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Genetics

AN OVERVIEW ON SMART BREEDING APPROACH

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ABSTRACT SMART Breeding is a term that refers to marker-assisted selection, which involves selecting plants based on genotype rather than phenotype. SMART Breeding has made a quiet revolution in recent years because it does not discourage the use of conventional breeding. Hence SMART Breeding approach for crop improvement helps in enhancing the efficiency of conventional methods and indirectly it helps in accelerating breeding cycle and feeding the entire population within short period of time. Among the various approaches, Several approaches like MAS, MABC, MAGP, Combined MAS, PPB has been discussed in this paper.

KEYWORDS : SMART, MABC, MAS, MAGP, PPB

INTRODUCTION

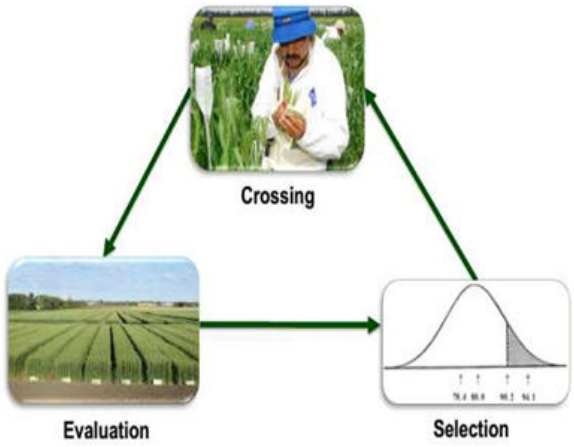

Fig-1 Areas where Breeding works

These are the three main areas where actually breeding work starts:-

1. Crossing
2. Selection and
3. Evaluation

Challenges faced during the screening of plants by conventional methods:-

Feeding the world within the planet's carrying capacity (2x more with 2x less)-Population in the country/world is rapidly growing, but production is not keeping up, so we may face a food shortage in the future. Since the time is short due to this population rate, the production should be increased and be able to meet out food demand of world by using some other modern techniques. Since we are running out of time, breeders should not scrimp on the selection process, which is a crucial step in any crop improvement. Instead, we should abandon traditional breeding and pursue a new method called SMART breeding to meet the world's food demand.

SMART :- Selection with Markers and Advanced Reproductive Technologies

SMART Breeding is a term that refers to marker-assisted selection, which involves selecting plants based on genotype rather than phenotype. SMART Breeding has made a quiet revolution in recent years because it does not discourage the use of conventional breeding. Rather, it seeks to improve the performance of the existing system.

STEPS INVOLVED IN MARKER ASSISTED SELECTION:-

- Selection of parents:- selection of plants is done based on phenotypically which are superior phenotypically.
- Development of breeding population:- Among the selected plants, breeding populations like F_2, Backcross progenies and RIL's are developed.
- Isolation of DNA from each plant:- From each of the plants DNA is taken out for running the gel and to identify banding pattern.
- Scoring markers:- Here markers with specific traits are known, which is used as base to screen in their segregating populations derived from the selected plants.
- Correlation with morphological traits:- By comparing with parental bands and progeny bands, we can able to identify the plants with a particular traits and presence of particular genes.

EARLY GENERATION MARKER-ASSISTED SELECTION:-

While markers can be used at any stage of a traditional plant breeding programme, MAS has a significant advantage in early generations because it allows undesirable gene combinations to be eliminated. This allows breeders to focus attention on a lesser number of high-priority lines in subsequent generations. Due to the high selection pressure, population sizes may quickly become very small, allowing for genetic drift at non-target loci. It is therefore recommended that large population sizes be used, or that this issue be reduced by using F3 populations rather than F2 populations, since the selected proportion of an F3 population is greater than that of an F2 population.

SLS-MAS (Single Large Scale MAS)

The main objective of SLS-MAS is to use marker once and to select plant only once in early generation from entire population.

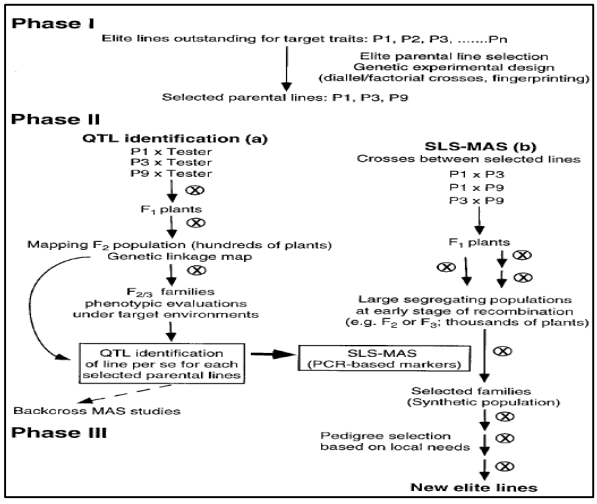

Fig-2 Scheme for SLS- MAS

In phase-1, the selected parental lines should have high GCA (to regain

its hybrid performance in its offsprings) and allelic complementality (should have favourable allele at non target loci also). In phase-2, QTL identification works on principle that gene and marker segregate during meiosis, so that we can analyse banding pattern in their progenies. QTL mapping is done in 3 steps:-

