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Principles and Requirements of Genetic Mapping in Plants

Jyoti Prakash Sahoo
Article ID: 7
Department of Agricultural Biotechnology, College of Agriculture, OUAT, Bhubaneswar – 751003,
Corresponding Author: jyotiprakashsahoo2010@gmail.com

Introduction

Genetic mapping refers to the determination of the relative positions of genes on a DNA molecule (chromosome or plasmid) and of their distance between them. Genetic map indicates the position and relative genetic distances between markers along chromosomes. The first genetic map was published in 191 by T. H. Morgan and his student, Alfred Sturtevant, who showed the locations of 6 sex linked genes on a fruit fly chromosome. Genetic mapping is based on the principle that genes (markers or loci) segregate via chromosome recombination during meiosis (i.e. sexual reproduction), thus allowing their analysis in the progeny (Paterson, 1996). When two genes are close together on the same chromosome, they do not assort independently and are said to be linked. Genes that are closer together or tightly-linked will be transmitted together from parent to progeny more frequently than those genes located far apart. Such process or set of processes is called recombination by which DNA molecules interact with one another to bring a rearrangement of the genetic information in an organism.

Requirements for Genetic Mapping

1. Develop appropriate mapping population and decide the sample size
2. Decide the type of molecular marker(s) for genotyping the mapping population
3. Screen parents for marker polymorphism and then genotype the mapping population
4. Perform linkage analyses using statistical programs

Mapping population

The first step in producing a mapping population is selecting two genetically divergent parents, which show clear genetic differences for one or more traits of interest (e.g., the recipient or recurrent parent can be a highly productive and commercially successful cultivar but lacks disease resistance, which is present in another donor parent).

Selection of molecular markers for mapping

Restriction fragment length polymorphisms (RFLPs), microsatellites or simple sequence repeats (SSRs), expressed sequence tags (ESTs), cleaved amplified polymorphic sequence (CAPS), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), inter simple sequence repeat (ISSR), diversity arrays technology (DArT), and single nucleotide polymorphism (SNP) have been used for map construction in several plants.

Polymorphism screening and genotyping of the mapping population

The third step in the construction of a linkage map is to identify sufficient number of markers that reveal differences between parents (i.e., polymorphic markers). In general, cross pollinating species possess higher levels of polymorphism compared to inbreeding species. Once sufficient numbers of polymorphic markers have been identified between parents, they must be used to genotype the entire mapping population.

Linkage analyses and map construction

Several computer packages are presently available for genetic linkage mapping but the most widely used are JoinMap, MAPMAKER/EXP, GMENDEL, LINKAGE and Map Manager QTX.

Test for segregation distortion

For each segregating marker, a chi-square analysis needs to be performed to test for deviation from the expected segregation ratio for the mapping population (1:1 for both dominant and codominant markers in BC, RIL, DH and NIL; 1:2:1 for codominant markers in F2; 3:1 for dominant markers in F2). Segregation distortion can occur due to statistical bias, genotyping and scoring errors and biological reasons like chromosome loss, competition among gametes for preferential fertilization, incompatibility genes, chromosome arrangements or non-homologous pairing.

Establishing linkage groups

Markers are assigned to linkage groups using the odds ratios, which refers to the ratio of the probability that two loci are linked with a given recombination value over a probability that the two are not linked. This ratio is called a logarithm of odds (LOD) value or LOD score. The critical LOD scores used to establish linkage groups and calculate map distances are called 'linklod' and 'maplod', respectively. Marker pairs with a recombination LOD score above a critical 'linklod' are considered to be linked whereas those with a LOD score less than 'linklod' are considered unlinked.

Determining map distance and locus order

For calculating map distances and determining locus order, several parameters, including a recombination threshold value, minimum 'maplod', jump threshold value, and mapping function (m.f.) is needed. Only information for marker pairs with a LOD score above 'maplod' is used in the calculation of map distances and its values can be as low as 0.01 to as high as 3.0. If the value of 'maplod' equal to 0.01, the program uses even very weak linkage information. At each step, a marker is added to the map on the basis of its total linkage information with the markers that were placed earlier on the map. When map distances are small (<10 cM), the map distance equals the recombination frequency. The researcher must select one of the two genetic mapping functions (Haldane or Kosambi), which translates recombination frequencies into map distances and vice versa. Haldane's mapping function assumes absence of interference between crossovers in meiosis, whereas Kosambi's mapping function assumes a certain degree of interference. Such mapping functions convert recombination fractions into map units called centimorgans (cM). By definition, one map unit (m.u.) is equal to one percent recombinant phenotypes or 1 cM.

Reference

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