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Insight into the various Mapping Populations in Crop Improvement

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ABSTRACT

A mapping population can be used to map genetic markers through linkage. Thus, the population can be constructed by hybridizing two dissimilar genotypes. It identifies the distance between the two linked genes, which in turn is used to construct a genetic map. Primary mapping populations are constructed by hybridizing two homozygous lines with distinct characters, while the secondary mapping population consists of hybridizing the individuals from a developed mapping population.

INTRODUCTION

In genetics and breeding, mapping populations are used to identify genes and locate genes in chromosomes. In self-pollination crops, F_2 and RILs act as a mapping population, while in the case of self-incompatibility, F_1 acts as a mapping population. Both self-pollination and cross-pollination crops may produce backcross and doubled haploid lines. Following the segregation of DNA region, the polymorphism was detected. By the recombination event, the traits can be fixed and used to construct the genetic map. Large populations are necessary for map-based gene cloning due to their high resolution. In this chapter, we have discussed the various mapping populations viz., F_2, Backcross population, Doubled haploid, Recombinant Inbred Lines (RIL's), Near Isogeneic Lines (NIL's), Chromosome Segment Substitution Lines (CSSL's), Backcross Inbred Lines (BIL's), Advanced Intercross Lines (AIL), Interconnected populations, Multiparent Advanced Generation Intercross Population (MAGIC), and Nested Association Mapping Population.

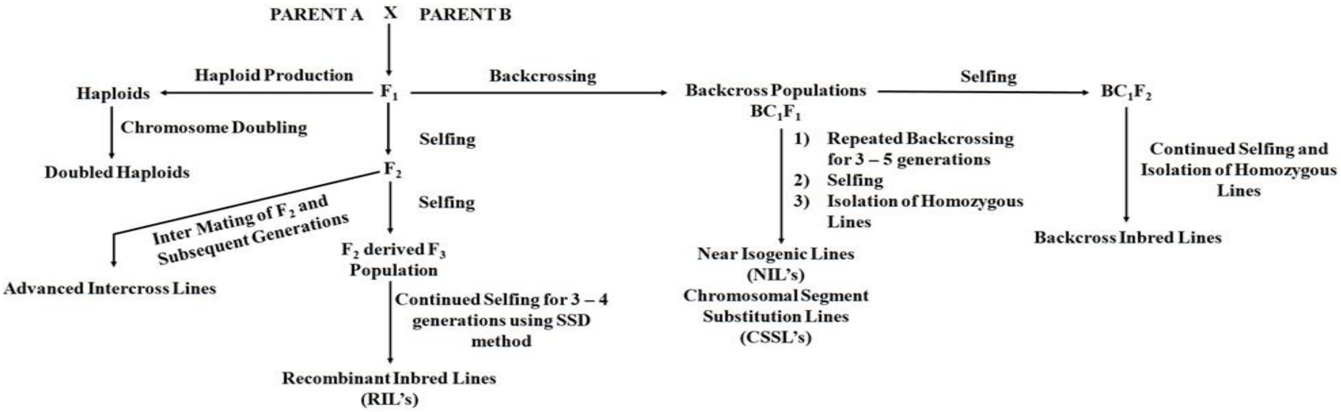

Figure 1. Mapping Population for Crop Improvement

F2 Population

The F_2 populations are obtained by selfing the F_1 which was obtained by crossing two distinct genotypes. Generally, the F_1 will be heterozygous for all the locus and expected to have more segregation in F_2 Thus, the Obtained F_2 will have a wider combination of linkage blocks from both parents. These differences served as a basic material for detecting the linkage between two genes. Since the F_2 plant is obtained from the selfing of F_1 plants, the chance of meiotic cell division would be single, which in turn produces a single round of recombination between any two genes. In the F_2 population, the expected ratio for dominant and codominant markers are 3:1 and 1:2:1 respectively. Hence the F_2 population is amenable for mapping the oligogenes. In addition, the F_2 population provides the estimate of additive, dominance, and epistasis components since it segregates for all the locus. Thus, this population covers the recombination events from both the parents involved in the cross.

Backcross Population

The backcross population is the progeny obtained by crossing the F_1 individual with any one of the parents. Genetic studies can be performed in the backcross, only when a detectable phenotypic change exhibits for the trait of interest in the backcross generations. For which the obtained F_1 are crossed to the recessive parents (Test Cross) and it exhibits 1:1 ratio for monohybrid and 1:1:1:1 for dihybrid. Test cross 1:1 represents the dominant markers on the coupling phase and the codominant marker on either phase. If the dominant marker is in the repulsion phase there is no segregation, the ratio will be 1:0. A Contrasting ratio will be produced when the backcross is made with the dominant parents whose dominant marker present in the coupling phase in relation to the gene of interest.

Doubled Haploids

Doubled haploids are the progeny doubling the chromosomes of the haploid plants derived from the culture of anther or pollens from the F1 individual. Generally, for doubling the ploidy level of chromosome, colchicine is used on the DH lines. Thus, the Doubled haploids are harvested individually and the marker ratio is 1:1 whether the marker is dominant and codominant. The Doubled haploids are evaluated in the replicated trials for both the oligogenic and polygenic traits. Here the genetic components of additive and additive x additive can be estimated since the population is homozygous. Hence the doubled haploid population is not suitable for estimating the heterotic QTLs.