- Population mapping (to get segregating populations)
- Identification of polymorphism (to distinguish between parental lines)
- Linkage analysis (computerised program, where we can know the presence of particular genes/traits in particular progenies)

Tester used should be of low value and recessive in nature, so that dominance of parental line can be easily known. Then, by using these QTL lines, early generation MAS is done among the F_2 progenies derived from parental lines. Once the progenies identified, then advancing generation of those lines is done in order to develop elite lines. In phase-3, the QTL identified lines which are superior can also be used as parental lines during breeding programme. This method was used by Ribaut and Betran, 1999.

MARKER-ASSISTED BACKCROSSING (MABC) :-

Backcrossing is crossing of F_1 with either of the parents

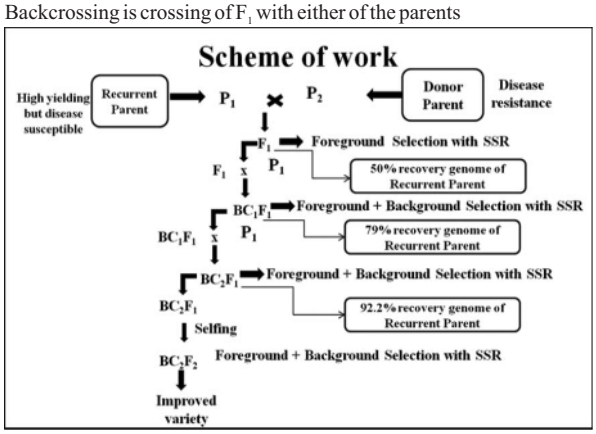

Fig-3 Schematic diagram for Marker assisted backcrossing

Here P_1 is recurrent parent with high yielding and P_2 is donor parent with disease resistance genes in it. Main aim is to transfer donor gene in to recurrent parent with background genome of recurrent parent. So, backcrossing of F_1 is done with parent1 and progenies with donor gene is selected based on foreground selection. For 2-3 generations, continuous backcrossing of F1 is performed to obtain recurrent parental genome, resulting in 92 percent recurrent parental genome at BC2F1. Finally, based on foreground and background selection, we will pick backcrossed progeny that look close to the recurrent parent and have the donor gene present (Hasan *et al*., 2015)

MABC involves 3 types of selection:-

- Foreground selection (controls donor gene)
- Recombinant selection (controls linkage drag)
- Background selection (controls recurrent parent)

Foreground selection :- The objective is to maintain the target locus in a heterozygous state (one donor allele and one RP allele) until the final backcross is completed. Then, the selected plants are self-pollinated and progeny plants identified that are homozygous for the donor allele.

Recombinant selection:- Recombinant selection is the process of selecting BC progeny with the target gene and recombination events between the target locus and related flanking markers. The aim of recombinant selection is to make the donor chromosome segment that contains the target locus smaller (i.e. size of the introgression). This Recombinant selection is important because the rate of decrease of this donor fragment is slower than for unlinked regions.

Background selection:- Background selection is when closely connected flanking markers are used to select recombinants and unlinked markers are used to select RP. Background markers are chromosome-wide markers that are unlinked to the target gene/QTL, or markers that can be used to discriminate against the donor genome. Since RP recovery can be significantly improved, this is extremely beneficial. The use of background selection during MABC to accelerate the development of an RP with an additional one or more genes has been referred to as 'variety development or enhancement' and 'complete line conversion'

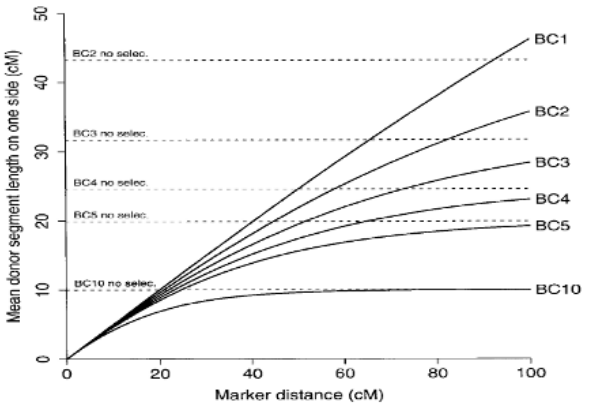

Fig-4 Graph showing the reduction in linkage drag

Length of reduction in donor fragment mainly depends on 3 factors:-

- Number of backcross generations performed
- Number of double recombinants formed
- Distance between marker and genes

But, number of backcross generations and double recombinants affect very less in reduction of linkage drag when compared to distance between marker and gene. For linked gene (i.e < 20 CM) reduction in length of donor segment is very less even for many backcrossing generations, but for unlinked genes, the number of backcross generations plays a very important role in reducing the linkage drag.

