DIFFERENT MAPPING POPULATIONS AND ITS UTILITY

[1]Prasenjit, D.,[2]Mallar, N. K., [3]Anirudha, S. K. and [4]Utpal, R.

[1,3] M.Sc.(Agri.), Dept. of Biotechnology, UAS, Dharwad, Karnataka

[2] M. Sc (Agri.), Dept. of Biotechnology, AAU, Jorhat

[4] PhD, Dept. of Genetics and Plant breeding, AAU, Jorhat

Correspondence mail id: prasenjitdebnath2@gmail.com

Mapping population:

Mapping populations are the progenies developed by controlled crossing in between two or more genetically diverse lines, suitable for mapping of genetic markers or to determine the genetic distance between loci/genes. Generally, the parents used for hybridization will be from the same species. But in some cases, related species may be used as one of the parents, in case the variation within the species is limited.

Choice of parents for deriving a mapping population:

Selection of diverse parents is most the important step of mapping population development. The two diverse lines selected as a parents should be completely homozygous in nature in case double haploid line can be used. Parents should be polymorphic for many molecular markers and as well as for the trait under study. It is desirable to choose parents which are adapted to the conditions where its progenies will be phenotyped. It is to be assured that the two parent lines are polymorphic both phenotypically and genotypically. Unadapted and exotic parents may pose difficulties in phenotypic evaluation.

Size of the mapping population:

The size of mapping population depends on type of mapping population, genetic nature of the target traits, objectives of the experiment, resources available for handling a sizable population. Depending on the need, the mapping population may vary from 100 to 3000

individuals. Generally 200 to 300 individuals would be suffice.

Different types of mapping populations

1. F_2 Population: A F_2 mapping population comprises the progeny produced by selfing or sib mating of the F_1 individuals from a cross between the selected parents. F_2 generation is the result of a single meiotic cycle (in F1 plants). In F_2 population the expected ratio for dominant and co dominant markers are 3:1 and 1:2:1. F_2 population are best suited for preliminary mapping of markers and oligogenes.

For mapping of genes F_2 population is not enough since segregation pattern is the most concerned matter regarding to F_2 population because F_2 population is not completely homozygous that's why we always need nearly 100% homozygous population

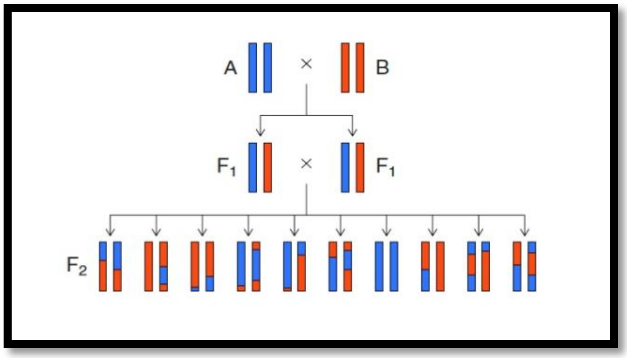

Fig. 1. Schematic representation of F_2 population development

Advantages:

1. Development of F_2 populations requires only two generations, which is minimum for any bi-parental population development.
2. It takes minimum efforts for development.
3. They are ideal for identifying heterosis QTLs.

Disadvantages:

1. Limited use of Fine mapping.
2. F_2 populations are cannot be easily preserved because F_2 plants are frequently immortal.
3. Difficult to map QTLs.

2. F_2 derived F_3 population($F_{2:3}$) :- A F_2 derived F_3 population is obtained by selfing the F_2 individuals for a single generation and harvesting the seeds from each F_2 plants sepeartely so that each F_2 plants can be represented as an individual progeny.

Advantages:

1. Suitable for mapping of oligogenic traits controlled by recessive genes.
2. $F_{2:3}$ family can be used for reconstructing the genotype of respective F_2 plants.