Recombinant Inbred Lines (RIL's)

RIL's, are the homozygous lines constructed by repeated selfing of F_2 individuals. In that Single Seed Descent method (SSD) is preferable and the pedigree method and bulk methods are preferred without selection for the particular traits. The advancement of generations are to be done in the optimal environment so that all the genotypes should have equal survival. From developing the population, the individuals should not be subjected to selection pressure since it leads to fixing the trait in the individual. For tapping the homozygous lines, it requires more than eight round of selfing under Single Seed Descent method. First two diversified parental populations were raised in the crossing block and crosses were made. The F_1's are bulked and space planted in the next generation. From this generation, any random single seed was selected from each plant and bulked to raise the next generation. After eight rounds of selfing, different RILs are obtained and the expected ratio of two homozygotes (Dominant and Recessive) is 1:1. RIL's population is used for constructing the linkage map and to detect the markers linked to genes governing the qualitative traits, *viz.,* race-specific vertical disease resistance and race-specific horizontal resistance.

Near Isogenic Lines (NIL's)

NIL's, are the homozygous lines that are identical in the genetic makeup except for the single locus. Near-isogenic lines are produced by the backcross method of plant breeding. For which, the donor parent (DP) carrying the gene of interest and the recurrent parent (RP) lacking the trait of interest are selected and the crossed were made to synthesis the F_1. The synthesized F_1 carried the gene of interest from the donor parent. Now the F_1's are backcrossed to the recurrent parent where the lacking trait of interest has to be improved. Here the marker expected ratio for the backcross population is 1: 1. Likewise, six to seven backcross generations to be advanced to improve the trait of interest in the recurrent parent from the donor parent (Schneider 2005). Strict foreground selection is to be followed to select the positive plants in the backcross generations since each round of backcrossing reduces the genome of the donor parents by 50%. Finally, the NIL's is the improved version of the recurrent parent. Repeated backcrossing leads to elimination of the genomic region flanking the gene of interest in the donor parents. This NIL's population can be used to construct high resolution mapping population. In addition, this population can be used for functional genomic studies, and gene expression profiling.

Chromosomal Segment Substitution Lines (CSSL)

Chromosomal Segment Substitution Lines is the homozygous lines having the particular chromosome segment from the Donor parent. Chromosomal Segment Substitution Lines are produced by backcrossing the F_1 with the recurrent parent for more than six generation followed by selfing the introgressed lines for two generation to isolate the homozygous derived lines or chromosome substituted version of recurrent parent. Stringent background selection is to be done to select the individuals with the highest recovery percent of Recovery of recurrent parent genome. These chromosomal segments substituted lines are used to map both the qualitative and quantitative traits (Eshed and Zamir 1994). Chromosomal segment substitution lines are evaluated in the replicated trials to select the individual plants with the desired chromosome segment from the donor parents. This population can be used to map and clone the genes for crop improvement.

Backcross Inbred Lines (BILs)

BILs are obtained by backcrossing the F_1 by crossing with the donor parents (Male) and the Recurrent parent (Female) with the recurrent parent followed by continuous selfing for more than six generations to obtain the homozygous lines. The significance of this backcross inbred line is that the frequency of alleles is higher among the contributing parents. Hence, it is advised to backcross with the parents having higher breeding value to synthesize the BC_1F_1 population.

Advanced Intercross Lines (AIL)

Advanced Intercross Lines (AIL) are obtained by sibbing the F_2 population obtained by the desirable cross. Intermating the segregating population allows for to maintenance of the heterozygosity which in turn enhances the recombination event between the QTL's and marker linked. This population allows precise mapping of QTL's. Mapping resolution will be more in the advanced intermating generation. The interval level of the QTL will be five-fold reduced in the Advanced Intercross Lines (AIL) compared to that of the $F_{2.}$

Interconnected Mapping Population

Interconnected mapping populations are developed by crossing the set of homozygous parental lines in such a way that two or more crosses with one parent in common. It may consist of F_2, Backcross populations, RILs, and doubled haploids generated from the individual cross. The biparental mapping population constructs the QTL maps for the concerned cross while the Interconnected Mapping Population provides different allelic combinations of QTL from different cross combinations or from different parental backgrounds. This Interconnected mapping population gives relative QTL from different populations through the Meta-QTL analysis.

Multiparent Advanced Generation Intercross Populations (MAGIC)

Multiparent Advanced Intercross Population is the collection of RILs from the various crosses involving several parents. The parents may be a inbred or clones. This mapping population can be used for association studies. Also serves as the source for the construction of high-density maps. This population can also be used for genomic selection.

Nested Association Mapping Population

A Nested Association Mapping Population is a population constructed crossing a diverse set of parents with one common parent (Yu et al. 2008) to synthesize the diverse set of F_1 followed by selfing using the Single Seed Descent method (SSD). This population can be used for the study of linkage mapping and association mapping. This population enables enables effective utilization of genetic and genomic resources for complex traits.

CONCLUSION

The review focussed on various mapping populations viz., F_2, Backcross population, Doubled haploid, Recombinant Inbred Lines (RIL's), Near Isogeneic Lines (NIL's), Chromosome Segment Substitution Lines (CSSL's), Backcross Inbred Lines (BIL's), Advanced Intercross Lines (AIL), Interconnected populations, Multiparent Advanced Generation Intercross Population (MAGIC), and Nested Association Mapping Population. Here, the mapping population helps to determine the genetic distance between the loci and mapping the specific location on the linkage group. Also, helps to identify the molecular markers linked to the gene of interest which in turn is used to map the QTL associated with the gene of interest. Thus, identifying the QTL's associated with the gene of interest helps to improve the plant idiotype by understanding the complex traits that could be utilized for further crop improvement.

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