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MARKER ASSISTED SELECTION: A POTENTIAL TOOL FOR CROP IMPROVEMENT PROGRAMME

Shaukeen Khan[1], Amit Dadheech[2], Baudh Bharti[3], Harikesh Jat[4] and Arjun Lal Regar[5]

Rajasthan College of Agriculture, MPUAT, Udaipur, Rajasthan- 313001, INDIA

Email of corresponding author: Shaukeen4@gmail.com

Marker assisted selection (MAS) refers to the use of DNA markers that are tightly-linked to target loci as a substitute for or to assist phenotypic screening. It is a combined product of traditional genetics and molecular biology. MAS allow for the selection of genes that controls traits of interest, such traits are colour, disease resistance, etc. Basic Assumption of DNA markers is to predict phenotype. MAS has become possible for traits both governed by major genes as well as quantitative trait loci (QTLs).

Knowledge of the genes for resistance to leaf rust caused by Puccinia recondita f. sp. tritici present in bread wheat (Triticum aestivum L.) cultivars and breeding lines is useful in developing resistant cultivars, estimating potential disease loss, and determining pathogen over-wintering (McVey DV, 1993). MAS refer to indirect selection for a desired plant phenotype based on the banding patterns of linked molecular markers. This technique is rapid, having high efficiency for crop improvement. This technique can bring a revolution in plant breeding for development of improved varieties. STS markers for identification of Lr19 and Lr24 in different genetic backgrounds have also been reported (Singh *et al.*, 2004). Barloy *et al.* (2006) pyramided the two CCN resistance genes in a wheat background through marker-assisted selection.

Why we require MAS?

1. To identify disease resistant plants out of big plant population based on morphological features is a complex task.
2. Moreover morphological characters are the result of gene and environment interaction.
3. Plant which appear resistant on the field does not necessarily posses resistant gene , the plant might have also escape the infection.
4. MAS has made this task very easy by precisely selecting desirable plants.

Role of MAS in crop improvement

1. Resistance breeding: Availability of tightly linked genetic markers for resistance genes will help in identifying plants carrying these genes simultaneously without subjecting them to pathogen or insect attack in early generations. The breeder would require a low amount of DNA from each individual plant to be tested without destroying the plant.

2. Gene pyramiding: Pyramiding of major/minor genes into cultivar for development of durable resistance/multiple resistance

3. Improvement of qualitative characters: It is Improvement in Quality traits by MAS like- Cooking Quality, Eating Quality, Appearance Quality in rice.

4. Molecular markers for hybrid vigour: Hybrids in crops such as maize, sorghum, rice, pearl millet, cotton, and several vegetable crops which have contributed greatly toward high yield potential of these crops through marker.

5. Abiotic resistance: Through molecular markers, biochemists and physiologists have identified specific traits which are useful in in improving drought responses such as osmotic adjustments, water use efficiency, and efficient root system. All these add to the yield improvement in crop plants.

6. Improvement of nutritional characters: Zn and Fe content in rice and bean are improved through MAS.

Conclusion : MAS is having potential role in population and inbred line development. The efficiency of MAS depends on the accuracy of phenotypic grouping of trait expression and the degree of linkage between the marker(s) andtarget traits. Marker allow desirable and useful alleles through pedigrees of breeding programmes or mined out of germplasm collections to serve as the basis for future varietals improvement. Molecular markers technique can be useful for breeding objectives by increase in the efficiency and reliability of selection. By Markers in combination with both QTL and association approaches may promotes the biotechnological innovative. Molecular markers offer great scope for improving efficiency of traditional plant breeding methods. Molecular marker genotyping can offer the gene pyramiding approach by reducing the number of generations. Gene Pyramiding technique with marker technology can integrate into existing plant breeding programme all over world to allow researchers to access, transfer and combine genes at a higher rate with precision.

References

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