Disadvantage:

1. It is not immortal.

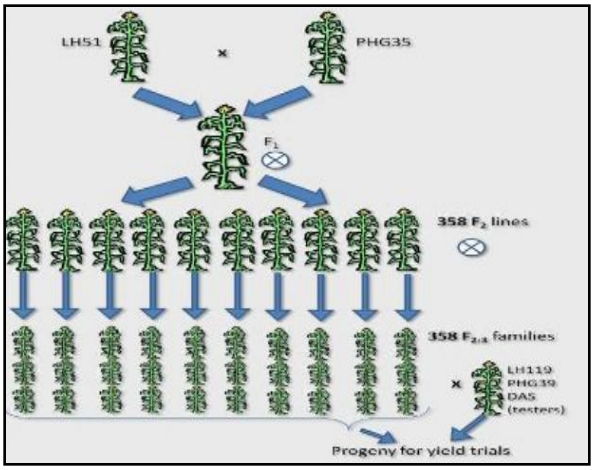

Fig. 2. Schematic representation of $F_{2:3}$ population

3. Double Haploids:-

Doubled haploid lines contain two identical sets of chromosomes in each cell. They are completely homozygous, as only one allele is available for all genes. Double haploids can be produced from haploid lines. Haploid lines either occur spontaneously, as in the case of rape and maize, or are artificially induced. Haploid plants are smaller and less vital than diploids and are nearly sterile. It is possible to induce haploids by culturing immature anthers on special media. Haploid plants can later be regenerated from the haploid cells of the gametophyte. A second option is microspore culture. In cultivated barley it is possible to induce the generation of haploid embryos by using pollen from the wild species Hordeum bulbosum. During the first cell divisions of the embryo, the chromosomes of H. bulbosum are eliminated, leaving the haploid chromosomal set derived from the egg cell. Occasionally in haploid plants the chromosome number doubles spontaneously, leadingto doubled haploid (DH) plants.

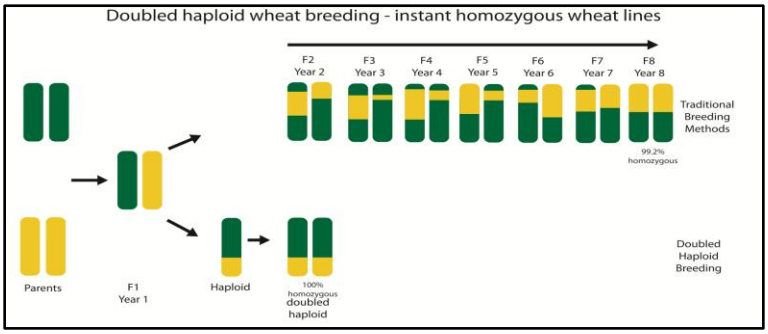

Fig. 3. Schematic representation of DH population development.

Adavantages:

1. Immortal population
2. Used in mapping of both quantitative and qualitative characters
3. The ability to produce homozygous lines after a single round recombination saves a lot of time for the plant breeders.
4. Fast development of large number of homozygous lines, efficient genetic analysis and development of markers for useful traits in much less time.

Disadvantages:

1. DH population is that selection cannot be imposed on the population.
2. In haploids produced from anther culture, it is observed that some plants are aneuploids and some are mixed haploid-diploid types.
3. Double haploidy is the cost involved in establishing tissue culture and growth facilities.
4. The over-usage of doubled haploidy may reduce genetic variation in breeding germplasm. hence one has to take several factors into consideration before deploying doubled haploidy in breeding programmes.
5. Somaclonal variation arises during DH production.

4. Backcross population:-

Backcross population are generated by crossing F_1 plants with either of the two parents of the concerned F_1.

Advantages:

1. The elite combination is not lost.
2. Less time require to develope.
3. Elite genotype of recurrent parent will produce elite genotype at the end of backcrossing programme.
4. Frequently used in resistance breeding.

