast resistance, bacterial blight resistance, brown planthopper resistance, submergence, salt, drought, cold tolerance, cooking quality, eating quality, yield, heading date, genetic male sterility, basal root thickness, root traits
14.	Wheat	<i>Fusarium</i> head blight (FHB) resistance, leaf rust resistance, powdery mildew resistance, stripe rust resistance, cereal cyst nematode resistance, glutenin quality, preharvest sprouting tolerance (PHST), grain protein content, dough properties, durable rust resistance and height.
15.	Barley	Barley yellow mosaic virus I-III resistance, cereal cyst nematode resistance, barley stripe rust resistance, leaf rust resistance, loose and covered smut resistance, malting quality, yield
16.	Soybean	Soybean mosaic virus (SMV) resistance, resistance to frogeye leaf spot (<i>Cercosporasojina</i>), earworm resistance

- **Identification/DNA Fingerprinting:** The use of DNA markers in cultivar identification is particularly important for the protection of proprietary germplasm. The markers were chosen to fingerprint depends on their availability, genomic coverage, cost- effectiveness and reproducibility. DNA markers have also been used to confirm the purity of hybrid cultivars where the high level of genetic purity is essential. Marker-based identification has also been used to check adulteration of commercial medicinal plants. Sex identification in some dioecious plants is also facilitated by the use of molecular markers.

Diversity analysis of germplasm and heterosis breeding: Genetic diversity could be used to exploits transgressive segregants in self-pollinated plants and heterotic hybrids/heterosis in cross-pollinated crops. A genome-wide assessment of genetic diversity using molecular markers makes parental selection more efficient. Many studies also indicated the use of molecular markers to construct haplotype blocks that have been successfully used to predict hybrid performance.

- **Characterization of germplasm resources:** Markers could be used in the identification and elimination of duplicate accessions, construction of reference collection or working

collections or core collections and diversity analysis. Identification of crop varieties with the help of molecular markers could be beneficial.

Markers used in selection (Marker-assisted selection)

MAS is a process in which a linked marker is used for indirect selection of a genetic determinant or determinants of a trait of interest. This method involves the selection of plants carrying genomic regions that are involved in the expression of traits of interest through the application of molecular markers. The development and availability of a wide array of molecular markers and dense genetic maps in crop plants have made the application of MAS possible for both qualitative and quantitative traits. The success of MAS mainly depends on the distance between the flanking markers and the target gene. Further, markers help in selection at the seedling stage, selection for complex traits and simultaneous selection of several traits could be possible

Table 2: MAS products developed in India

Crops	Gene/QTL	Hybrid/variety	Characteristics	Reference
Groundnut	<i>ahFAD2A</i> and <i>ahFAD2B</i>	Girnar 4 and Girnar 5	High content oleic acid	ICAR-DGR, SAUs and ICRISAT
Rice		MAS 946-1	Drought tolerance	University Agricultural Sciences
	<i>xa13</i> and <i>Xa21</i>	Pusa 1460	BLB resistance	IARI New Delhi
	<i>Xa21</i> , <i>xa13</i> and <i>xa5</i>	RP Bio 226	BLB resistance	ICAR-IIRR
	<i>xa13</i> and <i>Xa21</i>	Pusa Basmati 1728	BLB resistance	IARI New Delhi
	<i>xa13</i> and <i>Xa21</i>	Pusa Basmati 1718	BLB resistance	IARI New Delhi
Maize	<i>opaque2</i>	VivekQPM 9	High-Quality Protein	IARI New Delhi
		The pro-vitamin rich version of VivekQPM 9	Enhanced pro- vitamin A, Fe and Zn content and also rich in lysine and tryptophan content	IARI New Delhi
Pear millet		HHB 67-2	Disease resistance	Haryana Agricultural University/ ICRISAT
Wheat	Pyramided <i>Lr76</i> - <i>Yr70/Lr37</i> - <i>Yr17.Lr37-Yr17</i> and <i>Sr38</i> genes	UnnatPBW343	Resistance to stripe, leaf and stem rust	It is also the first commercial product from PAU, Ludhiana as a wide hybridization program
	<i>PHST</i> QTL, <i>Lr24</i> and <i>Lr28</i>	HD2329	Tolerance to pre- harvest sprouting and resistance to leaf rust disease	CCSU, Meerut and IARI New Delhi

Introgression/Backcrossing and elimination of linkage drag

Commercial elite cultivars can be improved for a desirable trait that exists in distantly related genotypes such as wild species but lacks in the commercially grown cultivar. Conventionally, this is achieved by gene introgression which involves crossing the elite cultivar with the donor plant, followed by repeated backcrossing of the progeny with the recipient line, while selecting simultaneously for the desirable allele in each generation. This takes about 6 or more generations but the use of DNA markers can effectively shorten this duration by reducing the number of backcrosses required. MAS also allows recovery of the maximum proportion of recurrent parent genomic regions at the non-target loci (background selection) and thus help minimize linkage drag. This method is termed marker-assisted backcrossing (MABC). MABB has been used for the transfer of the gene for fruit colour from *L. hirsutum* and fruit size from *L. pimpinifolium* to tomato and yields QTLs from *O. rufipogon* to cultivated rice. Successful, gene introgression from *L. peruvianum* to *L. esculentum* has been done for root-knot nematode-resistant in tomato.

- **Gene pyramiding:** Markers have also been widely utilized for gene pyramiding. Pyramiding is the accumulation of several desired alleles into a single line or cultivar (background). This is often cited as one of the major applications of MAS since gene pyramiding through conventional plant breeding is difficult. *Xa4*, *xa5*, *xa13* and *Xa21* genes have been pyramided in rice variety IR24.
- **Map-based gene cloning:** Map-based gene cloning or positional cloning is the process of identifying the genetic basis of a mutant phenotype by looking for linkage to markers whose physical location in the genome is known. Molecular markers have been used for gene cloning *pto* gene in tomato and *Xa21* gene in rice.

Conclusion

Molecular breeding could be used for crop production in different ways. Table 2 enlists the crop varieties that have been developed in India using MAS. To speed up the implementation of MAS in plant breeding, the coordination between the molecular biologists and plant breeders is required.

References

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