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Marker Assisted Breeding Programme

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SUMMARY

Use of Molecular Markers in Breeding Programme Marker aided selection is a tool for breeding, wherein genetic marker(s) tightly linked with the desired trait/gene(s) are utilized for indirect selection for that trait in segregating/non-segregating generations. In its simplest form it can be applied to replace evaluation of a trait that is difficult or expensive to evaluate. When a marker is found that co-segregates with a major gene for an important trait, it may be easier and cheaper to screen for the presence of the marker allele linked to the gene, than to evaluate the trait. From time to time the linkage between the marker and the gene should then be verified. When more complex, polygenic controlled traits are concerned, the breeder is faced with the problem how to combine as many as possible beneficiary alleles for the QTLs that were detected. In this case, the breeding material can be screened for markers that are linked to QTLs. Based on such an analysis specific crosses can be devised for creation of an optimal genotype by combining QTL alleles from different sources.

INTRODUCTION

Marker assisted selection, when applied within the current breeding material to enhance a breeding programme, does not solve the problem of limited genetic variability that is often seen in breeding stocks. A different application of marker assisted selection could contribute to a genetic enrichment of breeding material. Marker assisted selection may be used to facilitate a controlled inflow of new genetic material. The wild species often carries desired components that may be missing in cultivated material. Such components can be transferred to elite cultivated material by repeated backcrossing. However, breeders are often reluctant to apply this method because of unpredictable linkage drag. These are caused by other genes, which are unintentionally transferred along with the genes that control the target trait. It may take considerable effort and screening to get rid of the unwanted genes and return the material to an acceptable agronomic value. Markers can be used to pinpoint the genetic factors that are responsible for the desired characteristics in the unadapted material. In a backcross programme, the presence of the desired QTL alleles can be verified continuously by observing linked markers.

Material required for MAS

A set of authentic lines carrying trait of interest and a population to validate the markers to be used e.g., F2 or BCF2 for each of the individual traits/genes.

Following are the basic pre-requisites for MAS :

- Search of molecular markers that are linked to the trait of interest.
- Validate the available markers in parents and breeding population .
- If markers are not available, it has to be designed and validated before use (if mapping populations are not available in hand it may take 2-4 years to generate and validate markers)
- Design a selection scheme and breeding strategy
- Fix the minimum population to be assayed to capture all beneficial alleles □
- Meticulous record keeping
- Progeny testing for fixation of traits.

Steps involved in MAS

-Validation of molecular markers. Extract the DNA from test individuals and find out whether there is one to one relationship with marker and the trait.

-Extract the DNA of breeding population at the seedling stage and apply MAS. Select the individuals on the basis of presence of desired molecular markers for the concerned trait. For other traits, selection is based on classical breeding methods. Minimum individuals to be assayed should be as per the defined strategy and statistical considerations.

MAS procedure

Marker-assisted selection (MAS) refers to such a breeding procedure in which DNA marker detection and selection are integrated into a traditional breeding program.

Taking a single cross as an example, the general procedure can be described as follow:

- Select parents and make the cross, at least one (or both) possesses the DNA marker allele(s) for the desired trait of interest.
- Plant F1 population and detect the presence of the marker alleles to eliminate false hybrids.
- Plant segregating F2 population, screen individuals for the marker(s), and harvest the individuals carrying the desired marker allele(s).
- Plant F2:3 plant rows, and screen individual plants with the marker(s). A bulk of F3 individuals within a plant row may be used for the marker screening for further confirmation in case needed if the preceding F2 plant is homozygous for the markers. Select and harvest the individuals with required marker alleles and other desirable traits.
- In the subsequent generations (F4 and F5), conduct marker screening and make selection similarly as for F2:3s, but more attention is given to superior individuals within homozygous lines/rows of markers.
- In F5:6 or F4:5 generations, bulk the best lines according to the phenotypic evaluation of target trait and the performance of other traits, in addition to marker data.
- Plant yield trials and comprehensively evaluate the selected lines for yield, quality, resistance and other characters of interest.

The generations of MAS required vary with the number of markers used, the degree of association between the markers and the QTLs/genes of interest, and the status of marker alleles. In many cases, marker screening is performed for two to four consecutive generations in a segregating population. If fewer markers are used and the markers are in close proximity to the QTL or gene of interest, fewer generations are needed. If homozygous status of marker alleles of interest is detected in two consecutive generations, marker screening may not be performed in their progenies.

Limitations of MAS

- Cost factor
- Requirement of technical skill
- Automated techniques for maximum benefit
- Per se, DNA markers are not affected by environment but traits may be affected by the environment and show G x E interactions. Therefore, while developing markers, phenotyping should be carried out in multiple environments and implications of G x E should be understood and markers should be used judiciously.
- DNA marker has to be validated for each of the breeding population. Any apriori assumption regarding the validity of markers may be disastrous. Marker assisted backcross breeding A backcross breeding programme is aimed at gene introgression from a “donor” line into the genomic background of a “recipient” line. The potential utilization of molecular markers in such

CONCLUSION

Marker assisted selection (MAS) MAS is most useful for traits that are difficult to select e.g., disease resistance, salt tolerance, drought tolerance, heat tolerance, quality traits (aroma of basmati rice, flavour of vegetables). The approach involves selecting plants at early generation with a fixed, favourable genetic background at specific loci, conducting a single large scale marker assisted selection while maintaining as much as possible the allelic segregation in the population and the screening of large populations to achieve the objectives of the scheme. No selection is applied outside the target genomic regions, to maintain as much as possible the Mendelian allelic segregation among the selected genotypes. After selection with DNA markers, the genetic diversity at un-selected loci may allow breeders to generate new varieties and hybrids through conventional breeding in response to targets set in breeding programme.

REFERENCES

Datta, D., Gupta, Sanjeev, Chaturvedi, S.K. and Nadarajan, N. (2011): Molecular Markers in Crop Improvement. Indian Institute of Pulses Research, Kanpur - 208 024.

Kahraman A, Kusmenoglu I, Aydin N, Aydogan A, Erskine W, and Muehlbauer F J. 2004. QTL mapping of winter hardness genes in lentil. Crop Sci. 44: 13-22.

Kumpatla, S.P., R. Buyyarapu, I.Y. Abdurakhmonov, and J.A. Mammadov. 2012. Genomics-assisted plant breeding in the 21st century: technological advances and progress. In: I.Y. Abdurakhmonov (ed.), Plant Breeding, InTech, pp 131-184.

Lecomte, L., P. Duffé, M. Buret, B. Servin, F. Hospital, and M. Causse. 2004. Marker-assisted introgression of five QTLs controlling fruit quality traits into three tomato lines revealed interactions between QTLs and genetic backgrounds. Theor. Appl. Genet. 109: 568-668.