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Marker Assisted Selection and it's Schemes in Plant Breeding

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Introduction :

Marker assisted selection (MAS) is a process in which a marker (morphological, biochemical or DNA/RNA variation based) is used for indirect selection of a trait of interest. It is indirect selection process where a trait of interest is selected based on a marker linked to it. For instance, if MAS is being used to select individuals with a disease, the level of disease is not quantified but a marker allele which is linked with disease is used to define the presence of disease. The assumption is that linked allele associates with the gene or quantitative trait locus (QTL) of interest. MAS is suitable for the characters which are difficult to measure, have low heritability and are expressed late in the development. At first, Sax (1923) showed the association of a simply inherited genetic marker with quantitative character in plants while he had detected segregation of seed size associated with a seed coat colour marker in beans (*Phaseolus vulgaris* L.). Rasmusson (1935) demonstrated linkage of flowering time (a quantitative trait) in peas with a simply inherited gene for flower colour.

The Gene vs marker

The gene of interest is straight related with protein production. This protein produces certain phenotypes. In contrary markers should not effect the character in study but it is genetically linked. In many characters, genes are discovered. They can directly be examined for their presence with a great level of confidence. Nevertheless, if a gene is not isolated, then we have to take marker's help to tag a gene of interest. In this case, there may be some false positive results because of recombination between marker of interest and gene or QTL. A perfect marker would cause no false positive results.

Steps involved in Marker Assisted Selection

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Generally the first step is to map the gene or QTL of interest first by using different techniques and then use this information for marker assisted selection. Usually, the markers to be used should be close to gene of interest and there distance should be less than 5 recombination unit or centi Morgon (cM). This is because one have to ensure that only negligible fraction of the selected individuals will be recombinants. Normally, two markers are used so as to reduce the probabilities of an error as a result of homologous recombination. For instance, if two flanking markers are used at the same time with an interval of 20cM, so there is higher probability (99%) for recovery of the target gene.

Single Step Marker Assisted Selection and QTL mapping

Contrary to two-step QTL mapping and MAS, a single-step method for breeding characteristic plant populations has been advanced. In this approach, first few breeding cycles includes, identification of markers linked to the trait of interest by QTL mapping and then the same data is used in the same population. Again in this method, pedigree structures are derived from families. These families are created by crossing number of parents (in three-way or four way crosses). Phenotyping and genotyping is done using molecular markers and mapped the possible location of QTL of interest. This will categorize markers and their favourable alleles. Once these promising marker alleles are detected, the frequency of such alleles will be increased and response to marker assisted selection is calculated. Marker allele(s) with needed effect will be supplementary used in next selection cycle or other experiments.

Use of MAS for backcross breeding:

A minimum of five to six-backcross are needed to transfer a gene of interest from the donor to a recurrent-adapted cultivar. The recovery of the recipient genotype can be speeded with the use of molecular markers. If the F_1 is heterozygous for marker locus, plants with recurrent parent allele(s) at the marker locus in first or succeeding backcross will also carry a chromosome tagged by the marker.

Advantages of marker-assisted selection:

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Marker-assisted selection may significantly be enhances the productivity and efficiency for breeding as compared to conventional breeding. The important advantages of MAS compared to conventional phenotypic selection are enlisted here as,

1. Very simple as compared to phenotypic screening
2. Selection may be carried out at seedling stage
3. Single plants may be selected with high reliability.

These advantages may changes into (1) more efficiency or (2) enhanced line development in breeding programs. For example, time and labour savings may arise from the substitution of difficult or time-consuming field trials with DNA marker tests. Additionally, selection depends on DNA markers may be more consistent due to the effect of environmental factors on field trials. Additional benefit from MAS is that the, total number of lines that need to be tested may be reduced. As many lines can be discarded after MAS at early stage, this allows a more effective breeding design. The greater efficiency of target character selection which may allow certain traits to be 'fast-tracked', since some genotypes can be easily identified and selected. Furthermore, 'background' markers may also be used to hasten the recovery of recurrent parents during marker-assisted backcrossing.

Schemes of Marker Assisted Selection in plant breeding :

1. **Marker assisted backcrossing :**

   In total, there are three levels of selection in which markers may be useful in backcross breeding. In the first level, markers are used to screen for the trait of interest, which may be useful for those traits which are laborious in phenotypic screening procedures or those have recessive alleles. The second level of selection includes selection of backcross progeny with the gene of interest and tightly-linked flanking markers so as to minimize linkage drag i.e. recombinant selection. The third level of MAB involves selecting backcross progeny with 'background' markers. In other words, markers can be used to choose against the donor genome, which may speed up the genome recovery of recurrent parent. By using conventional backcrossing, it would takes minimum of five to six generations to recover the recurrent parent. As a minimum two but perhaps three or even four backcross generations can be set aside by using markers.

2. **Marker assisted pyramiding** :

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"Pyramiding is the process of simultaneously combining multiple genes or QTLs together into a single genotype". This is possible through conventional breeding but very much difficult at early generations. By using conventional phenotypic selection, specific plants must be phenotypically screened for all the characters tested. Hence, it may be very problematic to evaluate plants from certain population types (e.g. F_2). As DNA marker assays are non-destructive, DNA markers may ease selection and markers for multiple specific genes or QTLs can be tested using a single DNA sample without phenotyping. The most extensive use of pyramiding has been for merging several disease resistance genes in order to develop long-lasting or durable disease resistance.

3. **Early generation marker assisted selection :** One of the most spontaneous stage to use markers to select plants is at an initial generation. The key advantage is that many plants with undesirable gene combinations, particularly those that lack vital disease resistance traits and plant height, can be simply rejected. This has important significances in the advanced stages of the breeding program because the evaluation for other characters can be more efficiently and inexpensively planned for less breeding lines.