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Bi-parental mapping populations

a tool for QTL mapping in crops

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The population used for identification of genomic region controlling phenotypic traits is known as mapping population. Mapping populations developed by crossing of two genetically diverse parents are known as bi-parental mapping populations. The parents used for crossing may be from same species or related species. However, consideration of highly diverse parents having varied phenotypic and genotypic characters for the target trait of interest is pertinent to develop a suitable mapping population. Hence, it is important to perform the polymorphism survey for sufficient variation between the two parents before crossing both at the phenotypic and genotypic levels. The variation at genotypic level i.e, at DNA level is essential to find the recombination events. The more variation exists at DNA level, the easier it is to find polymorphic informative markers. If the parents are diverse at phenotypic level for a trait, there is a reasonable chance that genetic variation exists between the parents. However, sometimes environmental effects might affect the phenotypic variation, which may have no genetic basis for the effects. Similarly, the lack of phenotypic variation between the selected parents may not necessarily mean that there is no genetic variation for the trait, as different sets of genes could result in same phenotype (Mackay, 2001; Ribaut and Hoisington, 1998). There are several types of bi-parental mapping population may be produced from a cross between two parental lines for the target trait which can be used for QTL mapping. The following are different types of mapping populations:

1. **F_2 Population:** An F_2 mapping population is the population produced by selfing or intermating of the F_1 individuals from a cross between the selected parents and the product of single meiotic cycle is F_2 individuals. In an F_2 population, the ratios expected for dominant marker is 3:1 and for codominant marker 1:2:1. F_2 populations are relatively easy to produce with minimum efforts and considered as best population for preliminary mapping. Therefore, the target traits are scored on single plants. These populations cannot be used for fine mapping and have limited use in QTLs mapping. Each individual is genetically different in F_2 populations and cannot be evaluated in replicated trial over locations and years.

Hence, precise determination of genotype x environment interaction and its effect on the expression of quantitative traits become ineffective. Which so over, QTL x QTL interaction cannot be detected. Even though, QTLs having additive effects can be detected, it becomes unattainable either to develop exact replica or to enhance amount of seeds.

2. **F_2-Derived F_3 Population ($F_{2:3}$):** $F_{2:3}$ population is obtained by selfing the F_2 individuals for a single generation. The seeds from each F_2 plant harvested separately and each F_2 plant is represented as an individual plant progeny. For genotyping, DNA is obtained from individual F_2 plants or it can be from a bulk of at least 20 plants of each F_3 family and this bulked DNA may represent the genotype of the parental F_2 plant (Yu et al. 1997). Similarly with that of F_2 population F_2-derived F_3 population is immortal and it has more suitability for mapping quantitative traits and recessive genes.
3. **Backcross Population:** Backcross population are the population that developed from of crossing of F1 plants with any one of the two parents used for the initial cross. Generally, for genetic analysis, backcross with recessive parent is used which is known as testcross. It also requires less time to develop and recombination information is based on only one parent. Backcross populations can be utilized for marker-assisted backcrossing breeding to introgress the target traits. However, backcross populations are not perpetual as that of F_2 populations which evaluation cannot be done in replicated trials and so this is unsuitable for QTL mapping rather it is used for oligogene mapping. This method generally do not detected negative alleles from the recurrent parent and therefore QTL x QTL interaction cannot be estimated.
4. **Doubled Haploids (DHs):** Doubled haploid (DH) plants are developed by chromosome doubling of haploid plants obtained by another culture or pollen culture from F_1 plants. DH populations are permanent mapping population so it can be evaluated in replicated trials over location and years and multiplied without any genotypic change. They are suitable for mapping both quantitative and qualitative traits. Homozygous lines are produced in short period of time, thus save time. DHs are comparable to F_2 as both are products of one meiotic cycle. In a DH population, the expected ratio for dominant or codominant markers is 1:1. Its development involves tissue culture techniques so technical skill is required to compare with other mapping populations and so the same is not preferable population-for mapping heterosis QTLs.
5. **Recombinant Inbred Lines (RILs):** Recombinant Inbred Lines (RILs) are produced by continuous selfing or sib mating of individual F_2 plants until complete homozygosity is achieved by following single seed descent (SSD) method. In SSD method, one seed is harvested from each plant of the F_2 and in later generations seeds from all the plants are bulked. These bulked seeds are used to raise the next generation populations and the method is being followed for upto five or more generations to maintain the homozygosity. At the end, seeds from each plant are harvested separately to obtain as many RILs as the lines fixed for many recombination events. The genetic segregation ratio for both dominant and co-dominant markers is 1:1. RILs are immortal populations so it can be evaluated in replicated trials over location and years and multiplied without any further segregation since achieved homozygosity. RILs have been widely used for the mapping of QTLs. RILs are obtained after several cycles of meiosis, therefore very useful for identification of tightly linked markers. However, it requires many seasons or generation to develop and developing RILs in crops with high inbreeding depression is difficult.

6. **Immortalized F_2 Population:** Immortalized F_2 populations are produced by intercrossing a set of RILs. It is an immortal population so it can be evaluated in replicated trials over location and years. It can be used for heterotic QTL detection. It requires making of a large number of crosses for development.
7. **Near-Isogenic Lines (NILs):** Near-Isogenic Lines (NILs) are developed by either repeated selfing or backcrossing the F_1 plants to the recurrent parents. NILs are similar to recurrent parent except for the gene of interest when developed through backcrossing. However, NILs developed through selfing are similar in pair except for the gene of interest but differ a lot from recurrent parent. The genetic segregation ratio for both dominant and co-dominant markers is 1:1. Like DHs and RILs, NILs are immortal populations. They are useful for positional cloning. It requires many generations to develop and linkage drag problem is associated with NILs.
8. **Chromosomal Segment Substitution Lines (CSSLs):** They are a homozygous line having a distinct chromosome segment from a donor parent in the chromosome background of recurrent parent. It is useful for mapping of oligogenes as well as QTLs. Linkage drag is a major problem in CSSLs as undesirable traits might have linked to the target gene.
9. **Backcross Inbred Lines (BILs):** Backcross inbred lines (BILs) are obtained by backcrossing the F_1 from a cross between one of the two parents used in the initial cross and then continue selfing of the BC_1F_1 progeny to obtain homozygous lines.
10. **Advanced Intercross Lines (AILs):** Advanced intercross line (AIL) population is produced by intermating the individuals of F_2 and subsequent generations from a suitable cross. In the segregating generations intermating is done often to maintain heterozygosity that will further promote recombination between QTLs and the markers linked to them in every generation. This process furthermore guided to more specified region of the QTLs identifications.

Bi-parental mapping populations are simple to develop and therefore most widely used for identifying regions of genome controlling phenotypic variation. For QTL mapping, it is essential to develop a suitable experimental bi-parental mapping population using parental lines that are phenotypically diverse for the target trait as well as genetically diverse. The choice of a bi-parental mapping population depends upon the objectives of the experiment, the timeline as well as availability of markers for carrying QTL analysis. The development of bi-parental mapping populations requires time and effort. However, this may not be feasible for some species like tree species also each population type has their own advantages and disadvantages.

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