MARKER ASSISTED GENE PYRAMIDING (MAGP):-

Pyramiding is a breeding technique that involves stacking genes from various parents in one progeny. One of the most important applications of molecular markers to plant breeding is MAGP, which is one of the most successful methods for accumulating multiple resistance genes. It's used to describe quantitative characteristics (governed by many genes).

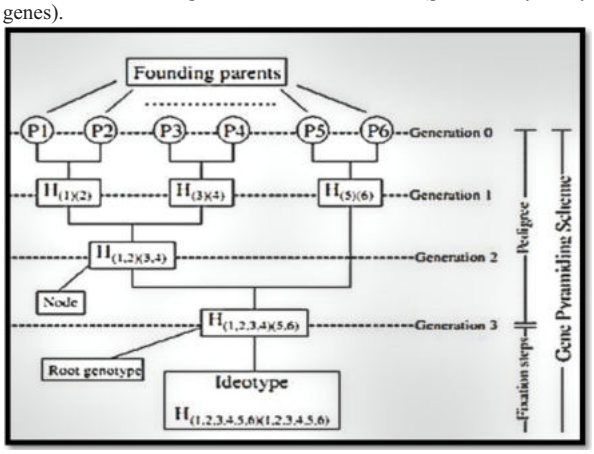

Fig 5- Distinct gene pyramiding scheme cumulating six target genes

Each of the tree's nodes is referred to as an intermediate genotype, and it has two parents. The intermediate genotypes are not just any offspring of a given cross; they are a specific genotype chosen from among the offspring that contains all of the parental target genes. A potential technique for the fixation steps is to generate a population of doubled haploids from the root genotype. Here, a population of gametes is obtained from the genotypes and their genetic material is doubled. This leads to a population of fully homozygous individuals, among which the ideotype can be found. Using this process, the ideal genotype can be obtained in just one additional generation after the root genotype is obtained. However, in some plant species, growing a large population of doubled haploids is difficult and time-consuming. Selfing the root genotype directly to obtain the ideal genotype is an alternative to this approach. Selfing the root genotype, on the other hand, will result in a break in linkage between the desired alleles, which will be difficult to detect because the linkage process is rarely

visible. (Tyagi *et al*., 2014). Similar study conducted by Rajpurohit *et al* 2011.

Crossing the root genotype with one of the founding parents. In such programs, the linkage will still be known, and the selection will be for genotypes that are homozygous for the target gene brought by the founding parent but heterozygous for other regions. Eibach *et al*., 2011 used this method in grape vine breeding.

COMBINED MARKER ASSISTED SELECTION:-

In some cases, a combination of phenotypic screening and MAS approach may be used when some QTLs have been unidentified from QTL mapping. It is used when the marker is not 100% accurate and for the traits where marker genotyping is cheaper or easier than phenotypic screening

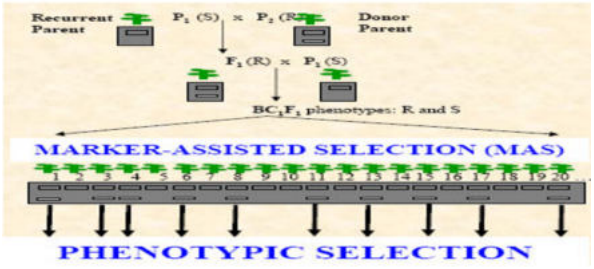

Fig-6 Schematic diagram for combined marker assisted selection

PARTICIPATORY PLANT BREEDING (PPB) :-

- PPB is the involvement of farmers in selection of parents/plants in which farmers prefered cultivars/ plants are taken as ideal plants for plant breeding programme. (Kanbar *et al*., 2011)

Methods :-

1) Consulatative :- Here at each and every stage of crop growth consultancy from farmers is taken for selection of plants during crop breeding
2) Collabrative:- Here farmers are allowed to grow crops and the lines which farmers feel good, such kind of lines are taken for crop breeding.

Drawbacks:-

- IPR issues makes it more complicated for private companies:- Because the benefits should also be shared to farmers since they are also involved in breeding programme.
- Competitors should gain access to genetic materials only which are grown in farmers field

How MAS outcompetes Genetic engineering:-

- MAS respects the species barrier::- Whatever genes used for introgression are taken from natural gene pool and related species only, unlike from unrelated species in genetic engineered crops.
- MAS raises fewer safety concerns:- These varities are as safe as that of conventionally bred varities and are not hazardous.
- MAS requires less investment:- It might have high cost than convention method, but when compared to GE varities it is less investment and it doesn't make sense if we use GE for low value and non commercial crops.
- MAS bred cultivars/lines are accepted by consumers:- These are not having any ethical beliefs of acceptance as like in GE varities i.e about harmfulness and consumption of food derived from GE crops
- Comparision between MAS bred varities & genetically engineered varities:- Till now 28 genes were developed in rice for drought resistance by MAS and all are available, but by GE approach only few lines were developed and are not yet commercialized..

CONCLUSION:-

SMART Breeding approach for crop improvement helps in enhancing the efficiency of conventional methods and indirectly it helps in accelerating breeding cycle and feeding the entire population within short period of time.

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