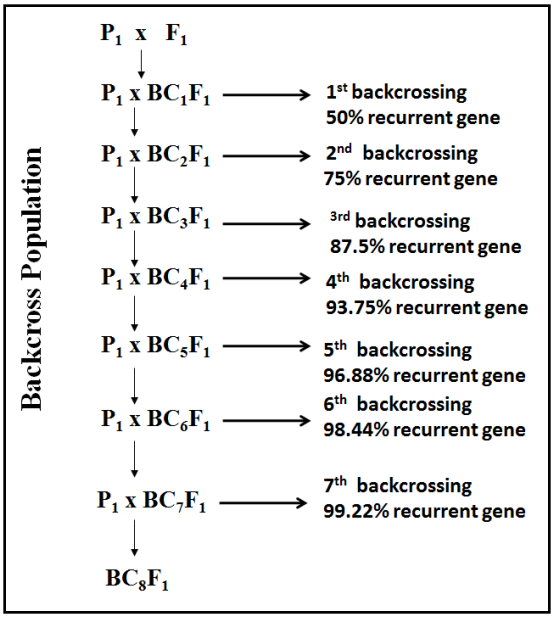

Fig. 4. Schematic representation of Backcross population

Disadvantages:

1. Process is not used to develope quantitative traits.
2. Population is not immortal.
3. It's require many seasons to get new cultivar.
4. More restricted for recessive traits.

5. Backcross inbred Lines (BILS):- These lines are developed by backcrossing the F_1 from a cross between two homozygous lines to one of the parents and continued selfing of the BC_1F_1 progeny to obtain homozygous lines. BILs may be the increased frequency of the alleles contributed by the parent used for backcrossing. Therefore it would be desirable to use the parents with the higher value of target trait for backcrossing with F_1 hybrids.

Advantages:

1. Each line in BIL population is inbred and can be propagated simply by self-pollination.
2. Traits can be measured on a plot basis rather than an individual plant basis. This allows the population to be evaluated in multiple environments over years.
3. BIL populations makes them a good population for mapping quantitative traits using single factor analysis.

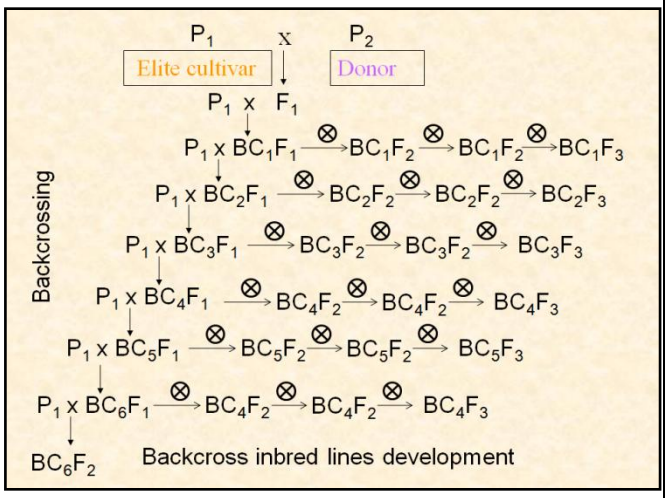

Fig.5. Schematic representation of BILs development

Disadvantages:

1. Developing a BIL population requires much time.
2. It is difficult to study the interaction of multiple, unlinked genes from the donor parent.
3. The structure of a BIL population is not a simple segregating population, the algorithms of the

majority of QTL mapping software are not designed to work with this population type. It is not practical to use interval or composite interval mapping methods on a BIL population.

6. Recombinant inbred lines:

RILs are useful for preliminary mapping of any trait that differs between the parental strains used to generate the population. The great thing about RILs is that the same mapping population can be maintained and used over and over again to map all kinds of different traits. They can also reveal multiple loci contributing to any trait of interest. The downside is that they are less statistically powerful for analyzing effects of any one particular locus, because each RIL also harbors potentially confounding background genetic variation.

