Marker-Assisted Backcrossing (MABC) in Plant Breeding

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Marker-assisted backcrossing (MABC) is a breeding technique that uses molecular markers to identify and select genes controlling resistance to those factors. It is one of the most promising approaches in breeding programs for gene introgression.

In marker-assisted backcrossing, the goal is to incorporate a major gene from an agronomically inferior source (the donor parent) into an elite cultivar or breeding line (the recurrent parent). The desired outcome is a group of plants within a species that are derived from a single plant.

In this procedure, main objective is to harness and incorporate genes from a donor parent (agronomically inferior source) into an elite recurrent parent (otherwise an agronomically superior line having one or two defects). It results into a pool of plants having derived from single plant within the same species.

Steps of Marker-Assisted Backcrossing

In general, MABC Involves Three Steps:

Step 1: Target gene(s) selection (Foreground selection): Foreground selection based upon marker becomes relatively useful, if the gene in question is recessive. Foreground selection becomes useful for the genes sensitive to environment or in case of costly phenotyping, for example, traits for grain quality. Thus, foreground selection based upon markers helps in early selection and rejection of plants with undesirable traits, hence leading to cost reduction caused by raising of entire crop plants.

Step 2: Background selection near the target gene(s) to reduce linkage drag when introgressing wild or exotic germplasm.

Step 3: Background selection throughout the genome. Markers enable the identification of progeny most similar to the recurrent parent. Thus, the use of markers helps accelerate a BC program.

Parameters to be optimized in MABC:

- Optimal distance between target locus and flanking markers for a given population size
- Minimal number of individuals for detecting recombinants in a given marker interval
- Minimal number of data points to achieve fast completion of BC program
- Allocation of marker analyses to different BC generations

Types of Back Cross Breeding

Type 1: Stepwise backcrossing: Recurrent parent (RP1) is crossed with donor parent (DP1) to produce the F1 hybrid and backcrossed up to third backcross generation (BC3) to produce the improved recurrent parent


RP1 X DP1
↓
F1 X RP1
↓
BC1F1 X RP1
↓
BC3F1
↓
IRP1 X DP2
↓
F1 X IRP1
↓
BC1F1 X IRP1
↓
BC3F1
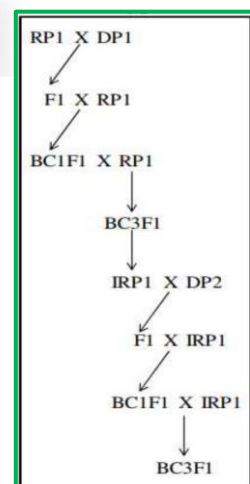
(IRP1). This improved recurrent parent is then crossed with other donor parent (DP2) to pyramid multiple genes.

Type 2: Simultaneous backcrossing : Recurrent parent (RP1) is crossed with donor parents (DP1, DP2, etc.) to get the F1 hybrids which are then undercrossed to produce improved F1. F1 is then backcrossed with the recurrent parent to get the improved recurrent parent.
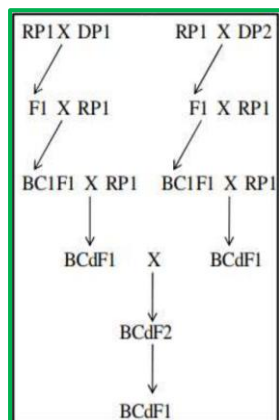
Type 3: Stepwise and parallel backcrossing: Simultaneous crossing of recurrent parent (RP1) with many donor parents and then backcrossing them up to the BC3 generation. Backcross populations with the individual gene are then inter-crossed with each other to get the pyramided lines.
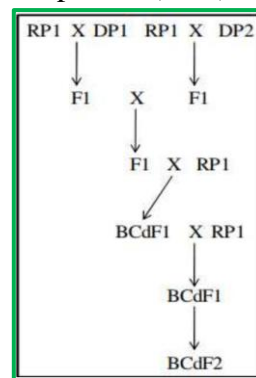
Advantages of marker assisted back cross breeding

Marker-assisted backcrossing (MAB) has several advantages over traditional backcrossing. It allows for selection to be carried out at the seedling stage, which can save time, resources and efforts. It is also simpler than phenotypic screening and can allow for the selection of single desired plants. MAB makes use of molecular markers in the backcrossing process to avoid problems associated with phenotypic selection of traits by selecting genes directly or indirectly. This allows for faster recovery of the recurrent parent genome with MAS compared to conventional backcrossing when foreground and background selection are combined[2].

Applications of marker assisted back cross breeding

Marker-assisted selection (MAS) has emerged as a potential tool to achieve desirable results in plants with the help of molecular markers and improves the traits of interest in a short duration[5]. It refers to indirect selection for a desired plant phenotype based on the banding pattern of linked molecular (DNA) markers. MAS is based on the concept that it is possible to infer the presence of a gene from the presence of a marker which is tightly linked to the gene of interest[1].

Marker-assisted backcross breeding (MABB) is an artistic tool to develop varieties within a short span of time which is nearly impossible to get a plant variety through conventional breeding approach within a short period. Plant varieties which are produced through MABB don't go through any type of regulation like transgenic crops[3].

Examples of traits improved using marker assisted backcrossing

Marker-assisted backcrossing has been used to improve a variety of traits in plants. For example, it has been used to introgress transgenes into an adapted variety or line, such as the introgression of the Bt insect resistance transgene into different maize genetic backgrounds[2]. Another example is the increase of soybean yields by using marker-assisted backcrossing to introgress a yield QTL from a wild accession into commercial genetic backgrounds[2].

Limitations of marker assisted backcrossing

1. The use of molecular markers requires specifi c experimental instruments, such as a PCR machine, gel electrophoresis apparatus, and gel imager for gel-based markers or high-throughput genotyping systems for single nucleotide polymorphism (SNP) markers.
2. Along with the experimental instruments needed for molecular marker work, knowledge of laboratory techniques and data analyses are required. Although acquiring this knowledge is not difficult, MAB is not possible without additional education and training beyond that needed for conventional breeding.

3. Besides cost, major limitations to the development of MAS might include the limited understanding of genetic phenomena such as gene networks, epistasis, and gene-environment interactions (GEI).

References

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