Advantage:

1. Used for QTL mapping.
2. Immortal Population.

Disadvantage:

1. Requires many season to develope RILs.
2. Development of RILs is difficult if crop having inbreeding depression.

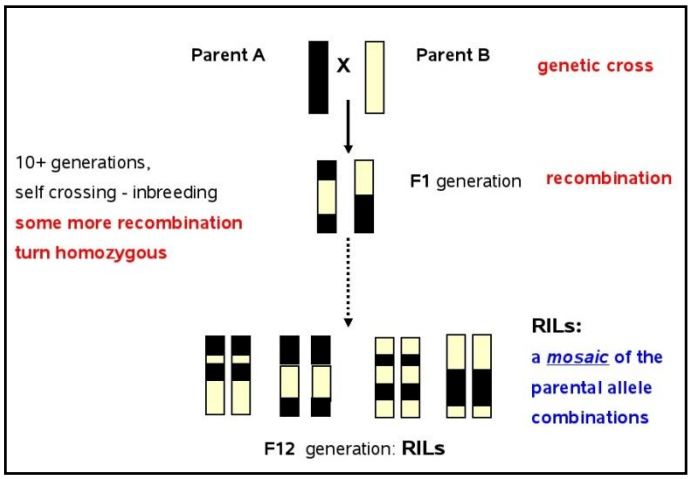

Fig.6. Schematic representation of recombinant inbred lines.

7. Near isogenic lines (NILs):

NILs can be generated through two different breeding procedures. It is developed through repeated selfing and selecting heterozygous individuals until sufficient homozygosity is attained for all traits except for the trait of interest. NILs can also be generated by backcrossing the F_1 plants to the recurrent parents and selecting the trait of interest in each generation. NILs developed through backcrossing are similar to recurrent parent except for the gene of interest, whereas the NILs generated though selfing are produced in pairs of near identical individuals (identical for all traits except for the loci of interest). Like DHs and RILs, NILs are also immortal

mapping population. NILs are quite useful in functional genomics. NILs have disadvantages too. They require many generations for development. These are directly useful only for molecular tagging of the concerned gene but not for linkage mapping. Linkage drag is a potential problem in constructing NILs.

Advantages:

1. NILs are immortal population.
2. These population is used to tagging different traits.
3. It is used to prepare fine mapping and map based cloning of QTLs.
4. It is used for functional genomics work.

Disadvantages:

1. Problem of Linkage drag is present
2. It cannot used to prepare linkage mapping
3. Increase cost, time and efforts.

8. Interconnected mapping population: These population is produced in such a way crossing a set of homozygous parental lines that two or more crosses having one parents common. Inter connected population is first used by Gilbert to partition single gene effects from the over all effect of polygenes estimated from diallel crosses.

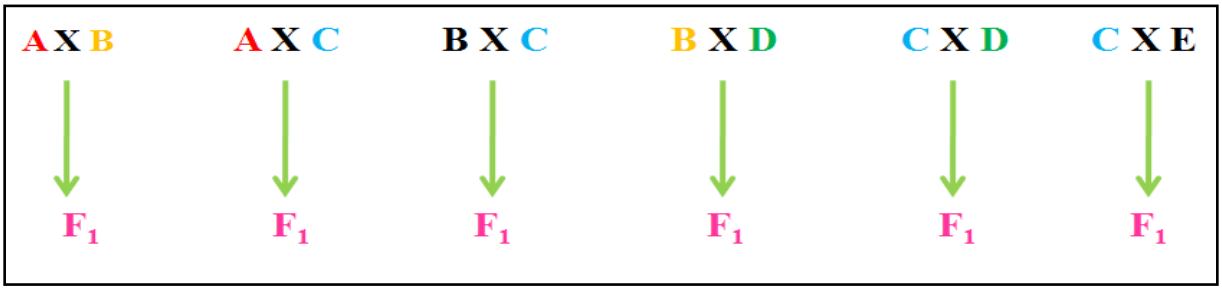

Fig.7. Schematic representation of an interconnected population.

An interconnected population may consist of F_2, backcross, RIL, or DH populations generated from each of the crosses produced as per the mating design used.

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